

12-22-99

PATENT

Attorney Docket No. GENSET.025CP1

Date: December 21, 1999

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ASSISTANT COMMISSIONER FOR PATENTS

WASHINGTON, D.C. 20231

ATTENTION: BOX PATENT APPLICATION

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): **Jean-Baptiste Dumas Milne Edwards, Aymeric Duclert, and Jean-Yves Giordano**

For: EXPRESSED SEQUENCE TAGS AND ENCODED HUMAN PROTEINS

Enclosed are:

- (X) Ten (10) sheets of drawings.
- (X) Sequence Submission Statement and Sequence Listing in 785 pages, along with a computer readable CD-Rom.
- (X) This application is a continuation-in-part of prior applications:
- PCT Patent Application Serial No. PCT/IB99/00712 filed April 9, 1999, which is a continuation-in-part of both United States Patent Application Serial No. 09/057,719 filed April 9, 1998 and Application Serial No. 09/069,047 filed April 28, 1998.
- (X) Return prepaid postcard.

CLAIMS AS FILED

FOR	NUMBER FILED	NUMBER EXTRA	RATE	FEE
Basic Fee			\$760	\$760
Total Claims	21 - 20 =	1 ×	\$18	\$ 18
Independent Claims	14 - 3 =	11 ×	\$78	\$858
If application contains any multiple dependent claims(s), then add			\$260	\$0
TOTAL FILING FEE		\$1,636		

- (X) A check in the amount of \$1,636 to cover the filing fee is enclosed.
- (X) The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Account No. 11-1410. A duplicate copy of this sheet is enclosed.

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(X) Please use Customer No. 20,995 for the correspondence address.



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Attorney Docket No. : GENSET.025CP1

Applicants : Jean-Baptist Dumas Milne Edwards, et al.

For : EXPRESSED SEQUENCE TAGS AND
ENCODED HUMAN PROTEINS

Attorney : Daniel Hart

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Date of Deposit : December 21, 1999



I hereby certify that the accompanying

Transmittal in Duplicate; Specification in ¹⁷⁶~~174~~ pages; 10 sheets of drawings;
Sequence Submission Statement and Sequence Listing in 785 pages, along with a
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EXPRESSED SEQUENCE TAGS AND ENCODED HUMAN PROTEINSRelated Applications

5 The present application is a continuation-in-part of PCT application PCT/IB99/00712 filed April, 9, 1999 which is a continuation-in-part of both United States Patent Application Serial No. 09/057,719 filed April 9, 1998 and United States Application Serial No. 09/069,047 filed April, 28, 1998, all the disclosures of which are hereby incorporated herein by reference in their entirety, including any figures, tables or drawings.

Background of the Invention

10 The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of specifically hybridizing to loci distributed throughout the human
15 genome find applications in the construction of high resolution chromosome maps and in the identification of individuals.

 In the past, the characterization of even a single human gene was a painstaking process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer technology have merged to greatly accelerate the rate at which human genes can be
20 isolated, sequenced, mapped, and characterized.

 Currently, two different approaches are being pursued for identifying and characterizing the genes distributed along the human genome. In one approach, large fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bioinformatics software. However, this approach entails
25 sequencing large stretches of human DNA which do not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In addition to requiring extensive sequencing, the bioinformatics software may mischaracterize the genomic sequences obtained, *i.e.*, labeling non-coding DNA as coding DNA and vice versa.

 An alternative approach takes a more direct route to identifying and characterizing human
30 genes. In this approach, complementary DNAs (cDNAs) are synthesized from isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended cDNAs which include sequences
35 adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST

which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters. Alternatively, ESTs having partially overlapping sequences may be identified and contigs comprising the consensus sequences of the overlapping ESTs may be identified.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs, are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs (Adams *et al.*, *Nature* **377**:3-174, 1996, Hillier *et al.*, *Genome Res.* **6**:807-828, 1996), the entire disclosures of which are incorporated herein by reference.

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region (5'UTR) of the mRNA from which the cDNA is derived. Indeed, 5'UTRs have been shown to affect either the stability or translation of mRNAs. Thus, regulation of gene expression may be achieved through the use of alternative 5'UTRs as shown, for instance, for the translation of the tissue inhibitor of metalloprotease mRNA in mitogenically activated cells (Waterhouse *et al.*, *J Biol Chem.* **265**:5585-9, 1990), the entire disclosure of which is incorporated herein by reference. Furthermore, modification of 5'UTR through mutation, insertion or translocation events may even be implied in pathogenesis. For instance, the fragile X syndrome, the most common cause of inherited mental retardation, is partly due to an insertion of multiple CGG trinucleotides in the 5'UTR of the fragile X mRNA resulting in the inhibition of protein synthesis via ribosome stalling (Feng *et al.*, *Science* **268**:731-4, 1995), the entire disclosure of which is incorporated herein by reference. An aberrant mutation in regions of the 5'UTR known to inhibit translation of the proto-oncogene *c-myc* was shown to result in upregulation of *c-myc* protein levels in cells derived from patients with multiple myelomas (Willis *et al.*, *Curr Top Microbiol Immunol* **224**:269-76, 1997), the entire disclosure of which is incorporated herein by reference. In addition, the use of oligo-dT primed cDNA libraries does not allow the isolation of complete 5'UTRs since such incomplete sequences obtained by this process may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5' ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. In some instances, the sequences used in such therapeutic or diagnostic techniques may be sequences which encode proteins which are secreted from the cell in which they are synthesized. Those sequences encoding secreted proteins as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells. In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon- α , interferon- β , interferon- γ , and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy-induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. These signal peptides can be used to direct the extracellular secretion of any protein to which they are operably linked. In addition, portions of the signal peptides called membrane-translocating sequences, may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cells in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Sequences coding for non-secreted proteins may also find application as therapeutics or diagnostics. In particular, such sequences may be used to determine whether an individual is likely to express a detectable phenotype, such as a disease, as a consequence of a mutation in the coding sequence of a protein. In instances where the individual is at risk of suffering from a disease or other undesirable phenotype as a result of a mutation in such a coding sequence, the undesirable phenotype may be corrected by introducing a normal coding sequence using gene therapy.

Alternatively, if the undesirable phenotype results from overexpression of the protein encoded by the coding sequence, expression of the protein may be reduced using antisense or triple helix based strategies.

The secreted or non-secreted human polypeptides encoded by the coding sequences may also be used as therapeutics by administering them directly to an individual having a condition, such as a disease, resulting from a mutation in the sequence encoding the polypeptide. In such an instance, the condition can be cured or ameliorated by administering the polypeptide to the individual.

In addition, the secreted or non-secreted human polypeptides or portions thereof may be used to generate antibodies useful in determining the tissue type or species of origin of a biological sample. The antibodies may also be used to determine the cellular localization of the secreted or non-secreted human polypeptides or the cellular localization of polypeptides which have been fused to the human polypeptides. In addition, the antibodies may also be used in immunoaffinity chromatography techniques to isolate, purify, or enrich the human polypeptide or a target polypeptide which has been fused to the human polypeptide.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross *et al.*, *Nature Genetics* 6: 236-244, 1994), the entire disclosure of which is incorporated herein by reference. The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al.*, *Genome Res.* 6:327-335, 1996), the entire disclosure of which is incorporated herein by reference. Both of these approaches have their limits due to a lack of specificity and of comprehensiveness. Thus, there exists a need to identify and systematically characterize the 5' portions of the genes.

The present 5' ESTs may be used to efficiently identify and isolate 5'UTRs and upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding sequences of genes.

5

Summary of the Invention

The present invention relates to purified, isolated, or enriched 5' ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. These sequences will be referred to hereinafter as "5' ESTs." The present invention also includes purified, isolated or enriched nucleic acids comprising contigs assembled by determining a consensus sequences from a plurality of ESTs containing overlapping sequences. These contigs will be referred to herein as "consensus contigated 5'ESTs."

As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4 - 10^6 fold purification of the native message. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5' EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5' ESTs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the

population of recombinant backbone molecules. More preferably, the enriched 5' ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5' ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

5 “Stringent,” “moderate,” and “low” hybridization conditions are as defined below.

 The term “polypeptide” refers to a polymer of amino acids without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl
10 groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as
15 other modifications known in the art, both naturally occurring and non-naturally occurring.

 As used interchangeably herein, the terms “nucleic acids,” “oligonucleotides,” and “polynucleotides” include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The term “nucleotide” as used herein as an adjective to describe molecules comprising RNA, DNA, or RNA/DNA hybrid sequences of any
20 length in single-stranded or duplex form. The term “nucleotide” is also used herein as a noun to refer to individual nucleotides or varieties of nucleotides, meaning a molecule, or individual unit in a larger nucleic acid molecule, comprising a purine or pyrimidine, a ribose or deoxyribose sugar moiety, and a phosphate group, or phosphodiester linkage in the case of nucleotides within an oligonucleotide or polynucleotide. Although the term “nucleotide” is also
25 used herein to encompass “modified nucleotides” which comprise at least one modifications (a) an alternative linking group, (b) an analogous form of purine, (c) an analogous form of pyrimidine, or (d) an analogous sugar, for examples of analogous linking groups, purine, pyrimidines, and sugars see for example PCT publication No. WO 95/04064. The polynucleotide sequences of the invention may be prepared by any known method, including
30 synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art.

 The terms “base paired” and “Watson & Crick base paired” are used interchangeably herein to refer to nucleotides which can be hydrogen bonded to one another by virtue of their sequence identities in a manner like that found in double-helical DNA with thymine or uracil

residues linked to adenine residues by two hydrogen bonds and cytosine and guanine residues linked by three hydrogen bonds (See Stryer, L., *Biochemistry*, 4th edition, 1995).

The terms “complementary” or “complement thereof” are used herein to refer to the sequences of polynucleotides which are capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. For the purpose of the present invention, a first polynucleotide is deemed to be complementary to a second polynucleotide when each base in the first polynucleotide is paired with its complementary base. Complementary bases are, generally, A and T (or A and U), or C and G. “Complement” is used herein as a synonym from “complementary polynucleotide,” “complementary nucleic acid” and “complementary nucleotide sequence” . These terms are applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind. Preferably, a “complementary” sequence is a sequence which an A at each position where there is a T on the opposite strand, a T at each position where there is an A on the opposite strand, a G at each position where there is a C on the opposite strand and a C at each position where there is a G on the opposite strand.

Thus, 5' ESTs in cDNA libraries in which one or more 5' ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are “enriched recombinant 5' ESTs” as defined herein. Likewise, 5' ESTs in a population of plasmids in which one or more 5' ESTs of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are “enriched recombinant 5' ESTs” as defined herein. However, 5' ESTs in cDNA libraries in which 5' ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in which backbone molecules having a 5' EST insert are extremely rare, are not “enriched recombinant 5' ESTs.”

The term “capable of hybridizing to the polyA tail of said mRNA” refers to and embraces all primers containing stretches of thymidine residues, so-called oligo(dT) primers, that hybridize to the 3' end of eukaryotic poly(A)+ mRNAs to prime the synthesis of a first cDNA strand. Techniques for generating said oligo(dT) primers and hybridizing them to mRNA to subsequently prime the reverse transcription of said hybridized mRNA to generate a first cDNA strand are well known to those skilled in the art and are described in *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989, the entire disclosures of which are incorporated herein by reference. Preferably, said oligo(dT) primers are present in a large excess in order to allow the hybridization of all mRNA 3'ends to at least one oligo(dT) molecule. The

priming and reverse transcription step are preferably performed between 37°C and 55°C depending on the type of reverse transcriptase used.

Preferred oligo(dT) primers for priming reverse transcription of mRNAs are oligonucleotides containing a stretch of thymidine residues of sufficient length to hybridize specifically to the polyA tail of mRNAs, preferably of 12 to 18 thymidine residues in length. More preferably, such oligo(T) primers comprise an additional sequence upstream of the poly(dT) stretch in order to allow the addition of a given sequence to the 5' end of all first cDNA strands which may then be used to facilitate subsequent manipulation of the cDNA. Preferably, this added sequence is 8 to 60 residues in length. For instance, the addition of a restriction site in 5' of cDNAs facilitates subcloning of the obtained cDNA. Alternatively, such an added 5' end may also be used to design primers of PCR to specifically amplify cDNA clones of interest.

In some embodiments, the present invention relates to 5' ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Such 5' ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5' ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5' ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5' ends of the coding sequences of the mRNAs from which the 5' ESTs are derived. These cDNAs will be referred to hereinafter as "full-length cDNAs." These cDNAs may comprise

a 3' untranslated region and eventually a polyadenylation tail. These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full-length cDNA sequences may be used to express the proteins corresponding to the 5' ESTs. As discussed above, secreted proteins and non-secreted proteins may be therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating and controlling a variety of human conditions. The 5' ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5' EST was derived.

Alternatively, the 5' ESTs may be used to obtain and express extended cDNAs encoding portions of the protein. In the case of secreted proteins, the portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off.

The present invention includes isolated, purified, or enriched "EST-related nucleic acids." The terms "isolated," "purified" or "enriched" have the meanings provided above. As used herein, the term "EST-related nucleic acids" means the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622, extended cDNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622, full-length cDNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622 or genomic DNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622. The present invention also includes the sequences complementary to the EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched "fragments of EST-related nucleic acids." The terms "isolated," "purified" and "enriched" have the meanings described above. As used herein the term "fragments of EST-related nucleic acids" means fragments comprising at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive nucleotides of the EST-related nucleic acids to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related nucleic acids being referenced. In particular, fragments of EST-related nucleic acids refer to "polynucleotides described in Table II," "polynucleotides described in Table III," and "polynucleotides described in Table IV." The present invention also includes the sequences complementary to the fragments of the EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched "positional segments of EST-related nucleic acids." As used herein, the term "positional segments of EST-related nucleic acids" includes segments comprising nucleotides 1-25, 26-50, 51-75, 76-100, 101-125, 126-150, 151-175, 176-200, 201-225, 226-250, 251-300, 301-325, 326-350, 351-375, 376-400, 401-425, 426-450, 451-475, 476-500, 501-525, 526-550, 551-575, 576-600 and 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the

lengths of the particular EST-related nucleic acids being referenced. The term “positional segments of EST-related nucleic acids” also includes segments comprising nucleotides 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 450-500, 501-550, 551-600 or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. The term “positional segments of EST-related nucleic acids” also includes segments comprising nucleotides 1-100, 101-200, 201-300, 301-400, 501-500, 500-600, or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. In addition, the term “positional segments of EST-related nucleic acids” includes segments comprising nucleotides 1-200, 201-400, 400-600, or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. The present invention also includes the sequences complementary to the positional segments of EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched “fragments of positional segments of EST-related nucleic acids.” As used herein, the term “fragments of positional segments of EST-related nucleic acids” refers to fragments comprising at least 10, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 150, or 200 consecutive nucleotides of the positional segments of EST-related nucleic acids. The present invention also includes the sequences complementary to the fragments of positional segments of EST-related nucleic acids.

The present invention also includes isolated or purified “EST-related polypeptides.” As used herein, the term “EST-related polypeptides” means the polypeptides encoded by the EST-related nucleic acids, including the polypeptides of SEQ ID NOs. 812-1599.

The present invention also includes isolated or purified “fragments of EST-related polypeptides.” As used herein, the term “fragments of EST-related polypeptides” means fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of an EST-related polypeptide to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related polypeptides being referenced. In particular, fragments of EST-related polypeptides refer to polypeptides encoded by “polynucleotides described in Table II,” “polynucleotides described in Table III,” and “polynucleotides described in Table IV.”

The present invention also includes isolated or purified “positional segments of EST-related polypeptides.” As used herein, the term “positional segments of EST-related polypeptides” includes polypeptides comprising amino acid residues 1-25, 26-50, 51-75, 76-100, 101-125, 126-150, 151-175, 176-200, or 201-the C-terminal amino acid of the EST-related polypeptides to the extent that such amino acid residues are consistent with the lengths of the particular EST-related

polypeptides being referenced. The term “positional segments of EST-related polypeptides also includes segments comprising amino acid residues 1-50, 51-100, 101-150, 151-200 or 201-the C-terminal amino acid of the EST-related polypeptides to the extent that such amino acid residues are consistent with the lengths of the particular EST-related polypeptides being referenced. The term

5 “positional segments of EST-related polypeptides” also includes segments comprising amino acids 1-100 or 101-200 of the EST-related polypeptides to the extent that such amino acid residues are consistent with the lengths of particular EST-related polypeptides being referenced. In addition, the term “positional segments of EST-related polypeptides” includes segments comprising amino acid residues 1-200 or 201-the C-terminal amino acid of the EST-related polypeptides to the extent

10 that amino acid residues are consistent with the lengths of the particular EST-related polypeptides being referenced.

The present invention also includes isolated or purified “fragments of positional segments of EST-related polypeptides.” As used herein, the term “fragments of positional segments of EST-related polypeptides” means fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100,

15 or 150 consecutive amino acids of positional segments of EST-related polypeptides to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related polypeptides being referenced.

The present invention also includes antibodies which specifically recognize the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In the case of secreted proteins, such as those of SEQ ID NOs. 1554-1580 antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides of SEQ ID

20 NOs. 812-1516 or 1554-1580 may also be obtained.

In some embodiments and in the case of secreted proteins, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids include a signal sequence. In other embodiments, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may

25 include the full coding sequence for the protein or, in the case of secreted proteins, the full coding sequence of the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may include regulatory regions upstream of the translation start site or downstream of the stop codon

30 which control the amount, location, or developmental stage of gene expression.

35

As discussed above, both secreted and non-secreted human proteins may be therapeutically important. Thus, the proteins expressed from the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may be useful in treating or controlling a variety of human conditions.

5 The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. In addition, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related
10 nucleic acids, or fragments of positional segments of nucleic acids are useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body.
15 Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of
20 nucleic acids, such as promoters or upstream regulatory sequences.

The present invention also comprises fusion vectors for making chimeric polypeptides comprising a first polypeptide and a second polypeptide. Such vectors are useful for determining the cellular localization of the chimeric polypeptides or for isolating, purifying or enriching the chimeric polypeptides.

25 The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may also be used for gene therapy to control or treat genetic diseases. In the case of secreted proteins, signal peptides may be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the sequence of
30 the non-aligned 5'ESTs, also referred to as singletons, and sequences of the 5'ESTs which were aligned to yield consensus contigated 5' ESTs are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under internal designations. The non-aligned 5'ESTs are those which comprise a single EST from a single tissue in the listing of Table V. The inserts may be recovered from the stored materials by growing the appropriate clones on a suitable medium. The Bluescript
35 DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art

such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be performed with primers designed at both ends of the inserted EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids. The PCR product which corresponds to the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive nucleotides, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

A further embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 24-811.

Yet another embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of the full coding sequences of a sequence selected from the group consisting of SEQ ID NOs. 766-792 wherein the full coding sequence comprises the sequence encoding the signal peptide and the sequence encoding the mature protein.

Still another embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of a contiguous span of a sequence selected from the group consisting of SEQ ID NOs. 766-792 which encodes the mature protein.

Another embodiment of the present invention is a purified nucleic acid comprising, consisting essentially of, or consisting of a contiguous span of a sequence selected from the group consisting of SEQ ID NOs. 24-728 and 766-792 which encodes the signal peptide.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

5 Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of the sequences of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising, consisting essentially of, or consisting of a mature protein included in a sequence selected from the group consisting of the sequences of SEQ ID NOs. 1554-1580.

10 Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising, consisting essentially of, or consisting of a signal peptide included in a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1516 and 1554-1580.

15 Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide, wherein said nucleic acid comprises, consists essentially of, or consists of

- a) a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622; and
- b) a polyadenylation tail.

20 Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide wherein said nucleic acid comprises, consists essentially of, or consists of

- a) a sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs. 812-1599; and
- b) a polyadenylation tail.

25 Another embodiment of the present invention is a purified nucleic acid at least 20, 25, 30, 35, 40, 50, 75, 100, 200, 300, 500 or 1000 nucleotides in length which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

30 Another embodiment of the present invention is a purified or isolated polypeptide comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a purified or isolated polypeptide comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising, consisting essentially of, or consisting of a mature protein of a polypeptide selected from the group consisting of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising, consisting essentially of, or consisting of a signal peptide of a sequence selected from the group consisting of the polypeptides of SEQ ID NOs. 812-1516 and 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising, consisting essentially of, or consisting of at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, hybridizing said primer to an mRNA in said collection that encodes said protein reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA, making a second cDNA strand complementary to said first cDNA strand and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

In one aspect of this embodiment, the cDNA encodes at least a portion of a human polypeptide. Preferably, said human polypeptide comprises at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. More preferably, said human polypeptide comprises the polypeptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. In one aspect of this embodiment, said cDNA comprises the complete coding sequence of said human polypeptide.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of contacting a cDNA collection with a detectable probe comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 under

conditions which permit said probe to hybridize to a cDNA, identifying said cDNA which hybridizes to said detectable probe, and isolating said cDNA.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

5 In one aspect of this embodiment, the cDNA encodes at least a portion of a human polypeptide. Preferably, said human polypeptide comprises at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. More
10 preferably, said human polypeptide comprises the polypeptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. In one aspect of this embodiment, said cDNA comprises the complete coding sequence of said human polypeptide.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of contacting a collection of mRNA molecules from human cells with a
15 first primer capable of hybridizing to the polyA tail of said mRNA, hybridizing said first primer to said polyA tail, reverse transcribing said mRNA to make a first cDNA strand, making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-
20 1622, and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

In one aspect of this embodiment, said cDNA encodes at least a portion of a human
25 polypeptide. Preferably, said human polypeptide comprises at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. More preferably, said human polypeptide comprises the polypeptide encoded by a sequence selected
30 from the group consisting of the sequences of SEQ ID NOs. 24-811. In one aspect of this embodiment, said cDNA comprises the complete coding sequence of said human polypeptide.

In another aspect of the preceding method the second cDNA strand is made by contacting said first cDNA strand with a second primer comprising at least 12, 15, 18, 20, 23, 25,
35 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and a third primer which sequence is fully

included within the sequence of said first primer, performing a first polymerase chain reaction with said second and third primers to generate a first PCR product, contacting said first PCR product with a fourth primer, said fourth primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of said sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and a fifth primer which sequence is fully included within the sequence of said third primer, wherein said fourth and fifth primers hybridize to sequences within said first PCR product, and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of this embodiment is a purified cDNA obtainable by the method of the preceding paragraph.

In another aspect of this embodiment, said cDNA encodes at least a portion of a human polypeptide. Preferably, said human polypeptide comprises at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. More preferably, said human polypeptide comprises the polypeptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. In one aspect of this embodiment, said cDNA comprises the complete coding sequence of said human polypeptide.

Alternatively, the second cDNA strand may be made by contacting said first cDNA strand with a second primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, hybridizing said second primer to said first strand cDNA, and extending said hybridized second primer to generate said second cDNA strand.

One aspect of the above embodiment is a purified cDNA obtainable by the method of the preceding paragraph.

In a further aspect of this embodiment said cDNA encodes at least a portion of a human polypeptide. Preferably, said human polypeptide comprises at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. More preferably, said human polypeptide comprises the polypeptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811. In one aspect of this embodiment, said cDNA comprises the complete coding sequence of said human polypeptide.

Another embodiment of the present invention is a method of making a polypeptide comprising the steps of obtaining a cDNA which encodes a polypeptide encoded by a nucleic

acid comprising, consisting essentially of, or consisting of a sequence selected from the group consisting of SEQ ID NOs. 24-811 or a cDNA which encodes a polypeptide comprising at least 6, 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive amino acids of a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NOs. 24-811, inserting
5 said cDNA in an expression vector such that said cDNA is operably linked to a promoter, introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA, and isolating said protein.

Another aspect of this embodiment is an isolated protein obtainable by the method of the preceding paragraph.

10 Another embodiment of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining genomic DNA located upstream of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, screening said genomic DNA to identify a promoter capable of directing
15 transcription initiation, and isolating said DNA comprising said identified promoter.

In one aspect of this embodiment, said obtaining step comprises walking from genomic DNA comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622. In another aspect of this embodiment, said screening step comprises
20 inserting genomic DNA located upstream of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 into a promoter reporter vector. For example, said screening step may comprise identifying motifs in genomic DNA located upstream of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-
25 1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 which are transcription factor binding sites or transcription start sites.

Another embodiment of the present invention is a isolated promoter obtainable by the method of the paragraph above.

Another embodiment of the present invention is an array of discrete ESTs or fragments
30 thereof of at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 nucleotides in length, said array comprising at least one sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of a sequence selected from the group
35 consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences

complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622. In some aspects of this embodiment, the array includes at least two sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622. In another aspect of this embodiment, the array includes at least one, three, five, ten, fifteen, or twenty sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is an enriched population of recombinant nucleic acids, said recombinant nucleic acids comprising an insert nucleic acid and a backbone nucleic acid, wherein at least 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 5%, 10%, or 20% of said insert nucleic acids in said population comprise a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a polypeptide comprising at least 6, 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive amino acids of a sequence selected from the group consisting of SEQ ID NOs. 812-1599.

Yet, another embodiment of the present invention is an antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide comprising a contiguous span of at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 amino acids of any of SEQ ID NOs. 812-1599, wherein said antibody is polyclonal or monoclonal.

Another embodiment of the present invention is a computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599. In one aspect of this embodiment the computer system further comprises a sequence comparer and a data storage device having reference sequences stored thereon. For example, the sequence comparer may comprise a computer program which indicates polymorphisms. In another aspect of this embodiment, the computer system further comprises an identifier which identifies features in said sequence.

Another embodiment of the present invention is a method for comparing a first sequence to a reference sequence wherein said first sequence is selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of reading said first sequence and said reference sequence through use of a computer program which compares sequences and determining differences between said first sequence and said reference sequence with said computer program. In some aspects of this embodiment, said step of determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

Another embodiment of the present invention is a method for identifying a feature in a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of reading said sequence through the use of a computer program which identifies features in sequences and identifying features in said sequence with said computer program.

Another embodiment of the present invention is a vector comprising a nucleic acid according to any one of the nucleic acids described above.

In one aspect of this embodiment, the vector encodes a fusion protein comprising a signal peptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811 and 1600-1622 operably linked to a second nucleic acid encoding an heterologous polypeptide.

Another embodiment of the present invention is a host cell containing any of the above vectors.

Another embodiment of the present invention is a method for directing the secretion of a polypeptide comprising the steps of culturing a host cell containing a vector encoding a fusion

protein, said fusion protein comprises a signal peptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs. 24-811 and 1600-1622 operably linked to a second nucleic acid encoding an heterologous polypeptide, under conditions which allow the secretion of said fusion protein and recovering said fusion protein. In one aspect of this embodiment, said fusion protein is secreted into the extracellular environment. In another aspect of this embodiment, said fusion protein is inserted into the membrane of said host cell

Another embodiment of the present invention is a method for importing a polypeptide into a cell comprising the step of contacting said cell with a fusion protein comprising a signal peptide encoded by a sequence selected from the group consisting of the sequences of SEQ ID NOs: 38-270, operably linked to said polypeptide.

Another embodiment of the present invention is a method of making any of the nucleic acids described above comprising the steps of introducing said nucleic acid into a host cell such that said nucleic acid is present in multiple copies in each host cell and isolating said nucleic acid from said host cell.

Another embodiment of the present invention is a method of making a nucleic acid of any of the nucleic acids described above comprising the step of sequentially linking together the nucleotides in said nucleic acids.

Another embodiment of the present invention is a method of making any of the polypeptides described above wherein said polypeptides is 150 amino acids in length or less comprising the step of sequentially linking together the amino acids in said polypeptide.

Another embodiment of the present invention is a method of making any of the polypeptides described above wherein said polypeptides is 120 amino acids in length or less comprising the step of sequentially linking together the amino acids in said polypeptides.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they derived. In the first step (1), the cap of intact mRNAs is oxidized to be chemically ligated to an oligonucleotide tag. In the second step (2), a reverse transcription is performed using random primers to generate a first cDNA strand. In the third step (3), mRNAs are eliminated and the second strand synthesis is carried out using a primer contained in the oligonucleotide tag.

Figure 2 is an analysis of the 43 amino terminal amino acids of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5'ESTs.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags.

Figure 5 describes the transcription factor binding sites present in each of the promoters of Figure 4.

Figure 6 is a block diagram of an exemplary computer system.

Figure 7 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 8 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous.

Figure 9 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence.

Figure 10 is a table with all of the parameters that can be used for each step of extended cDNA analysis.

Detailed Description of the Preferred Embodiment

I. Obtaining 5'ESTs from cDNA libraries including the 5'Ends of their Corresponding mRNAs

The 5' ESTs of the present invention were obtained from cDNA libraries including cDNAs which include the 5'end of their corresponding mRNAs. The general method used to obtain such cDNA libraries is described in Examples 1 to 5.

EXAMPLE 1

Preparation of mRNA

Total human RNAs or polyA⁺ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as described below. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczynski and Sacchi, *Analytical Biochemistry* **162**:156-159, 1987) , the entire disclosure of which is incorporated herein by reference. PolyA⁺ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* **69**:1408-1412, 1972) , the entire disclosure of which is incorporated herein by reference, in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA⁺ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded.

Contamination of the polyA⁺ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

EXAMPLE 2

Methods for Obtaining mRNAs having Intact 5' Ends

Following preparation of the mRNAs from various tissues as described above, selection of mRNA with intact 5' ends and specific attachment of an oligonucleotide tag to the 5' end of such mRNA was performed using either a chemical or enzymatic approach. Both techniques takes advantage of the presence of the "cap" structure, which characterizes the 5' end of intact mRNAs and which comprises a guanosine generally methylated once, at the 7 position. The chemical approach is illustrated in Figure 1.

The chemical modification approach involves the optional elimination of the 2', 3'-cis diol of the 3' terminal ribose, the oxidation of the 2', 3', -cis diol of the ribose linked to the cap of the 5' ends of the mRNAs into a dialdehyde, and the coupling of the such obtained dialdehyde to a derivatized oligonucleotide tag. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in International Application No. WO96/34981, published November 7, 1996, the entire disclosure of which is incorporated herein by reference.

The enzymatic approach for ligating the oligonucleotide tag to the 5' ends of mRNAs with intact 5' ends involves the removal of the phosphate groups present on the 5' ends of uncapped incomplete mRNAs, the subsequent decapping of mRNAs with intact 5' ends and the ligation of the phosphate present at the 5' end of the decapped mRNA to an oligonucleotide tag. Further detail regarding the enzymatic approaches for obtaining mRNAs having intact 5' ends are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al.*, *Gene* **150**:243-250 (1994), the entire disclosures of which are incorporated herein by reference.

In either the chemical or the enzymatic approach, the oligonucleotide tag has a restriction enzyme site (e.g. EcoRI sites) therein to facilitate later cloning procedures. Following attachment of the oligonucleotide tag to the mRNA, the integrity of the mRNA was then examined by performing a Northern blot using a probe complementary to the oligonucleotide tag.

EXAMPLE 3

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags, first strand cDNA synthesis was performed using a reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of mRNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

The second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5' end of the ligated oligonucleotide. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

EXAMPLE 4

Cloning of cDNAs derived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

EXAMPLE 5

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

Clones containing the oligonucleotide tag attached were then selected as follows. The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows. Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, **Gene** 127:95-8, 1993), the entire disclosure of which is incorporated herein by reference, such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, **13**: 124-131, 1992, the entire disclosure of which is incorporated herein by reference. In this procedure, the single stranded DNA was hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide

tag. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated using dot blot analysis to typically be between 90 and 98%.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 6

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE-9600 thermocyclers (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

EXAMPLE 7

Obtaining 5' ESTs from Extended cDNA libraries

Obtained from mRNA with Intact 5' Ends

Alternatively, 5'ESTs may be isolated from other cDNA or genomic DNA libraries. Such cDNA or genomic DNA libraries may be obtained from a commercial source or made using other

techniques familiar to those skilled in the art. One example of such cDNA library construction, a full-length cDNA library, is as follows.

PolyA⁺ RNAs are prepared and their quality checked as described in Example 1. Then, the caps at the 5' ends of the polyA⁺ RNAs are specifically joined to an oligonucleotide tag as described in Example 2. The oligonucleotide tag may contain a restriction site such as Eco RI to facilitate further subcloning procedures. Northern blotting is then performed to check the size of mRNAs having the oligonucleotide tag attached thereto and to ensure that the mRNAs are actually tagged.

First strand synthesis is subsequently carried out for mRNAs joined to the oligonucleotide tag as described in Example 3 above except that the random nonamers are replaced by an oligo-dT primer. For instance, this oligo-dT primer may contain an internal tag of 4 nucleotides which is different from one tissue to the other. Following second strand synthesis using a primer contained in the oligonucleotide tag attached to the 5' end of mRNA, the blunt ends of the obtained double stranded full-length DNAs are modified into cohesive ends to facilitate subcloning. For example, the extremities of full-length cDNAs may be modified to allow subcloning into the Eco RI and Hind III sites of a Bluescript vector using the Eco RI site of the oligonucleotide tag and the addition of a Hind III adaptor to the 3' end of full-length cDNAs.

The full-length cDNAs are then separated into several fractions according to their sizes using techniques familiar to those skilled in the art. For example, electrophoretic separation may be applied in order to yield 3 or 6 different fractions. Following gel extraction and purification, the cDNA fractions are subcloned into appropriate vectors, such as Bluescript vectors, transformed into competent bacteria and propagated under appropriate antibiotic conditions. Subsequently, plasmids containing tagged full-length cDNAs are positively selected as described in Example 5.

The 5' end of full-length cDNAs isolated from such cDNA libraries may then be sequenced as described in Example 6 to yield 5'ESTs.

II. Computer Analysis of the Isolated 5' ESTs: Construction of the SignalTag™ Database

The sequence data from the cDNA libraries made as described above were transferred to a database, where quality control and validation steps were performed. A base-caller, working using a Unix system, automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may

contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5' ESTs were entered in a database for storage and manipulation as described below. Before searching the ESTs in the database for sequences of interest, ESTs derived from mRNAs which were not of interest were identified. Briefly, such undesired sequences may be of three types. First, contaminants of either endogenous (ribosomal RNAs, transfer RNAs, mitochondrial RNAs) or exogenous (prokaryotic RNAs and fungal RNAs) origins were identified. Second, uninformative sequences, namely redundant sequences, small sequences and highly degenerate sequences were identified. Third, repeated sequences (Alu, L1, THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats) were identified and masked in further processing.

In order to determine the accuracy of the sequencing procedure as well as the efficiency of the 5' selection described above, the analyses described in Examples 8 and 9 respectively were performed on 5' ESTs obtained from the database following the elimination of endogenous and exogenous contaminants and following the masking of repeats.

EXAMPLE 8

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described in Example 6, the sequences of 5' ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database available at the time of filing the priority applications. The 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy. This analysis revealed that the sequences incorporated in the database had an accuracy of more than 99.5%.

EXAMPLE 9

Determination of Efficiency of 5' EST Selection

To determine the efficiency at which the above selection procedures isolated 5' ESTs which included sequences close to the 5' end of the mRNAs from which they derived, the sequences of the ends of the 5' ESTs derived from the elongation factor 1 subunit α and ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the

transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5' ESTs which included the authentic transcription start sites. For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for comparison. The 5' ends of more than 85% of 5' ESTs derived from mRNAs included in the GenBank database were located close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends of their corresponding mRNAs.

EXAMPLE 10

Calculation of Novelty Indices for 5'EST Libraries

In order to evaluate the novelty of 5'EST libraries, the following analysis was performed. For each sequenced 5'EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others and the longest sequence found in the cluster was used as representative of the group. A novelty rate (NR) was then defined as: $NR = 100 \times (\text{Number of new unique sequences found in the library} / \text{Total number of sequences from the library})$. Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the 5'EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

EXAMPLE 11

Generation of Consensus Contigated 5' ESTs

Since the cDNA libraries made above include multiple 5' ESTs derived from the same mRNA, overlapping 5'ESTs may be assembled into continuous sequences. The following method describes how to efficiently align multiple 5'ESTs in order to yield not only consensus contigated 5'EST sequences for mRNAs derived from different genes but also consensus contigated 5'EST sequences for different mRNAs, so called variants, transcribed from the same gene such as alternatively spliced mRNAs.

The whole set of sequences was first partitioned into small clusters containing sequences which exhibited perfect matches with each other on a given length and which derived

from a small number of different genes. Some 5'EST sequences, so called singletons, were not aligned using this approach because they were not homologous to any other sequence.

Thereafter, all variants of a given gene were identified in each cluster using a proprietary software. 5'EST sequences belonging to the same variant were then contiguated and consensus contiguated 5'EST sequences generated for each variant. All consensus contiguated 5'EST sequences were subsequently compared to the whole set of individual 5'EST sequences used to obtained them.

If desired, the consensus contiguated 5'EST sequences may be verified by identifying clones in nucleic acid samples derived from biological tissues, such as cDNA libraries, which hybridize to the probes based on the sequences of the consensus contiguated 5'ESTs using any methods described herein and sequencing those clones.

Application of this alignment method to a selected set of 5'ESTs free from endogenous contaminants and uninformative sequences, and following the masking of repeats, yielded consensus contiguated 5'EST sequences or variants of clustered genes encompassing many individual 5'ESTs. Both non aligned 5'ESTs, *i.e.* singletons, and consensus contiguated 5'ESTs were then compared to already known sequences and those sequences matching human mRNA sequences were eliminated from further analysis.

EXAMPLE 12

Identification of Open Reading Frames in 5' ESTs

Subsequently, consensus contiguated 5'ESTs and 5'ESTs were screened to identify those having an open reading frame (ORF).

Such open reading frames were simply defined as uninterrupted nucleic acid sequences longer than 45 nucleotides and beginning with an ATG codon.

Alternatively, the nucleic acid sequence was first divided into several subsequences which coding propensity was evaluated separately using one or several different methods known to those skilled in the art such as the evaluation of N-mer frequency and its variants (Fickett and Tung, *Nucleic Acids Res*;20:6441-50 (1992)) , the entire disclosure of which is incorporated herein by reference, or the Average Mutual Information method (Grosse *et al*, International Conference on Intelligent Systems for Molecular Biology, Montreal, Canada. June 28-July 1, 1998), the entire disclosure of which is incorporated herein by reference. Each of the scores obtained by the techniques described above were then normalized by their distribution extremities and then fused using a neural network into a unique score that represents the coding probability of a given subsequence. The coding probability scores obtained for each subsequence, thus the probability score profiles obtained for each reading frame, was then

linked to the initiation codons present on the sequence. For each open reading frame, defined as a nucleic acid sequence beginning with an ATG codon, an ORF score was determined. Preferably, this score is the sum of the probability scores computed for each subsequence corresponding to the considered ORF in the correct reading frame corrected by a function that negatively accounts for locally high score values and positively accounts for sustained high score values. The most probable ORF with the highest score was selected.

In some embodiments, nucleic acid sequences encoding an “incomplete ORF”, as referred therein, namely an open reading frame in which a start codon has been identified but no stop codon has been identified, were obtained.

In other embodiments, nucleic acid sequences encoding a “complete ORF”, as used therein, namely an open reading frame in which a start codon and a stop codon have been identified, are obtained.

In a preferred embodiment, open reading frames encoding polypeptides of at least 50 amino acids were obtained.

To confirm that the chosen ORF actually encodes a polypeptide, the consensus contigated 5’EST or 5’EST may be used to obtain an extended cDNA using any of the techniques described therein, and especially those described in Examples 19 and 20. Then, such obtained extended cDNAs may be screened for the most probable open reading frame using any of the techniques described therein. The amino acid sequence of the ORF encoded by the consensus contigated 5’EST or 5’EST may then be compared to the amino acid sequence of the ORF encoded by the extended cDNA using any of the algorithms and parameters described therein in order to determine whether the ORF encoded by the extended cDNA is basically the same as the one encoded by the consensus contigated 5’EST or 5’EST.

Alternatively, to confirm that the chosen ORF actually encodes a polypeptide, the consensus contigated 5’EST or 5’EST may be used to obtain an extended cDNA using any of the techniques described therein, and especially those described in Examples 19 and 20. Such an extended cDNA may then be inserted into an appropriate expression vector and used to express the polypeptide encoded by the extended cDNA as described therein. The expressed polypeptide may be isolated, purified, or enriched as described therein. Several methods known to those skilled in the art may then be used to determine whether the expressed polypeptide is the one actually encoded by the chosen ORF, therein referred to as the expected polypeptide. Such methods are based on the determination of predictable features of the expressed polypeptide, including but not limited to its amino acid sequence, its size or its charge, and the comparison of these features to those predicted for the expected polypeptide. The following paragraphs present examples of such methods.

One of these methods consists in the determination of at least a portion of the amino acid sequence of the expressed polypeptide using any technique known to those skilled in the art. For example, the amino-terminal residues may be determined using techniques either based on Sanger's technique of acid hydrolysis of a polypeptide which N-terminal residue has been covalently labeled or using techniques based on Edman degradation of polypeptides which N-terminal residues are sequentially labeled and cleaved from the polypeptide of interest. The amino acid sequence of the expressed polypeptide may then be compared to the one predicted for the expected polypeptide using any algorithm and parameters described therein.

Alternatively, the size of the expressed polypeptides may be determined using techniques familiar to those skilled in the art such as Coomassie blue or silver staining and subsequently compared to the size predicted for the expected polypeptide. Generally, the band corresponding to the expressed polypeptide will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, specific antibodies or antipeptides may be generated against the expected polypeptide as described in Example 34 and used to perform immunoblotting or immunoprecipitation studies against the expressed polypeptide. The presence of a band in samples from cells containing the expression vector with the extended cDNA which is absent in samples from cells containing the expression vector encoding an irrelevant polypeptide indicates that the expected polypeptide or portion thereof is being expressed. Generally, the band corresponding to the expressed polypeptide will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

EXAMPLE 13

Identification of Potential Signal Sequences in 5' ESTs

The 5'ESTs or consensus contigated 5'ESTs found to encode an ORF were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res.* 14:4683-4690, 1986, the entire disclosure of which is incorporated herein by reference. Those sequences encoding a 15 amino acid long stretch with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those nucleic acid sequences which match a known human mRNA or EST sequence and have a 5' end located downstream of the known 5' end, preferably by more than 20 nucleotides,

were excluded from further analysis. The remaining nucleic acids having signal sequences therein were included in a database called SignalTag™.

EXAMPLE 14

Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figure 2.

Using the above method of identification of secretory proteins, 5' ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs or consensus contigated 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs or consensus contigated 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5' EST or consensus contigated 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST or consensus contigated 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637, the entire disclosure of which is incorporated herein by reference. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST or consensus contigated 5' EST signal sequence confirms that the 5' EST or consensus contigated 5' ESTs encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs or consensus contigated 5' ESTs into expression vectors such as pXT1 as described below, or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

EXAMPLE 15

Analysis of the Sequences of the Invention

The set of the nucleic acid sequences of the invention (SEQ ID NOs. 24-811 and 1600-1622) was obtained as described in Example 11. Subsequently, the most probable open reading frame was determined and signal sequences were searched, as described in Examples 12 and 13, for all sequences of the invention.

The nucleotide sequences of the SEQ ID NOs. 24-811 and 1600-1622 and the polypeptides sequences encoded by SEQ ID NOs. 24-811 (*i.e.* polypeptide sequences of SEQ ID NOs. 812-1599) are provided in the appended sequence listing which structure is as follows.

SEQ ID NOs. 24-728 are nucleic acids having an incomplete ORF which encodes a signal peptide. The locations of the incomplete ORFs and sequences encoding signal peptides are listed in the accompanying Sequence Listing. In addition, the von Heijne score of the signal peptide computed as described in Example 13 is listed as the "score" in the accompanying Sequence Listing. The sequence of the signal-peptide is listed as "seq" in the accompanying Sequence Listing. The "/" in the signal peptide sequence indicates the location where proteolytic cleavage of the signal peptide occurs to generate a mature protein.

SEQ ID NOs. 729-765 are nucleic acids having an incomplete ORF in which no sequence encoding a signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a sequence encoding a signal peptide in these nucleic acids. The locations of the incomplete ORFs are listed in the accompanying Sequence Listing.

SEQ ID NOs. 766-792 are nucleic acids having a complete ORF which encodes a signal peptide. The locations of the complete ORFs and of the signal peptides, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the proteolytic cleavage site are indicated as described above.

SEQ ID NOs. 793-811 are nucleic acids having a complete ORF in which no sequence encoding a signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a sequence encoding a signal peptide in these nucleic acids. The locations of the complete ORFs are listed in the accompanying Sequence Listing.

5 SEQ ID NOs. 812-1516 are “incomplete polypeptide sequences” which include a signal peptide. “Incomplete polypeptide sequences” are polypeptide sequences encoded by nucleic acids in which a start codon has been identified but no stop codon has been identified. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 24-728. The location of the signal peptide, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the
10 proteolytic cleavage site are indicated as described above.

 SEQ ID NOs. 1517-1553 are incomplete polypeptide sequences in which no signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a signal peptide in these polypeptides. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 729-765.

15 SEQ ID NOs. 1554-1580 are “complete polypeptide sequences” which include a signal peptide. “Complete polypeptide sequences” are polypeptide sequences encoded by nucleic acids in which a start codon and a stop codon have been identified. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 766-792. The location of the signal peptide, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the proteolytic cleavage site are indicated
20 as described above..

 SEQ ID NOs. 1581-1599 are complete polypeptide sequences in which no signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a signal peptide in these polypeptides. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 793-811.

25 SEQ ID NOs. 1600-1622 are nucleic acid sequences in which no open reading frame has been conclusively identified to date. However, it remains possible subsequent analysis will identify an open reading frame in these nucleic acids.

 In the accompanying Sequence Listing, all instances of the symbol “n” in the nucleic acid sequences mean that the nucleotide can be adenine, guanine, cytosine or thymine. In some
30 instances the polypeptide sequences in the Sequence Listing contain the symbol “Xaa.” These “Xaa” symbols indicate either (1) a residue which cannot be identified because of nucleotide sequence ambiguity or (2) a stop codon in the determined sequence where applicants believe one should not exist (if the sequence were determined more accurately). In some instances, several possible identities of the unknown amino acids may be suggested by the genetic code.

In the case of secreted proteins, it should be noted that, in accordance with the regulations governing Sequence Listings, in the appended Sequence Listing, the full protein (*i.e.* the protein containing the signal peptide and the mature protein) extends from an amino acid residue having a negative number through a positively numbered C-terminal amino acid residue. Thus, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid number 1, and the first amino acid of the signal peptide is designated with the appropriate negative number.

If one of the nucleic acid sequences of SEQ ID NOs. 24-811 and 1600-1622 are suspected of containing one or more incorrect or ambiguous nucleotides, the ambiguities can readily be resolved by resequencing a fragment containing the nucleotides to be evaluated. If one or more incorrect or ambiguous nucleotides are detected, the corrected sequences should be included in the clusters from which the sequences were isolated, and used to compute other consensus contigated sequences on which other ORFs would be identified. Nucleic acid fragments for resolving sequencing errors or ambiguities may be obtained from deposited clones or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein, and determining its sequence.

In addition, if one of the sequences of SEQ ID NOs. 812-1599 is suspected of containing a truncated ORF as the result of a frameshift in the sequence, such frameshifting errors may be corrected by combining the following two approaches. The first one involves thorough examination of all double predictions, *i.e.* all cases where the probability scores for two ORFs located on different reading frames are high and close, preferably different by less than 0.4. The fine examination of the region where the two possible ORFs overlap may help to detect the frameshift. In the second approach, homologies with known proteins are used to correct suspected frameshifts.

Of the identified clusters, some were shown to be multivariant, *i.e.* to contain several variants of the same gene. Table I gives for each of the multivariant clusters named by its internal reference (first column), the list of all variant consensus contigated 5'ESTs (second column), each being represented by a different sequence identification number.

TABLE I

Cluster Internal Reference	SEQ ID NOs of Variants
C1	687, 791
C2	744, 798
C3	640, 811
C4	59, 66
C5	84, 97
C6	287, 289
C7	286, 775, 777
C8	762, 768
C9	783, 784
C10	80, 1603
C11	655, 736
C12	805, 806

Table II provides a list preferred polynucleotide fragments which are derivatives of the consensus contigated 5'ESTs. As used herein the term "polynucleotide described in Table II" refers to the all of the preferred polynucleotide fragments defined in Table II in the following manner. The fragments are referred to by their SEQ ID numbers in the first column. The preferred polynucleotide fragments are then defined by a range of nucleotide positions from the SEQ IDs of the consensus contigated 5'ESTs as indicated in the second column entitled "positions of preferred fragments." The preferred polynucleotide fragments correspond to the individual 5'ESTs aligned to obtain the consensus contigated 5'EST and to those filed in the priority documents. The third column entitled "variant nucleotides" describes the nucleotide sequence variations observed between the consensus contigated 5'EST and preferred nucleic acid fragments as follows:

A) Substitutions in the sequence of a consensus contigated 5'EST to derive a preferred polynucleotide fragment are denoted by an "S", followed by a number indicating the first nucleotide position in a specific SEQ ID to be substituted in a string of substituted nucleotides or the position of the substituted nucleotide in the case of a single substituted nucleotide. Then there is a coma followed by one or more lower case letters indicating the identity of the nucleotide(s) occurring in the substituted position(s). For example, SEQ ID NO: 3401; Position of preferred fragments: 1-250; Variant nucleotides S45,atc would indicate that a preferred polynucleotide fragment had the sequence of positions 1 to 250 of SEQ ID NO. 3401, except that the nucleotides at positions 45, 46, and 47 were substituted with A, T, and C, respectively, in the preferred polynucleotide as compared with the sequence of SEQ ID No. 3401.

B) Insertions in the sequence of a consensus contigated 5'EST to derive a preferred polynucleotide fragment are denoted by an "I", followed by a number indicating

the nucleotide position in a specific SEQ ID after which a string of nucleotides is inserted or the position after which the nucleotide is inserted in the case of a single inserted nucleotide. Then there is a coma followed by one or more lower case letters indicating the identity of the nucleotide(s) occurring in the inserted position(s). For example, SEQ ID NO: 7934; Position of preferred fragments: 1-500; Variant nucleotides: I36,gataca would indicate that a preferred polynucleotide fragment had the sequence of positions 1 to 500 of SEQ ID NO. 7934, except that after the nucleotides at position 36 a GATACA string of nucleotides is inserted in the preferred polynucleotide as compared with the sequence of SEQ ID No. 7934.

C) Deletions in the sequence of a consensus contigated 5'EST to derive a preferred nucleic acid fragment are denoted by an "D", followed by a number indicating the first nucleotide position in a specific SEQ ID to be deleted in a string of deleted nucleotides or the position of the deleted nucleotide in the case of a single deleted nucleotide. Then there is a coma followed by number indicating the number of nucleotide(s) deleted from the sequence provided in the sequence ID. For example, SEQ ID NO: 5398; Position of preferred fragments: 56-780; Variant nucleotides D114,5 would indicate that a preferred polynucleotide fragment had the sequence of positions 56 to 780 of SEQ ID NO. 5398, except that the nucleotides in positions 114 to 118 had been deleted in the preferred polynucleotide as compared with the sequence of SEQ ID No. 5398.

The present invention encompasses isolated, purified, or recombinant nucleic acids which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, or 500 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular polynucleotide, of a polynucleotide described in Table II, or a sequence complementary thereto, wherein said polynucleotide described in Table II is selected individually or in any combination from the polynucleotides described in Table II. The present invention also encompasses isolated, purified, or recombinant nucleic acids which consist of or consist essentially of a polynucleotide described in Table II, or a sequence complementary thereto, wherein said polynucleotide is selected individually or in any combination from the polynucleotides described in Table II. The present invention further encompasses isolated or purified polypeptides which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, or 100 amino acids encoded by a polynucleotide described in Table II.

Table II

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
35	1-423	S124, s; I135, a; S293, w; I363, a; S377, r; D424, 15
41	1-427	I117, m; S120, r; S124, g; D373, l; S376, b; S378, b; I427, gggg; D428, 109
43	1-276	S114, m; S118, rg; S123, r; S139, nr; I142, t; D148, l; D152, l; I228, t; I276, gg; D277, 136
45	126-420	D1, 125; I420, ggg; D421, 100
46	1-255	S139, r; I145, r; S146, mm; S150, ar; S254, g; D256, 128
48	4-437	D1, 3; S49, a; S55, g; S79, a; S90, a; I437, tctctg
59	1-471	S26, a; S44, t; S48, t; S109, a; S191, t; S200, gc; S203, a; S210, g; S237, a; S240, g; S255, a; S272, a; S277, a; S279, a; S284, t; S297, g; S305, g; S316, a; I471, ggtca
66	1-428	I428, tactgggg
82	1-399	S251, t; S277, d; I399, aagccggg
84	5-488	D1, 4; S210, g; S293, a; S325, g; S339, a; S348, g; S353, g; S395, g; I488, cacca
93	1-508	I508, gattt
96	26-315	D1, 25; S28, a; S62, c; I315, cagatgg
97	4-460	D1, 3; S19, g; S31, g; S114, gt; S118, a; S123, tc; S127, c; S132, a; S186, g; S190, c; S203, t; S210, g; S232, c; I460, acgtt
105	1-281	S273, a; I281, g; D282, 211
114	10-315	I0, t; D1, 9; S91, m; S267, n; S276, w; S292, h; S295, m; I315, tggg; D316, 19
118	1-145	S57, d; S126, d; I145, ccctc
120	2-348	D1, 1; S104, t; I348, g; D349, 38
121	1-190	I121, c; I190, ccctt
123	1-353	I117, m; I186, w; S187, y; I353, caccgggg
124	1-249	I249, ggrvgggg
125	114-375	D1, 113; S206, wn; I231, a; I375, ccctagg
126	1-437	S297, cc; S307, tg; S312, a; S318, g; S341, a; S351, t; S353, g; S383, c; S387, a; D404, 1
136	82-428	D1, 81; I428, aaagtg
139	1-268	I268, gggaaggg
148	6-405	D1, 5; I405, ggtgt
159	1-230	S227, ta; I230, ccctggg
165	3-256	I0, tat; D1, 2; I17, c; S18, t; S111, d; I115, t; S123, r; I256, aagcgagg
170	1-280	I103, t; S104, c; I111, t; I280, cgttcggg
194	1-215	S50, s; S186, sn; S199, k; I215, gcagcggg
213	1-158	S128, m; I132, w; S143, d; I158, tgcccggg

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
223	3-431	D1, 2; S28, s; S79, c; S82, s; S308, nr; S328, nb; I431, ccggc
247	1-359	I76, gttt; I359, tccctgg
258	1-236	S72, r; S81, g; S197, s; I205, ss; S232, k; I236, acttcggg
264	5-283	D1, 4; S64, g; S122, m; S134, yy; I137, c; I151, t; I283, gttgc
269	1-143	S111, s; I143, ggggcggg
286	5-207	D1, 4; S204, a; S206, c; I207, gg; D208, 567
287	1-277	S114, r; I125, t; S131, ag; S256, tg; S259, tt; S262, at; S267, t; S269, c; S273, c; I277, ccggg; D278, 337
289	69-416	D1, 68; I416, agccaggg
289	1-278	S114, r; I125, t; S131, ag; S277, c; I278, cggg; D279, 138
292	20-254	D1, 19; I254, aaagagg
293	1-414	I414, tagcag
300	1-285	S16, m; S67, y; I285, baccacggg; D286, 1
349	23-431	D1, 22; I118, a; S214, y; I431, caactgg
350	3-386	D1, 2; S42, w; I263, c; I386, gggat
368	3-446	D1, 2; I446, tctct
385	1-193	I35, t; I108, t; I134, r; S135, a; S137, r; S143, w; I178, c; I193, gagcgggg
411	6-391	D1, 5; S17, r; S27, t; S334, y; D392, 244
412	1-185	S49, s; S127, s; I185, gctggg; D186, 150
415	2-229	D1, 1; S3, a; I229, caaatggg
435	1-386	S4, s; I386, ccggg
436	4-472	D1, 3; S61, sa; D238, 1; S239, s; I472, agtgtgg
437	1-340	I340, ggg; D341, 129
441	1-409	S109, smag; I409, cgcacggg
454	1-492	S72, nn; S115, t; S121, bwy; S181, yn; I492, gagtc
455	1-177	I14, w; I16, a; I177, gagctggg
459	1-311	S39, n; S74, rg; I311, accatggg
460	1-425	I425, agtac
461	5-420	D1, 4; I420, tcgtc
481	1-429	I10, w; S262, d; S333, n; I429, ctccaggg
489	1-414	D72, 1; S117, n; S396, d; I414, ggaca
496	1-215	I215, ttttcggg
501	1-430	S275, n; I430, aggat
502	91-413	D1, 90; I413, aaacgggg
504	21-420	D1, 20; S47, w; S83, n; I280, n; S281, na; S292, v; S314, sm; S368, ww; S373, w; I420, cccca
505	18-457	D1, 17; D36, 1; S182, g; S273, n; S283, a; S416, bh; I457, ctcga
514	1-303	I303, accca

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
515	1-455	S11, t; I12, n; S30, r; S256, wr; I333, t; I455, cataa
517	24-453	D1, 23; I453, agagcggg
519	1-275	I119, gt; S125, w; I129, w; S133, k; S137, k; S167, k; I275, gcccc
522	1-313	I313, agcgtggg
526	4-366	I0, t; D1, 3; I366, ggcccggg
530	1-434	S328, g; I434, aagat
535	1-379	S128, g; S162, m; D380, 5
561	2-341	D1, 1; I341, raagagg
568	1-246	I118, g; S137, g; I246, aaaccggg
570	1-207	I207, tttt
576	1-288	I34, c; I288, cccgtgg
588	1-390	S218, a; S224, k; S314, dh; S358, s; D376, 1; I390, atg; D391, 23
597	31-274	D1, 30; S49, n; I274, tccatgg
606	1-354	I141, g; D174, 1; S229, rr; D355, 72
627	1-415	S7, a; I415, cattt
634	1-178	D179, 212
640	6-428	D1, 5; D429, 79
641	64-483	D1, 63; I165, d; D183, 1; S185, y; S253, t; D279, 2; S416, a; I483, atata
655	1-280	S58, c; I84, g; S88, k; S204, ac; S244, g; S247, g; I280, ggg; D281, 90
672	34-489	D1, 33; S316, k; S331, k; S333, w; S486, g; S488, c; D490, 4
687	116-473	D1, 115; S142, n; I473, cctcgggg
697	1-202	S142, s; S144, sr; S148, d; S152, d; I155, a; I164, a; S174, k; I202, gcc; D203, 291
708	8-384	D1, 7; S104, b; I384, gaaaa
710	1-167	S40, k; S49, db; I167, tatct
722	1-191	I125, c; I191, tttt
723	1-316	I316, aggg; D317, 157
729	15-373	D1, 14; S139, t; I373, cgcag; D374, 99
730	29-372	D1, 28; I155, g; S192, ka; S333, d; I372, m; D373, 93
731	1-290	S10, kk; S30, b; S32, t; S92, t; S197, dy; S278, g; I290, aggg; D291, 55
732	8-277	D1, 7; I113, a; S127, w; I131, s; S132, r; S156, w; S160, r; S211, n; S215, w; I247, a; D278, 121
733	20-375	D1, 19; S306, sbs; I325, h; S326, nr; S338, ywd; S344, v; I375, aggg; D376, 68
734	1-359	D66, 1; D360, 14
735	25-322	D1, 24; S30, r; I193, a; I322, ccaaggg
736	9-181	D1, 8; S58, g; I181, aactaggg
737	1-160	S97, ta; I160, aggtc

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
738	1-227	D228, 7
739	45-514	D1, 44; S178, s; I182, c; S436, dmn; S461, v; S476, c; S506, t; D515, 75
740	11-388	D1, 10; I388, cgacaggg
741	1-478	S118, s; S125, a; I126, s; S134, k; S421, vn; I478, aatse
742	217-553	I0, tt; D1, 216; S286, r; S294, m; S311, r; S317, s; S338, r; S442, dm; S469, h; S476, r; S485, s; S491, w; I495, ht; S496, v; S513, r; D521, 1; S536, m; D554, 199
743	1-459	I11, s; S258, m; I270, m; I304, c; I308, amta; S313, c; S438, v; I459, agggag
744	25-316	D1, 24; S315, g; D317, 95
745	21-283	D1, 20; I40, g; S41, c; D123, 1; S181, sr; S227, r; I283, ccgag; D284, 121
746	1-256	D257, 173
747	1-179	S134, w; S138, w; S140, kt; I179, cacca
748	1-235	S46, t; I72, t; S189, cc; S222, c; D236, 148
749	2-370	D1, 1; S32, cg; D144, 1; S341, g; D371, 76
750	18-410	I0, aag; D1, 17; I410, aatcc
751	22-355	D1, 21; D148, 1; S150, c; S152, a; S313, n; D356, 181
752	1-139	S50, t; I118, g; I139, ccct
753	1-189	S26, r; S115, s; I121, r; S122, r; S128, s; S143, r; I146, w; S156, r; D190, 4
754	1-395	S212, wd; I395, cggca
755	19-460	D1, 18; S26, c; S156, a; S253, n; I460, tagaagg
756	2-142	D1, 1; I106, gc; S107, t; S110, c; I142, ccaccggg
757	28-296	D1, 27; I119, s; I122, t; S128, s; S255, t; S267, m; D297, 66
758	11-368	D1, 10; I200, g; S201, c; S281, d; S317, c; I368, ccatcggg
759	19-452	D1, 18; S421, w; I452, a
760	25-175	D1, 24; S34, yk; I175, ccggg; D176, 120
761	1-212	I212, cactcggg
762	1-374	S320, s; S349, a; D375, 249
763	8-152	D1, 7; I152, acggg; D153, 109
764	1-160	I127, g; I145, g; I160, cgccccggg
765	137-313	D1, 136; S272, m; I279, s; S310, t; I313, ggg; D314, 203
766	1-320	S278, ag; S281, cagacc; S288, ta; S291, caag; S296, c; S317, m; I320, cggg; D321, 306
767	6-336	I0, aa; D1, 5; S149, w; S245, y; D337, 137
768	1-374	S320, s; D375, 299
769	53-435	D1, 52; S59, b; S344, nnkw; D436, 104
770	24-448	D1, 23; S25, g; S411, w; S416, m; D449, 31

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
771	1-370	S3, c; S180, m; S275, r; D371, 122
772	1-388	I299, c; S326, c; D389, 8
773	1-143	S18, c; S66, a; I143, ggg; D144, 274
774	1-347	S194, a; S205, c; I347, ggg; D348, 107
775	5-207	D1, 4; S111, tg; S158, g; S171, c; S191, a; S204, a; S206, c; I207, gg; D208, 324
776	1-368	I200, c; S201, a; S291, ta; I332, c
777	5-207	D1, 4; S204, a; S206, c; I207, gg; D208, 262
778	39-342	D1, 38; S184, r; D343, 126
779	4-360	D1, 3; S13, m; S15, c; S22, s; S24, m; S48, r; S56, s; S335, c; S345, rs; I360, ggg; D361, 119
780	1-472	I347, c; D473, 32
781	116-426	D1, 115; S219, m; S424, g; D427, 118
782	1-391	S386, k; D392, 64
783	1-453	D109, l; S110, y; S125, y; I128, g; S132, k; I453, ctctc
784	29-494	D1, 28; S72, r; D495, 93
785	99-461	D1, 98; S218, r; I461, gaccgggg
786	2-465	D1, 1; S8, y; S388, s; I398, g; S400, t; S403, at; S417, g; D466, 24
787	28-271	D1, 27; S99, t; S230, c; S266, ga; S269, c; I271, g; D272, 126
788	1-285	D280, l; I285, g; D286, 310
789	1-209	S205, c; D210, 150
790	51-297	D1, 50; I297, ggggg; D298, 539
791	113-327	D1, 112; S218, g; I226, g; D280, l; I327, cgcaggg; D328, 224
792	17-218	D1, 16; S58, t; S217, t; I218, gggg; D219, 219
793	11-92	D1, 10; S91, c; I92, a; D93, 258
794	9-431	D1, 8; I431, taagt
795	30-341	D1, 29; I341, a; D342, 175
796	1-442	S17, w; S19, wr; D35, l; S134, t; S264, n; S322, nr; S369, s; S420, s; S422, y; I442, tctcggg
797	1-420	S136, c; S150, c; I245, ccc; I420, ggagtg
798	25-316	D1, 24; S315, g; D317, 97
799	1-344	D345, 57
800	7-465	D1, 6; S59, k; S146, a; S186, km; I465, gtcca
801	121-422	D1, 120; I269, c; S419, cc; I422, gg; D423, 207
802	46-477	D1, 45; S132, bn; I477, actac
803	15-467	D1, 14; S45, k; S65, t; S418, ys; D452, l; D468, 119
804	1-341	S42, t; S97, d; S326, gtg; S331, tgt; S336, a; S338, c; I341, cccccggg; D342, 218
805	2-409	D1, 1; S334, d; I409, aggg; D410, 161
806	5-384	D1, 4; I384, actaa

SEQ ID NO.	Positions of Preferred Fragments	Variant nucleotides
807	1-301	S113, a; S117, c; S123, t; D128, l; D134, l; S282, g; S284, a; I301, gacggagggg; D302, 70
808	2-314	D1, l; S306, g; I314, ggg; D315, l21
809	1-394	S53, g; S228, n; S272, vk; I301, g; I358, m; S368, nb; S375, w; I383, mm; I388, yt; I394, nhaccggg
810	6-205	I0, a; D1, 5; I141, t; I205, ggg; D206, 630
811	6-270	D1, 5; I270, gggg; D271, l15
1600	1-247	S45, m; S114, k; I122, m; S123, yc; S158, rr; S221, k; I247, ccccaggg
1601	1-225	S109, bm; S195, m; I225, tgcacggg
1602	23-245	D1, 22; D138, l; S139, s; S242, t; S244, g; I245, g; D246, l3
1603	1-303	S71, c; D277, l; I303, ggagggg; D304, 38
1604	1-242	S47, w; S50, c; S81, h; S85, d; S91, k; S106, r; I242, tgtggg; D243, 50
1605	2-225	D1, l; S20, k; S91, c; I225, ggg; D226, l32
1606	15-293	D1, l4; S156, g; S193, g; I200, t; I293, acaaaggg
1607	1-361	S323, c; I361, ccca
1608	1-151	I151, taagggg; D152, l54
1609	1-242	S55, s; I135, a; S152, h; I242, cagtaggg
1610	1-196	I151, w; S190, k; I196, cctgtgg
1611	1-228	S115, k; S174, rk; I228, cgtttggg
1612	1-221	S108, v; I221, tgatcggg
1613	1-281	I66, w; I137, a; D282, 79
1614	1-171	S53, k; S76, k; I80, k; S81, kw; S86, r; S92, k; S126, k; I171, gccgagg
1615	2-193	D1, l; S67, c; I121, s; S122, mm; S126, g; S130, r; S146, r; S156, gm; I193, cctca
1616	1-349	S251, ww; S259, rs; S275, k; I279, w; S285, y; S292, y; I320, m; I331, m; I338, w; I341, s; I349, accccggg
1617	1-129	I118, t; D130, 26
1618	1-184	D9, l; D185, l
1619	1-169	I122, t; I169, gcccgagg
1620	1-187	S106, k; S118, m; S122, cg; S132, k; D188, 59
1621	1-153	D125, l; I131, ttt; S152, t; I153, gg; D154, l27
1622	1-400	S43, s; I126, g; I129, y; S353, d; I400, tatat

EXAMPLE 16

Categorization of 5' ESTs and Consensus Contigated 5'ESTs

5 The nucleic acid sequences of the present invention (SEQ ID NOs. 24-811 and 1600-1622) were grouped based on their homology to known sequences as follows. All sequences were compared to EMBL release 57 and daily releases available at the time of filing using BLASTN.

All matches with a minimum of 25 nucleotides with 90% homology were retrieved and used to compute Tables III and IV.

In some embodiments, 5'ESTs or consensus contigated 5'ESTs nucleic acid sequence do not match any known vertebrate sequence nor any publicly available EST sequence, thus being completely new.

In other embodiments, 5'ESTs or consensus contigated 5'ESTs match a known sequence. Tables III and IV gives for each sequence of the invention in this category referred to by its sequence identification number in the first column, the positions of their preferred fragments in the second column entitled "Positions of preferred fragments." As used herein the term "polynucleotide described in Table III" refers to the all of the preferred polynucleotide fragments defined in Table III in this manner, and the term "polynucleotide described in Table IV" refers to the all of the preferred polynucleotides fragments defined in Table IV in this manner. The present invention encompasses isolated, purified, or recombinant nucleic acids which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, or 500 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular polynucleotide, of a polynucleotide described in Table III or Table IV, or a sequence complementary thereto, wherein said polynucleotide described in Table III or Table IV is selected individually or in any combination from the polynucleotides described in Table III or Table IV. The present invention also encompasses isolated, purified, or recombinant nucleic acids which consist of or consist essentially of a polynucleotide described in Table III or Table IV, or a sequence complementary thereto, wherein said polynucleotide is selected individually or in any combination from the polynucleotides described in Table III or Table IV.

Table III

SEQ ID NO	Positions of preferred fragments
24	1-251
25	1-83
28	227-276
29	1-27
30	130-242, 283-315, 365-461
32	314-399
33	89-321
34	1-38
35	1-52, 171-222
36	1-30, 408-441
37	1-138
39	115-140

SEQ ID NO	Positions of preferred fragments
40	1-97
41	1-112
42	1-177
46	1-38
48	376-400
51	400-466
54	1-259
55	189-320
56	265-457
58	246-469
59	81-123, 418-444
60	1-348
61	78-123, 418-457
62	386-439
63	1-214
64	109-297
65	1-370
66	92-428
68	1-180
69	165-259
70	1-178
71	1-27
72	1-179
73	1-65, 107-192
75	1-314
77	263-388
78	1-64
79	1-149
80	101-142, 302-380
82	1-192
83	1-398
85	1-290
86	1-118, 149-336
87	1-262
88	1-149
89	1-315
90	1-74
91	1-335, 364-423
92	1-316
93	338-508
94	179-321
95	219-402
96	26-315
97	348-460
98	1-230
99	391-467
101	214-336
102	1-289

SEQ ID NO	Positions of preferred fragments
103	1-383
104	1-211
105	1-36
106	1-126
107	1-49
108	294-336
109	1-128
111	1-154
112	407-441
113	1-80, 139-184
114	10-79
116	1-292
117	1-304
119	1-288
120	2-348
121	1-122
123	188-353
124	1-249
125	295-375
128	1-244
129	1-232
130	196-312
131	178-276
132	37-174
133	1-344
134	1-244
135	1-217
136	82-428
137	1-29, 103-155, 274-434
138	1-395
139	1-268
140	1-170
141	1-396
142	1-73, 227-357
143	1-159
144	1-433
145	61-116
146	1-71, 179-205
147	177-300
149	1-146
151	1-166
152	1-382
153	1-208
154	121-251
155	1-147
157	1-115
158	1-175
159	1-44, 80-230

SEQ ID NO	Positions of preferred fragments
160	1-346
161	1-277
162	1-235
163	1-34
164	1-195
165	19-78, 175-217
166	1-209
167	1-65
168	128-218
169	49-245
170	179-280
171	1-103
172	1-218
173	1-380
174	1-139
175	1-122
176	1-300
177	1-466
179	1-86
180	1-245
181	1-241
182	1-263
183	1-170
184	58-106, 399-443
185	1-427
186	1-365
187	1-260
188	1-172
189	1-150
190	161-271, 301-339
191	1-91
192	1-264
193	1-246
194	1-150
195	1-209
196	1-363
197	1-155
198	1-135
200	1-125
201	1-210
202	1-338
203	1-188
204	228-347
205	1-440
206	56-221
208	1-422
209	169-195
210	1-363

SEQ ID NO	Positions of preferred fragments
211	1-368
212	1-448
213	1-134
214	1-193
215	1-214
216	1-134
218	1-189
219	1-248
220	1-115
221	1-113
222	1-370
224	1-251
225	1-198
226	45-141
227	1-206
228	1-480
229	1-144
230	1-42, 281-351, 432-457
231	1-112
233	1-301
234	1-109
235	1-393
236	1-222
237	1-154
238	1-439
239	112-137
240	1-194
241	1-44
242	1-242
244	1-324
245	1-38, 217-280
246	1-60
247	77-359
248	1-236
249	1-342
250	80-382
251	1-303
252	62-259
253	1-165
254	1-328
255	1-320
256	1-305
257	1-181
258	116-174
259	1-265
260	1-272
261	1-62
263	1-371

SEQ ID NO	Positions of preferred fragments
266	1-274
267	1-342
268	364-427
269	31-143
270	1-79
271	1-121
272	229-292
273	1-158
274	1-113
275	1-254
276	1-333
277	1-130
278	1-184
279	1-265
280	1-188
281	1-177
282	1-336
283	1-294
284	1-171
285	1-297
288	1-42
290	1-170
292	20-155
294	1-334
295	1-375
296	1-226
297	1-232
299	40-139
300	1-285
301	1-242
302	1-136
303	1-175
304	1-493
305	1-214
306	89-458
307	1-328
308	1-380
309	1-236
310	1-357
311	1-470
312	1-187
313	1-159
315	1-162
316	1-404
317	1-450
318	1-395
319	1-257
320	56-325

SEQ ID NO	Positions of preferred fragments
321	1-201
322	1-159
323	1-420
324	1-210
325	1-192
326	88-181
327	1-185
328	128-210
330	1-223
331	1-362
332	1-89
334	1-188
335	1-115
336	1-300
337	1-307
338	1-123
339	1-297
340	1-34
341	1-44
342	1-37
343	141-169
344	1-112
345	1-235, 266-349
346	1-191
347	1-229
348	1-210
350	139-266
351	1-307
352	1-170
353	1-293
354	30-161, 192-331
355	1-93
356	1-178
357	1-107
358	1-29, 168-209
359	1-298
360	1-193
362	1-360
363	1-45, 100-212
364	39-170, 202-242
365	1-248
366	1-351
367	1-208
368	228-446
369	1-62
370	1-132
371	1-127
372	1-196

SEQ ID NO	Positions of preferred fragments
373	1-148
374	1-126
375	1-112
376	1-146
378	1-143
379	1-261
380	202-228
382	1-151
383	1-45
384	1-190, 250-456
385	1-55, 141-181
386	1-281
387	1-111
388	1-374
389	1-192
390	1-371
392	1-303
394	1-126
395	1-329
396	1-99
397	1-316
398	1-251
399	1-120
401	1-206
402	1-330
403	1-311
405	1-153
406	1-206
407	1-479
408	1-289
410	229-321
413	1-158
415	95-229
416	1-265
417	1-228
418	1-225
419	207-293
420	1-194
421	1-90
422	1-161
423	1-420
424	1-432
425	1-276, 309-419
426	1-232
427	1-81
428	1-96
429	1-165
431	1-58, 186-237, 327-354

SEQ ID NO	Positions of preferred fragments
433	1-65
434	1-83
435	1-386
436	405-447
438	1-106
439	45-105, 168-255, 284-447
441	1-409
442	1-320
443	1-256
444	1-284
445	1-240
446	1-149
447	1-360
448	1-123
449	1-94
450	1-302
452	1-349
453	1-270
454	1-492
455	17-105
456	1-102
457	1-108
458	1-285
459	1-311
460	1-191
461	312-420
462	1-257
463	1-117
464	1-142
466	1-235
467	1-29
468	1-41
469	1-438
470	1-131
471	1-211
472	1-150
473	1-352
474	1-141
476	1-232
478	1-201
479	1-151
480	1-104
481	7-429
482	1-385
486	1-226
488	1-296
489	1-72, 323-377
491	1-348

SEQ ID NO	Positions of preferred fragments
492	33-126
493	1-300
494	1-295
495	1-244
496	1-215
497	1-255
499	1-174, 384-474
500	1-50, 102-241
501	153-430
502	91-132
503	1-64
504	21-63, 356-420
505	37-68, 187-234
506	1-315
507	101-208
510	1-402
511	1-343
512	1-140, 170-246, 276-420
513	1-324
514	1-303
515	13-340
516	1-263, 293-360
518	1-245
519	111-275
520	62-182
521	1-218
523	1-502
524	1-118
525	1-276
526	223-366
527	1-428
528	297-342
529	1-244
530	1-88, 375-434
531	1-406
533	1-149
534	1-145
535	1-116
536	1-207
537	1-394
538	1-415
539	1-160
540	1-327
541	1-38, 73-396
542	1-247
543	1-221
544	1-375
545	1-376

SEQ ID NO	Positions of preferred fragments
546	1-109
547	1-160, 223-306
548	1-148
551	1-231
552	1-229
553	1-232
554	1-141
555	1-376
556	1-279
557	1-340
558	1-51
559	1-354
562	1-188
563	1-229
564	184-352
566	308-341
567	1-218
568	1-79
569	1-142
570	1-207
571	1-373
572	1-195
573	1-352
574	1-121
575	1-222
576	151-288
577	1-264
578	1-205
580	1-171, 273-328
581	1-356
582	1-239
583	1-144
584	1-282
585	1-338
586	1-436
588	1-380
589	1-60
590	1-178
592	1-66
593	1-215
594	1-161
596	1-407
597	31-83
598	1-417
599	1-329
600	1-311
601	1-61, 99-214
602	1-154, 197-463

SEQ ID NO	Positions of preferred fragments
603	135-269
604	1-351
605	1-195
608	1-357
609	1-201
612	1-176
613	1-342
615	1-272
616	1-114
617	1-46
618	1-208
619	1-257
620	1-28
621	1-26
622	1-221
623	1-432
624	1-233
625	1-26
627	1-43
628	1-318
629	1-170
630	1-196
631	248-339
632	1-433
633	1-154
634	1-41
635	1-137
636	1-172
637	1-253
638	1-185
639	1-206
641	334-483
642	1-309
643	1-75, 162-213
644	107-211
645	1-98
646	1-347
647	1-49, 81-143
648	1-232
649	74-133
650	1-37
651	1-276
652	1-170
653	1-178
654	1-121
656	1-197
657	1-246
659	1-197

SEQ ID NO	Positions of preferred fragments
660	116-172
661	1-411
662	1-146
663	1-65
664	1-182
665	1-320
666	1-273
667	1-149
668	1-122
670	1-160
671	1-137
673	1-263
674	1-263
675	1-107
677	1-441
678	134-191
679	1-235
680	1-26
682	1-58, 269-328
683	1-447
684	1-217
685	1-132
686	1-60
688	1-107
689	132-221, 327-377
690	1-388
691	1-141, 171-408
692	1-322
693	1-153
695	1-455
698	1-58, 117-174
699	240-300
700	1-159
701	1-69
702	1-175
703	1-298
704	1-136
705	1-168
706	1-419
707	1-382
708	8-245, 296-384
709	1-149
710	1-167
711	1-35
712	1-80, 116-156, 206-241
713	33-376
714	1-304
715	1-242

SEQ ID NO	Positions of preferred fragments
717	1-145
718	1-350
720	1-257
721	1-360
722	1-191
724	1-139
726	1-207
727	99-164
728	1-321
730	156-372
731	1-109, 256-290
735	25-192
737	1-160
738	1-227
739	441-514
742	217-280
743	10-275
747	1-179
749	2-31, 139-168
750	349-410
752	1-119
753	1-121
754	1-28
760	25-175
761	1-212
763	8-75
766	1-59, 102-248, 295-320
769	53-85
771	1-370
774	1-347
776	1-200
778	39-342
779	4-28
780	1-49, 407-472
781	116-426
782	1-59
783	1-53, 219-453
784	29-53, 219-263, 426-494
785	99-347, 386-461
786	2-28
788	1-279
789	1-58
790	226-268
792	129-218
794	265-431
796	5-86
797	1-34
799	1-344

SEQ ID NO	Positions of preferred fragments
802	46-477
806	64-384
807	135-301
808	2-314
810	6-39
1600	1-25
1601	1-225
1602	23-139
1603	1-294
1606	15-44
1607	1-361
1611	85-228
1612	1-221
1613	138-281
1614	65-171
1615	2-142
1616	1-46
1617	1-95
1620	1-187
1621	1-136
1622	32-280, 311-400

Table IV

SEQ ID NO	Positions of Preferred Fragments
35	1-52
41	1-115
45	1-47
46	1-33
66	400-428
82	83-149
93	399-508
105	1-36
114	1-79
120	1-386
121	1-190
124	1-249
125	295-328
139	1-81, 125-268
159	1-139, 180-230
165	1-78
170	179-205, 248-280
194	1-150
213	1-158
247	1-104, 155-183, 280-359
269	31-143
350	139-386
368	228-446
385	1-72, 143-193
415	95-229
435	1-386
436	446-472
441	1-361
454	1-349
455	1-105
459	35-161, 200-311
460	1-26, 56-140
481	1-429
489	1-84
496	1-44, 84-215
501	153-430
502	1-91
504	1-63
505	1-68
514	1-303
515	237-351
519	1-145
526	231-366
530	1-88
535	1-55

SEQ ID NO	Positions of Preferred Fragments
570	76-207
576	168-218, 261-288
588	1-331
597	1-83
627	1-43
634	1-41
641	1-55, 334-483
672	1-34
687	1-129
708	1-245, 296-384
710	1-26, 104-167
722	1-191
730	1-465
731	1-43
735	1-91
737	1-160
738	1-186
739	1-48
742	1-62, 99-248
743	1-315, 412-459
744	1-31
747	1-63
749	1-32
750	1-38
752	1-139
753	1-193
754	1-28
759	1-38
760	1-115
763	1-62
765	1-126
769	1-85
770	1-40
771	1-148
774	1-134
775	265-531
776	71-203
777	333-469
778	144-468
779	1-28
780	1-49
781	1-102
782	1-59
783	1-53
784	1-220, 262-390
785	1-339, 408-461
786	1-28
789	1-58

SEQ ID NO	Positions of Preferred Fragments
791	1-126
792	1-31, 129-220
793	1-31
794	355-431
795	1-33
797	1-31
798	1-31
799	1-401
801	1-117
802	1-92
806	64-384
807	1-331
808	1-351
810	1-39
1600	1-25
1603	1-341
1606	1-31
1607	1-361
1608	164-305
1611	85-228
1612	1-221
1613	112-360
1614	1-171
1615	94-193
1617	1-155
1620	1-246

III. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5'ESTs, Consensus Contigated 5'ESTs, or EST-related nucleic acids

5

EXAMPLE 17

Expression Patterns of mRNAs From Which the 5'ESTs were obtained

Each of the SEQ ID NOs. 24-811 and 1600-1622 was also categorized based on the tissue from which its corresponding mRNA was obtained, as follows.

10

Table V shows the spatial distribution of each nucleic acid sequence of the invention (SEQ ID NOs. 24-811 and 1600-1622) referred to by its sequence identification number in the first column. In the second column entitled tissue distribution, the spatial distribution is represented by the number of individual 5'ESTs used to assemble the consensus contigated 5'ESTs for a given tissue. Each type of tissue listed in Table V is encoded by a letter. The correspondence between the letter code and the tissue type is given in Table VI.

15

Table V

SEQ ID NO	Tissue Distribution
24	AA:1
25	S:1
26	P:1
27	W:1
28	P:1
29	S:1
30	P:1
31	P:1
32	P:1
33	P:1
34	AB:1
35	G:3; P:1; S:1; W:3; AA:4
36	P:1
37	S:1
38	Q:1
39	P:1
40	AB:1
41	B:1; C:3; F:1; G:1; H:4; S:2; T:8; W:1; Z:1; AA:3; AC:1; AD:3
42	A:1
43	N:2
44	P:1
45	C:2; K:1; O:1; S:5
46	K:1; S:2; AA:1
47	AA:1
48	C:1; O:1; P:8
49	P:1
50	P:1
51	P:1
52	S:1
53	AA:1
54	T:1
55	P:1
56	P:1
57	P:1
58	P:1
59	P:7; T:2; Z:1
60	R:1
61	C:1
62	P:1
63	F:1
64	AA:1
65	F:1
66	P:4; T:2; Z:1

SEQ ID NO	Tissue Distribution
67	S:1
68	AA:1
69	P:1
70	P:1
71	S:1
72	W:1
73	G:1
74	P:1
75	N:1
76	P:1
77	S:1
78	U:1
79	B:1
80	P:1
81	AC:1
82	K:1; O:1
83	G:1
84	C:1; K:2; P:29; S:2; T:1; X:2; Y:1; AA:2
85	K:1
86	C:1
87	F:1
88	AB:1
89	H:1
90	M:1
91	B:1
92	K:1
93	AC:2
94	P:1
95	M:1
96	Z:2
97	K:1; P:11; S:1; X:1; AA:1
98	W:1
99	X:1
100	P:1
101	AB:1
102	F:1
103	AA:1
104	K:1
105	B:4; C:6; E:2; H:3; O:2; Q:1; S:3; AC:2
106	T:1
107	O:1
108	P:1
109	G:1
110	AA:1
111	T:1

SEQ ID NO	Tissue Distribution
112	P:1
113	F:1
114	B:3; C:4; K:5; S:4; Y:1
115	U:1
116	W:1
117	T:1
118	T:2
119	T:1
120	H:3
121	AA:3
122	K:1
123	H:2
124	AA:2
125	B:1; G:1; J:3; T:13; Y:5; AA:5; AD:2
126	H:1; P:1
127	K:1
128	F:1
129	G:1
130	P:1
131	B:1
132	AA:1
133	W:1
134	P:1
135	K:1
136	B:1; C:1
137	B:1
138	H:1
139	AC:2
140	T:1
141	B:1
142	H:1
143	T:1
144	H:1
145	B:1
146	R:1
147	P:1
148	C:1; H:2; O:1; S:2; T:1; AC:2
149	H:1
150	AA:1
151	W:1
152	S:1
153	F:1
154	M:1
155	B:1
156	R:1

SEQ ID NO	Tissue Distribution
157	W:1
158	T:1
159	C:1; AA:1
160	F:1
161	H:1
162	D:1
163	AA:1
164	AA:1
165	W:3
166	AA:1
167	W:1
168	F:1
169	B:1
170	G:2
171	E:1
172	B:1
173	F:1
174	B:1
175	W:1
176	K:1
177	AA:1
178	S:1
179	K:1
180	AA:1
181	W:1
182	K:1
183	T:1
184	P:1
185	B:1
186	W:1
187	R:1
188	T:1
189	T:1
190	W:1
191	A:1
192	F:1
193	B:1
194	G:3
195	W:1
196	O:1
197	T:1
198	O:1
199	B:1
200	AA:1
201	G:1

SEQ ID NO	Tissue Distribution
202	B:1
203	G:1
204	P:1
205	AA:1
206	Y:1
207	Y:1
208	AA:1
209	G:1
210	H:1
211	C:1
212	H:1
213	W:2
214	Y:1
215	AB:1
216	K:1
217	M:1
218	AD:1
219	A:1
220	AA:1
221	G:1
222	G:1
223	G:1; H:2; S:2; X:1
224	G:1
225	G:1
226	B:1
227	P:1
228	O:1
229	G:1
230	T:1
231	T:1
232	K:1
233	S:1
234	O:1
235	F:1
236	T:1
237	B:1
238	W:1
239	G:1
240	R:1
241	A:1
242	W:1
243	P:1
244	H:1
245	D:1
246	C:1

SEQ ID NO	Tissue Distribution
247	B:2
248	P:1
249	F:1
250	AB:1
251	W:1
252	H:1
253	B:1
254	S:1
255	T:1
256	W:1
257	T:1
258	AA:2
259	P:1
260	W:1
261	H:1
262	K:1
263	K:1
264	C:1; E:1; F:1; I:4; L:1; N:22; O:1; P:1; S:1; T:9; AA:1
265	A:1
266	T:1
267	K:1
268	H:1
269	T:2
270	T:1
271	T:1
272	B:1
273	Y:1
274	T:1
275	G:1
276	AA:1
277	T:1
278	AB:1
279	T:1
280	W:1
281	F:1
282	K:1
283	H:1
284	O:1
285	W:1
286	B:21; C:7; H:5; K:5; O:8; S:16; W:1; Y:3; Z:4; AA:2; AC:1
287	K:2; P:12; W:1; AC:2
288	S:1
289	K:2; P:8; W:1; AC:2
290	S:1
291	H:1

SEQ ID NO	Tissue Distribution
292	B:11; C:2; E:1; H:7; K:1; N:3; S:1; T:8; W:1; AA:28; AC:1
293	B:6; C:3; G:1; H:6; K:4; N:4; O:3; Q:2; S:5; T:1; U:1; V:2; Y:3; AA:1
294	B:1
295	H:1
296	AA:1
297	T:1
298	T:1
299	T:1
300	H:1; S:1
301	H:1
302	W:1
303	W:1
304	H:1
305	G:1
306	K:1
307	H:1
308	A:1
309	H:1
310	H:1
311	Y:1
312	G:1
313	H:1
314	K:1
315	Y:1
316	P:1
317	H:1
318	AA:1
319	H:1
320	O:1
321	Y:1
322	B:1
323	P:1
324	P:1
325	K:1
326	H:1
327	H:1
328	Q:1
329	S:1
330	B:1
331	T:1
332	T:1
333	B:1
334	T:1
335	W:1
336	P:1

SEQ ID NO	Tissue Distribution
337	A:1
338	AA:1
339	AA:1
340	G:1
341	C:1
342	K:1
343	S:1
344	G:1
345	B:1
346	Y:1
347	G:1
348	F:1
349	AA:5
350	B:15; C:1; G:1; H:1; O:1; Q:2; S:1; X:1; Y:1
351	F:1
352	R:1
353	O:1
354	H:1
355	W:1
356	F:1
357	T:1
358	S:1
359	X:1
360	T:1
361	K:1
362	K:1
363	G:1
364	K:1
365	G:1
366	AA:1
367	F:1
368	C:2; H:2; X:1
369	E:1
370	T:1
371	H:1
372	G:1
373	AA:1
374	G:1
375	F:1
376	F:1
377	R:1
378	AA:1
379	AA:1
380	C:1
381	H:1

SEQ ID NO	Tissue Distribution
382	T:1
383	W:1
384	S:1
385	AA:2
386	D:1
387	O:1
388	W:1
389	F:1
390	W:1
391	K:1
392	W:1
393	K:1
394	T:1
395	H:1
396	T:1
397	T:1
398	G:1
399	C:1
400	K:1
401	B:1
402	H:1
403	B:1
404	B:1
405	H:1
406	AB:1
407	O:1
408	P:1
409	X:1
410	H:1
411	B:9; C:3; K:3; L:2; O:1; S:2; X:1; AA:1
412	G:1; S:2; V:2; W:1; Y:1; Z:1
413	W:1
414	G:1
415	B:3; C:3; F:1; G:2; H:4; J:1; K:1; O:1; P:3; S:1; V:1
416	I:1
417	F:1
418	F:1
419	F:1
420	AA:1
421	F:1
422	T:1
423	P:1
424	B:1
425	Y:1
426	W:1

SEQ ID NO	Tissue Distribution
427	AA:1
428	W:1
429	H:1
430	Y:1
431	J:1
432	AA:1
433	G:1
434	AA:1
435	B:3; H:1
436	B:9; G:4; H:8; K:2; O:2; W:1; Z:2; AA:2; AD:3
437	H:1; T:1
438	T:1
439	R:1
440	M:1
441	H:2
442	W:1
443	B:1
444	W:1
445	AB:1
446	F:1
447	AD:1
448	AB:1
449	N:1
450	T:1
451	W:1
452	O:1
453	AA:1
454	D:28
455	W:1
456	T:1
457	G:1
458	W:1
459	Y:4
460	B:3
461	P:2
462	K:1
463	T:1
464	H:1
465	G:1
466	AC:1
467	R:1
468	S:1
469	B:1
470	S:1
471	T:1

SEQ ID NO	Tissue Distribution
472	AA:1
473	W:1
474	T:1
475	S:1
476	T:1
477	AA:1
478	G:1
479	W:1
480	B:1
481	O:2
482	K:1
483	P:1
484	W:1
485	P:1
486	B:1
487	Y:1
488	H:1
489	P:1; Q:1; S:3
490	C:1
491	S:1
492	H:1
493	B:1
494	H:1
495	G:1
496	N:2
497	B:1
498	G:1
499	P:1
500	G:1
501	C:1; K:1; Q:1
502	B:4
503	R:1
504	B:5; H:2; W:2
505	G:2; H:1
506	W:1
507	B:1
508	W:1
509	AB:1
510	H:1
511	N:1
512	J:1
513	AA:1
514	T:2
515	AA:5
516	F:1

SEQ ID NO	Tissue Distribution
517	C:1; O:1
518	W:1
519	T:4
520	B:1
521	H:1
522	H:2; T:3
523	H:1
524	AA:1
525	W:1
526	C:2; E:1; J:1; R:3; S:4; AA:1
527	H:1
528	S:1
529	P:1
530	B:1; H:1
531	O:1
532	Y:1
533	H:1
534	T:1
535	T:2
536	B:1
537	AD:1
538	AA:1
539	T:1
540	F:1
541	AD:1
542	W:1
543	W:1
544	F:1
545	T:1
546	F:1
547	K:1
548	Y:1
549	S:1
550	B:1
551	B:1
552	B:1
553	H:1
554	P:1
555	G:1
556	H:1
557	K:1
558	B:1
559	R:1
560	AB:1
561	C:1; S:1; V:1

SEQ ID NO	Tissue Distribution
562	AA:1
563	K:1
564	P:1
565	K:1
566	G:1
567	W:1
568	E:1; W:2
569	W:1
570	B:2
571	O:1
572	T:1
573	B:1
574	T:1
575	B:1
576	B:3
577	B:1
578	X:1
579	H:1
580	AA:1
581	AA:1
582	AA:1
583	AA:1
584	AA:1
585	D:1
586	H:1
587	H:1
588	AA:3
589	K:1
590	W:1
591	K:1
592	W:1
593	B:1
594	V:1
595	R:1
596	P:1
597	G:1; X:2; Z:1
598	X:1
599	F:1
600	F:1
601	Y:1
602	F:1
603	W:1
604	H:1
605	G:1
606	C:2; H:1; S:3; W:2; AD:3

SEQ ID NO	Tissue Distribution
651	W:1
652	T:1
653	T:1
654	P:1
655	B:1; H:2; N:1; T:3; Y:1
656	B:1
657	T:1
658	R:1
659	K:1
660	W:1
661	AA:1
662	Y:1
663	W:1
664	G:1
665	S:1
666	Y:1
667	F:1
668	T:1
669	B:1
670	F:1
671	T:1
672	A:2; B:6; C:1; G:1; H:3; J:1; L:1; P:2; Q:1; S:4; T:1; V:3; W:2; Y:1; AA:3; AD:2
673	T:1
674	G:1
675	F:1
676	M:1
677	G:1
678	Y:1
679	D:1
680	P:1
681	D:1
682	AA:1
683	G:1
684	K:1
685	G:1
686	P:1
687	B:3; C:2; D:2; E:2; J:4; V:2; AC:6
688	AA:1
689	S:1
690	AA:1
691	H:1
692	AA:1
693	S:1
694	AB:1

SEQ ID NO	Tissue Distribution
695	T:1
696	H:1
697	B:4; E:1; F:1; P:1; T:2; Z:2
698	O:1
699	W:1
700	S:1
701	O:1
702	B:1
703	AB:1
704	H:1
705	B:1
706	H:1
707	G:1
708	F:1; H:1; K:1; W:2; AA:1
709	H:1
710	T:2
711	C:1
712	G:1
713	Y:1
714	C:1
715	Y:1
716	Z:1
717	P:1
718	G:1
719	S:1
720	K:1
721	M:1
722	T:2
723	O:1; P:2; S:2
724	T:1
725	T:1
726	N:1
727	T:1
728	T:1
729	C:2; H:2; K:2; V:1; AC:1
730	B:7; H:2; Y:1
731	B:5; W:3
732	B:1; C:2; G:2; S:2; AA:9
733	B:6; C:2; G:1; H:10; O:2; P:6; Q:1; S:2; W:4; AC:2
734	B:6; O:1; V:1
735	C:1; O:2
736	B:1; H:2; N:1; T:3; Y:1
737	T:2
738	T:2

SEQ ID NO	Tissue Distribution
739	B:3; C:8; D:1; E:6; G:3; H:11; I:1; J:1; N:1; O:3; P:12; Q:3; S:2; T:2; W:1; AC:1; AD:8
740	H:2; Y:1
741	C:2; H:1
742	B:12; C:1; G:1; H:4; K:2; O:2; S:4; T:2; Y:2
743	AA:4
744	B:1; G:1; H:6; T:1; W:1
745	C:7; E:1; G:3; H:2; P:2; S:2; T:1; W:1; AD:2
746	G:2; S:1
747	T:2
748	S:3
749	H:1; O:2; S:2
750	Y:1; AD:1
751	B:8; G:2; H:2; I:1; Q:2; S:2; T:1; W:2
752	T:3
753	P:4
754	B:1; H:2
755	B:7; C:1; G:6; H:2; K:1; U:2; V:1; Z:1
756	C:1; H:1; J:2; O:2; S:1; T:2; W:1; AA:1
757	B:1; C:1; K:3; S:1; V:1; Y:1
758	E:1; H:2; K:1; P:1; Q:1; AD:5
759	B:6; C:1; Y:1
760	B:4
761	W:2
762	B:3; C:7; H:9; N:1; S:1; T:1; Y:1; AA:1
763	N:1; S:1; AA:5
764	H:3
765	B:3; G:1; W:1
766	H:2
767	C:1; AA:3
768	B:2; C:6; H:9; N:1; S:1; T:1; Y:1; AA:1
769	A:1; B:4; C:4; F:4; G:6; H:10; K:2; O:8; P:2; R:1; S:8; T:2; W:3; AA:2; AC:1
770	A:2; P:16; X:1
771	AA:3
772	O:4
773	B:1; C:1; W:1
774	P:2; X:4
775	B:18; C:6; H:5; K:3; O:7; S:10; W:1; Y:3; Z:2; AA:2; AC:1
776	H:7
777	B:26; C:8; H:5; K:4; O:10; S:17; W:1; Y:4; Z:4; AA:4; AC:2
778	B:6
779	B:3; C:1; G:1; H:2; K:1; Q:1; S:8; W:2; Y:9; AA:4
780	B:3; C:1; F:1; P:1; W:1; AC:1
781	I:2; N:1; P:1; R:3; AA:1

SEQ ID NO	Tissue Distribution
782	B:2
783	H:1; P:2; S:3; AD:1
784	H:1; P:1; S:4; AD:1
785	T:2
786	D:1; AC:9
787	H:1; L:1; S:1
788	B:6; S:4
789	S:1; T:1
790	B:1; C:2; H:5; W:1; AD:1
791	B:3; C:2; D:3; E:2; J:4; V:3; AC:5
792	B:3; D:1; K:2; S:2; Y:1
793	B:2; G:2; AA:1
794	B:25; C:4; D:1; E:1; F:3; G:6; J:1; K:6; N:1; O:1; P:2; R:1; S:3; T:2; W:2; X:1; Y:1; Z:1; AA:1; AC:2; AD:1
795	B:4; C:1; E:2; H:4; J:1; L:1; O:4; S:1; V:1; Y:3; Z:1
796	H:5
797	B:2; E:1; N:2
798	B:1; G:1; H:6; T:1; W:1
799	H:2
800	H:2; I:2; AA:1
801	A:2; B:4; C:14; D:1; H:2; K:1; N:2; S:4; T:1; W:2; AA:20
802	AA:17
803	B:2; G:3; H:3; S:1; U:1; AC:1; AD:2
804	C:1; S:2; T:2; X:2; AA:1; AC:1
805	B:5; C:6; D:5; H:17; J:2; K:4; N:1; O:6; P:2; S:5; T:5; W:1; X:1; Z:2; AA:13; AC:3
806	B:2; C:3; D:3; H:6; J:2; K:1; N:1; O:3; P:1; S:2; T:4; W:1; X:1; Z:1; AA:5; AC:1
807	H:1; AC:4
808	R:13
809	B:3; W:4
810	B:16; S:1; Y:14
811	B:8; C:5; G:1; H:1; K:5; O:2; Q:2; R:2; S:2; T:3; Y:4; Z:2; AA:1; AC:1; AD:2
1600	T:4
1601	AA:3
1602	C:3; H:1
1603	H:2; AC:2
1604	B:7; C:1; E:1; H:1; P:2; R:3; S:2; T:2; Z:3; AA:2
1605	C:4; H:3; O:1
1606	A:3; B:13; C:14; D:2; E:10; F:3; G:19; H:32; K:11; O:5; P:2; R:3; S:16; T:4; W:2; Y:10; Z:8; AA:1; AC:3
1607	T:3
1608	B:3; P:2
1609	R:4

SEQ ID NO	Tissue Distribution
1610	B:4
1611	B:3; T:1
1612	T:2
1613	V:5
1614	D:3
1615	AA:10
1616	B:4
1617	T:2
1618	K:2; S:8; AA:1
1619	B:2
1620	W:2
1621	H:1; AB:1
1622	H:2

Table VI

Tissue code	Tissue type
A	Bone Marrow
B	Brain
C	Cancerous prostate
D	Cerebellum
E	Colon
F	Dystrophic muscle
G	Fetal brain
H	Fetal kidney
I	Fetal liver
J	Heart
K	Hypertrophic prostate
L	Kidney
M	Large intestine
N	Liver
O	Lung
P	Lymph ganglia
Q	Lymphocytes
R	Muscle
S	Prostate
T	Ovary
U	Pancreas
V	Placenta
W	Spinal cord
X	Spleen
Y	Substantia nigra
Z	Surrenals
AA	Testis
AB	Thyroid
AC	Umbilical cord
AD	Uterus

In addition to categorizing the 5' ESTs and consensus contigated 5' ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs, as well as their expression levels, may be determined as described in Example 18 below.

Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5' ESTs and consensus contigated 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of expression, over expression, or under expression of a mRNA corresponding to a 5' EST or consensus contigated 5' EST. By comparing mRNA expression patterns and quantities in

samples taken from healthy individuals with those from individuals suffering from a particular disease, 5' ESTs or consensus contigated 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs and consensus contigated 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs and consensus contigated 5' ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the 5' ESTs or consensus contigated 5' ESTs themselves.

EXAMPLE 18

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to EST-Related Nucleic Acids

Expression levels and patterns of mRNAs corresponding to EST-related nucleic acids may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277, the entire disclosure of which is incorporated herein by reference. Briefly, an EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3, T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid is 100 or more nucleotides in length. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (*i.e.* biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (*i.e.* RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A, the entire disclosure of which is incorporated herein by reference. In this method, cDNAs are prepared from a cell, tissue, organism or other

source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so called tagging endonuclease is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2 to 200 ditags. The tag sequences are then determined and compared to the sequences of the EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid to determine which 5' ESTs, consensus contigated 5' ESTs, or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs, consensus contigated 5' ESTs, or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids. Preferably, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 nucleotides in length. More preferably, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are at least 100 nucleotide long. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids may be more than 500 nucleotides long.

For example, quantitative analysis of gene expression may be performed with EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids in a complementary DNA microarray as described by Schena *et al.* (*Science* **270**:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* **93**:10614-10619, the entire disclosure of which is incorporated herein by reference, 1996). EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm² microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids in complementary DNA arrays as described by Pietu *et al.* (*Genome Research* **6**:492-503, 1996), the entire disclosure of which is incorporated herein by reference. The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology* **14**: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* **94**:1119-1123, 1997), the entire disclosures of which are incorporated

herein by reference. Oligonucleotides of 15-50 nucleotides corresponding to sequences of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides are about 20 to 25 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al.*, *supra* and application of different electric fields (Sonowsky *et al.*, *supra.*), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST, consensus contigated 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

IV. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs or consensus contigated 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs or consensus contigated 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site. If the extended cDNA encodes a secreted protein, it may contain the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide.

Extended cDNAs which include the entire coding sequence of the protein encoded by the corresponding mRNA are referred to herein as "full-length cDNAs." Alternatively, the extended cDNAs may not include the entire coding sequence of the protein encoded by the corresponding mRNA, although they do include sequences adjacent to the 5'ESTs or consensus contigated 5' ESTs. In some embodiments in which the extended cDNAs are derived from an mRNA encoding a secreted protein, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Examples 19 and 20 below describe a general method for obtaining extended cDNAs using 5' ESTs or consensus contigated 5' ESTs and nucleic acid homologous thereto. Example 21

below describes the cloning and sequencing of several extended cDNAs, including full-length cDNAs which include the authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 19 and 20 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of proteins encoded by the genes corresponding to the 5' ESTs or consensus contigated 5'ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the proteins encoded by the sequences of SEQ ID NOs. 24-811 and 1600-1622. In some embodiments, the extended cDNAs isolated using these methods encode at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the proteins encoded by the sequences of SEQ ID NOs. 24-811.

EXAMPLE 19

General Method for Using 5' ESTs or Consensus Contigated 5'ESTs to Clone and Sequence Extended cDNAs which Include the Entire Coding Region and the Authentic 5'End of the Corresponding mRNA

The following general method may be used to quickly and efficiently isolate extended cDNAs including sequence adjacent to the sequences of the 5' ESTs or Consensus Contigated 5'ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST or consensus contigated 5' EST of the invention, including those 5' ESTs and consensus contigated 5' ESTs encoding secreted proteins. This method is illustrated in Figure 3.

1. Obtaining Extended cDNAs

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly dT primer containing a nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. Such a primer and a commercially-available reverse transcriptase enzyme are added to a buffered mRNA sample yielding a reverse transcript anchored at the 3' polyA site of the RNAs. Nucleotide monomers are then added to complete the first strand synthesis.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer can be eliminated with an exclusion column.

Subsequently, a pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST or consensus contigated 5' EST and the known 3' end added by the poly dT primer used in the first strand synthesis. Software used to design primers are either based on

GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), the entire disclosure of which is incorporated herein by reference, or based on the octamer frequency disparity method (Griffais *et al.*, *Nucleic Acids Res.* 19: 3887-3891, 1991), the entire disclosure of which is incorporated herein by reference such as PC-Rare (http:// bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html). Preferably, the nested primers at the 5' end and the nested primers at the 3' end are separated from one another by four to nine bases. These primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

A first PCR run is performed using the outer primer from each of the nested pairs. A second PCR run using the inner primer from each of the nested pairs is then performed on a small sample of the first PCR product. Thereafter, the primers and remaining nucleotide monomers are removed.

2. Sequencing Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the entire coding sequence. Such an extended cDNA may be used in a direct cloning procedure as described in section a below. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b below.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST or consensus contigated 5' EST sequence, it is directly cloned in an appropriate vector as described in section 3.

b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are then designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.*

the polyA tract and sometimes the polyadenylation signal, as illustrated in Figure 3. Such extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs can be performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence long PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et al.*, *Genome Science Technol.* 1: 9-19, 1995), the entire disclosure of which is incorporated herein by reference, to construct contigs of walking sequences including the initial 5' tag. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment may be assessed by comparing the sequence length to the size of the corresponding nested PCR product. When Northern blot data are available, the size of the mRNA detected for a given PCR product may also be used to finally assess that the sequence is complete. Sequences which do not fulfill these criteria are discarded and will undergo a new isolation procedure.

3. Cloning Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into any expression vector known in the art, such as pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA).

Cloned PCR products are then entirely sequenced in order to obtain at least two sequences per clone. Preferably, the sequences are obtained from both sense and antisense strands according to the aforementioned procedure with the following modifications. First, both 5' and 3' ends of cloned PCR products are sequenced in order to confirm the identity of the clone. Second, primer walking is performed if the full coding region has not been obtained yet. Contigation is then performed using primer walking sequences for cloned products as well as walking sequences that have already contigated for uncloned PCR products. The sequence is considered complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends. All the contigated sequences for each cloned amplicon are then used to obtain a consensus sequence.

4. Selection of Cloned Full length Sequences

a) Computer analysis of extended cDNAs

Following identification of contaminants and masking of repeats, structural features, e.g. polyA tail and polyadenylation signal, of the sequences of extended cDNAs are subsequently determined using methods known to those skilled in the art. For example, algorithm, parameters and criteria defined in Figure 10 may be used. Briefly, a polyA tail is

defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 20 nucleotides of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 nucleotides preceding the polyA tail are searched for the canonic polyadenylation AAUAAA signal allowing one mismatch to account for possible sequencing errors as well as known variation in the canonical sequence of the polyadenylation signal.

Functional features, e.g. ORFs and signal sequences, of the sequences of extended cDNAs are subsequently determined as follows. The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 80 amino acids are preferred. If extended cDNAs encoding secreted proteins are desired, each found ORF is then scanned for the presence of a signal peptide using the matrix method described in Example 13.

Sequences of extended cDNAs are then compared, on a nucleotidic or proteic basis, to public sequences available at the time of filing.

b) Selection of full-length cDNAs of interest

A negative selection may then be performed in order to eliminate unwanted cloned sequences resulting from either contaminants or PCR artifacts as follows. Sequences matching contaminant sequences such as vector DNA, tRNA, mtRNA, rRNA sequences are discarded as well as those encoding ORF sequences exhibiting extensive homology to repeats. Sequences obtained by direct cloning (section 1a) but lacking polyA tail may be discarded. Only ORFs ending either before the polyA tail (section 1a) or before the end of the cloned 3'UTR (section 1b) may be selected. If extended cDNAs encoding secreted proteins are desired, ORFs containing a signal peptide are considered. In addition, ORFs containing unlikely mature proteins such as mature proteins which size is less than 20 amino acids or less than 25% of the immature protein size may be eliminated.

Then, for each remaining full length cDNA containing several ORFs, a preselection of ORFs may be performed using the following criteria. The longest ORF is preferred. If extended cDNAs encoding secreted proteins are desired and if the ORF sizes are similar, the chosen ORF is the one which signal peptide has the highest score according to Von Heijne method.

Sequences of full length cDNA clones may then be compared pairwise after masking of the repeat sequences. Full-length cDNA sequences exhibiting extensive homology may be clustered in the same class. Each cluster may then be subjected to a cluster analysis that detects sequences resulting from internal priming or from alternative splicing, identical sequences or sequences with several frameshifts. A selection may be operated between clones belonging to the

same class in order to detect clones encoding homologous but distinct ORFs which may be both selected if they both contain sequences of interest.

Selection of full-length cDNA clones encoding sequences of interest may subsequently be performed using the following criteria. Structural parameters (initial tag, polyadenylation site and signal) are first checked. Then, homologies with known nucleic acids and proteins are examined in order to determine whether the clone sequence match a known nucleotide/protein sequence and, in the latter case, its covering rate and the date at which the sequence became public. If there is no extensive match with sequences other than ESTs or genomic DNA, or if the clone sequence brings substantial new information, such as encoding a protein resulting from alternative splicing of an mRNA coding for an already known protein, the sequence is kept. Examples of such cloned full-length cDNAs containing sequences of interest are described in Example 21. Sequences resulting from chimera or double inserts or located on chromosome breaking points as assessed by homology to other sequences may be discarded during this procedure.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences may be obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only part of the coding sequences. In the case of nucleic acids encoding secreted proteins, nucleic acids containing only the coding sequence for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides may be obtained.

Similarly, nucleic acids containing any other desired portion of the coding sequences for the encoded protein may be obtained. For example, the nucleic acid may contain at least 10, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 consecutive bases of an extended cDNA.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

In addition to PCR based methods for obtaining cDNAs which include the authentic 5' end of the corresponding mRNA as well as the complete protein coding sequence of the corresponding mRNA, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs or consensus contigated 5' ESTS were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs, 5' ESTs, or consensus contigated 5' ESTs. Example 20 below provides examples of such methods.

EXAMPLE 20

Methods for Obtaining Extended cDNAs which Include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA or Nucleic Acids Homologous to Extended cDNAs, 5' ESTs or Consensus Contigated 5' ESTs

A full-length cDNA library can be made using the strategies described in Example 7. Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art.

Such cDNA or genomic DNA libraries may be used to isolate extended cDNAs obtained from 5' ESTs or consensus contigated 5' ESTs or nucleic acids homologous to extended cDNAs, 5' ESTs, or consensus contigated 5' ESTs as follows. The cDNA library or genomic DNA library is hybridized to a detectable probe. The detectable probe may comprise at least 10, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 consecutive nucleotides of the 5' EST, consensus contigated 5' EST, or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual 2d Ed.*, Cold Spring Harbor Laboratory Press, 1989, the entire disclosure of which is incorporated herein by reference. The same techniques may be used to isolate genomic DNAs. Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. The detectable probe described in the preceding paragraph is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, *in vitro* transcription, and non radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify cDNAs or genomic DNAs which hybridize to the detectable probe, cDNAs or genomic DNAs having different levels of homology to the probe can be identified and isolated as described below.

1. Identification of cDNA or Genomic DNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log(Na^+)) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $T_m = 81.5 + 16.6(\log(Na^+)) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the T_m . Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

cDNAs or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

2. Obtaining cDNA or Genomic DNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify cDNAs or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain cDNAs or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be “moderate” conditions above 50°C and “low” conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be “moderate” conditions above 25% formamide and “low” conditions below 25% formamide. cDNAs or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology between the Obtained cDNAs or Genomic DNAs and 5'ESTs, Consensus Contigated 5'ESTs, or Extended cDNAs or Between the Polypeptides Encoded by the Obtained cDNAs or Genomic DNAs and the Polypeptides Encoded by the 5'ESTs, Consensus Contigated 5'ESTs, or Extended cDNAs

To determine the level of homology between the hybridized cDNA or genomic DNA and the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived are compared. The sequences of the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived and the sequences of the cDNA or genomic DNA which hybridized to the detectable probe may be stored on a computer readable medium as described below and compared to one another using any of a variety of algorithms familiar to those skilled in the art, those described below.

To determine the level of homology between the polypeptide encoded by the hybridizing cDNA or genomic DNA and the polypeptide encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived, the polypeptide sequence encoded by the hybridized nucleic acid and the polypeptide sequence encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived are compared. The sequences of the polypeptide encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which

the probe was derived and the polypeptide sequence encoded by the cDNA or genomic DNA which hybridized to the detectable probe may be stored on a computer readable medium as described below and compared to one another using any of a variety of algorithms familiar to those skilled in the art, those described below.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Thompson *et al.*, 1994, *Nucleic Acids Res.* 22(2):4673-4680; Higgins *et al.*, 1996, *Methods Enzymol.* 266:383-402; Altschul *et al.*, 1990, *J. Mol. Biol.* 215(3):403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272), the entire disclosures of which are incorporated herein by reference.

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1993, *Nature Genetics* 3:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res.* 25:3389-3402), the entire disclosures of which are incorporated herein by reference. In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by

means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science* 256:1443-1445; Henikoff and Henikoff, 1993, *Proteins* 17:49-61), the entire disclosures of which are incorporated herein by reference. Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation), the entire disclosure of which is incorporated herein by reference.

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2267-2268), the entire disclosure of which is incorporated herein by reference.

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some embodiments, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

In some embodiments, the level of homology between the hybridized nucleic acid and the extended cDNA, 5'EST, or 5' consensus contigated 5'EST from which the probe was derived may be determined using the FASTDB algorithm described in Brutlag *et al.* *Comp. App. Biosci.* 6:237-245, 1990, the entire disclosure of which is incorporated herein by reference. In such analyses the parameters may be selected as follows: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the sequence which hybridizes to the probe, whichever is shorter. Because the FASTDB program does not consider 5' or 3' truncations when calculating homology levels, if the sequence which hybridizes to the probe is truncated relative to the sequence of the extended cDNA, 5'EST, or consensus contigated 5'EST from which the probe was derived the homology level is manually adjusted by calculating the number of nucleotides of the extended cDNA, 5'EST, or consensus contigated 5' EST which are not matched or aligned with the hybridizing sequence, determining the percentage of total nucleotides of the hybridizing sequence which the non-matched or non-aligned nucleotides represent, and subtracting this percentage from the homology level. For example, if the hybridizing sequence is 700 nucleotides in length and the extended cDNA, 5'EST, or consensus contigated 5' EST sequence is 1000 nucleotides in length wherein the first 300 bases at the 5' end of the extended cDNA, 5'EST, or consensus contigated 5' EST are absent from the hybridizing sequence, and wherein the overlapping 700 nucleotides are identical, the homology level would be adjusted as follows. The

non-matched, non-aligned 300 bases represent 30% of the length of the extended cDNA, 5'EST, or consensus contigated 5' EST. If the overlapping 700 nucleotides are 100% identical, the adjusted homology level would be $100-30=70\%$ homology. It should be noted that the preceding adjustments are only made when the non-matched or non-aligned nucleotides are at the 5' or 3' ends. No adjustments are made if the non-matched or non-aligned sequences are internal or under any other conditions.

For example, using the above methods, nucleic acids having at least 95% nucleic acid homology, at least 96% nucleic acid homology, at least 97% nucleic acid homology, at least 98% nucleic acid homology, at least 99% nucleic acid homology, or more than 99% nucleic acid homology to the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived may be obtained and identified. Such nucleic acids may be allelic variants or related nucleic acids from other species. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived.

Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied, for example the default parameters used by the algorithms in the absence of instructions from the user, one can obtain nucleic acids encoding proteins having at least 99%, at least 98%, at least 97%, at least 96%, at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the protein encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived. In some embodiments, the homology levels can be determined using the "default" opening penalty and the "default" gap penalty, and a scoring matrix such as PAM 250 (a standard scoring matrix; see Dayhoff *et al.*, in: Atlas of Protein Sequence and Structure, Vol. 5, Supp. 3 (1978)), the entire disclosure of which is incorporated herein by reference.

Alternatively, the level of polypeptide homology may be determined using the FASTDB algorithm described by Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990, the entire disclosure of which is incorporated herein by reference. In such analyses the parameters may be selected as follows: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=Sequence Length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the homologous sequence, whichever is shorter. If the homologous amino acid sequence is shorter than the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST as a result of an N terminal and/or C terminal deletion the results may be manually corrected as follows. First, the number of amino acid residues of the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus

contiguated 5' EST which are not matched or aligned with the homologous sequence is determined. Then, the percentage of the length of the sequence encoded by the extended cDNA, 5'EST, or consensus contiguated 5' EST which the non-matched or non-aligned amino acids represent is calculated. This percentage is subtracted from the homology level. For example wherein the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contiguated 5' EST is 100 amino acids in length and the length of the homologous sequence is 80 amino acids and wherein the amino acid sequence encoded by the extended cDNA or 5'EST is truncated at the N terminal end with respect to the homologous sequence, the homology level is calculated as follows. In the preceding scenario there are 20 non-matched, non-aligned amino acids in the sequence encoded by the extended cDNA, 5'EST, or consensus contiguated 5' EST. This represents 20% of the length of the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contiguated 5' EST. If the remaining amino acids are 100% identical between the two sequences, the homology level would be $100\% - 20\% = 80\%$ homology. No adjustments are made if the non-matched or non-aligned sequences are internal or under any other conditions.

In addition to the above described methods, other protocols are available to obtain extended cDNAs using 5' ESTs or consensus contiguated 5'ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 24-811 and 1600-1622. Preferably, the primer comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides from the sequences of SEQ ID NOs 24-811 and 1600-1622. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 24-811 and 1600-1622. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequences of SEQ ID NOs. 24-811 and 1600-1622 with a primer comprising a complementary to a fragment of an EST-related nucleic acid hybridizing the primer to

the mRNAs, and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides of the sequences complementary to SEQ ID NOs. 24-811 and 1600-1622.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized.
5 The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral
10 vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA
15 are well known to those skilled in the art and are described in *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. 1997 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989.

Alternatively, other procedures may be used for obtaining full-length cDNAs or extended cDNAs. In one approach, full-length or extended cDNAs are prepared from mRNA and cloned
20 into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1 and an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993), the entire disclosure of which is incorporated herein by reference. A biotinylated oligonucleotide comprising the sequence of a fragment of an EST-related nucleic acid is hybridized to the single stranded phagemids.
25 Preferably, the fragment comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides of the sequences of SEQ ID NOs. 24-811 and 1600-1622.

Hybrids between the biotinylated oligonucleotide and phagemids are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992), the entire disclosure of which is
30 incorporated herein by reference. Thereafter, the resulting phagemids are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST or consensus contigated 5'EST sequence used to design the biotinylated oligonucleotide. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs or full length cDNAs containing the 5' EST or
35 consensus contigated 5'EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full-length protein coding sequences or portions of the protein coding sequences may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

5

EXAMPLE 21

Full Length cDNAs

The procedures described in Example 19 and 20 were used to obtain extended cDNAs or full length cDNAs derived from 5' ESTs in a variety of tissues. The following list provides a few

10 examples of cDNAs obtained by these means.

Using this procedure, the full length cDNA of SEQ ID NO:1 (internal identification number 58-34-2-E7-FL2) was obtained. This cDNA encodes the signal peptide MWWFQQGLSFLPSALVIWTS (SEQ ID NO:2) having a von Heijne score of 5.5.

Using this approach, the full length cDNA of SEQ ID NO:3 (internal identification number

15 48-19-3-G1-FL1) was obtained. This cDNA encodes the signal peptide MKKVLLITAILAVAVG (SEQ ID NO: 4) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:5 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:6) having a von Heijne score of 10.7.

Furthermore, the polypeptides encoded by the extended or full-length cDNAs may be

20 screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The results obtained for the polypeptides encoded by a few full-length cDNAs derived from 5'ESTs that were screened for the presence of known protein signatures and motifs using the

25 Proscan software from the GCG package and the Prosite 15.0 database are provided below.

The protein of SEQ ID NO: 8 encoded by the full-length cDNA SEQ ID NO: 7 (internal designation 78-8-3-E6-CL0_1C) and expressed in adult prostate belong to the phosphatidylethanolamine-binding protein from which it exhibits the characteristic PROSITE signature from positions 90 to 112. Proteins from this widespread family, from nematodes to

30 fly, yeast, rodent and primate species, bind hydrophobic ligands such as phospholipids and nucleotides. They are mostly expressed in brain and in testis and are thought to play a role in cell growth and/or maturation, in regulation of the sperm maturation, motility and in membrane remodeling. They may act either through signal transduction or through oxidoreduction reactions (for a review see Schoentgen and Jollès, *FEBS Letters*, 369:22-26 (1995), the entire

35 disclosure of which is incorporated herein by reference). Taken together, these data suggest that

the protein of SEQ ID NO: 8 may play a role in cell growth, maturation and in membrane remodeling and/or may be related to male fertility. Thus, these protein may be useful in diagnosing and/or treating cancer, neurodegenerative diseases, and/or disorders related to male fertility and sterility.

5 The protein of SEQ ID No. 10 encoded by the full-length cDNA SEQ ID NO. 9 (internal designation 108-013-5-O-H9-FLC) shows homologies with a family of lysophospholipases conserved among eukaryotes (yeast, rabbit, rodents and human). In addition, some members of this family exhibit a calcium-independent phospholipase A2 activity (Portilla *et al*, *J. Am. Soc. Nephro.*, **9** :1178-1186 (1998), the entire disclosure of which is incorporated herein by reference).
10 All members of this family exhibit the active site consensus GX SXG motif of carboxylesterases that is also found in the protein of SEQ ID NO. 10 (position 54 to 58). In addition, this protein may be a membrane protein with one transmembrane domain as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, **10** :685-686 (1994), the entire disclosure of which is incorporated herein by reference). Taken together, these data suggest that
15 the protein of SEQ ID NO:10 may play a role in fatty acid metabolism, probably as a phospholipase. Thus, this protein or part therein, may be useful in diagnosing and/or treating several disorders including, but not limited to, cancer, diabetes, and neurodegenerative disorders such as Parkinson's and Alzheimer's diseases. It may also be useful in modulating inflammatory responses to infectious agents and/or to suppress graft rejection.

20 The protein of SEQ ID NO: 12 encoded by the full-length cDNA SEQ ID NO: 11 (internal designation 108-004-5-0-D10-FLC) shows remote homology to a subfamily of beta4-galactosyltransferases widely conserved in animals (human, rodents, cow and chicken). Such enzymes, usually type II membrane proteins located in the endoplasmic reticulum or in the Golgi apparatus, catalyzes the biosynthesis of glycoproteins, glycolipid glycans and lactose.
25 Their characteristic features defined as those of subfamily A in Breton *et al*, *J. Biochem.*, **123**:1000-1009 (1998), the entire disclosure of which is incorporated herein by reference are pretty well conserved in the protein of SEQ ID NO: 12, especially the region I containing the DVD motif (positions 114-116) thought to be involved either in UDP binding or in the catalytic process itself. In addition, the protein of SEQ ID NO: 12 has the typical structure of a type II
30 protein. Indeed, it contains a short 28-amino-acid-long N-terminal tail, a transmembrane segment from positions 29 to 49 and a large 278-amino-acid-long C-terminal tail as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, **10** :685-686 (1994)). Taken together, these data suggest that the protein of SEQ ID NO: 12 may play a role in the biosynthesis of polysaccharides, and of the carbohydrate moieties of glycoproteins and
35 glycolipids and/or in cell-cell recognition. Thus, this protein may be useful in diagnosing

and/or treating several types of disorders including, but not limited to, cancer, atherosclerosis, cardiovascular disorders, autoimmune disorders and rheumatic diseases including rheumatoid arthritis.

The protein of SEQ ID NO: 14 encoded by the full-length cDNA SEQ ID NO: 13 (internal designation 108-009-5-0-A2-FLC) shows extensive homology to the bZIP family of transcription factors, and especially to the human protein (Lu *et al.*, *Mol. Cell. Biol.*, 17 :5117-5126 (1997), the entire disclosure of which is incorporated herein by reference). The match include the whole bZIP domain composed of a basic DNA-binding domain and of a leucine zipper allowing protein dimerization. The basic domain is conserved in the protein of SEQ ID NO: 14 as shown by the characteristic PROSITE signature (positions 224-237) except for a conservative substitution of a glutamic acid with an aspartic acid in position 233. The typical PROSITE signature for leucine zipper is also present (positions 259 to 280). Taken together, these data suggest that the protein of SEQ ID NO: 14 may bind to DNA, hence regulating gene expression as a transcription factor. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the insertion. The PCR product which corresponds to the cDNA insert can then be manipulated using standard cloning techniques familiar to those skilled in the art.

V. Expression of Proteins or Polypeptides Encoded by EST-related nucleic acids or Fragments thereof

EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, and fragments of positional segments of EST-related nucleic acids may be used to express the polypeptides which they encode. In particular, they may be used to express EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In some

embodiments, the EST-related nucleic acids, positional segments of EST-related nucleic acids, and fragments of positional segments of EST-related nucleic acids may be used to express the full polypeptide (*i.e.* the signal peptide and the mature polypeptide) of a secreted protein, the mature protein (*i.e.* the polypeptide generated after cleavage of the signal peptide), or the signal peptide of a secreted protein. If desired, nucleic acids encoding the signal peptide may be used to facilitate secretion of the expressed protein. It will be appreciated that a plurality of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 22

Expression of the Proteins Encoded by the Genes Corresponding to the 5'ESTs or Consensus Contigated 5' ESTs

To express their encoded proteins, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are cloned into a suitable expression vector. In some instances, nucleic acids encoding EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides may be cloned into a suitable expression vector.

In some embodiments, the nucleic acids inserted into the expression vector may comprise the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 24-811. In other embodiments, the nucleic acids inserted into the expression vector may comprise may comprise the full coding sequence (*i.e.* the nucleotides encoding the signal peptide and the mature polypeptide) of one of SEQ ID Nos. 766-792. In some embodiments, the nucleic acid inserted into the expression vector may comprise the nucleotides of one of the sequences of SEQ ID Nos. 766-792 which encode the mature polypeptide (*i.e.* the nucleotides encoding the polypeptide generated after cleavage of the signal peptide). In further embodiments, the nucleic acids inserted into the expression vector may comprise the nucleotides of 24-728 and 766-792 which encode the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid inserted into the expression vector may encode a polypeptide comprising the one of the sequences of SEQ ID Nos. 812-1599. In some embodiments, the nucleic acid

inserted into the expression vector may encode the full polypeptide sequence (*i.e.* the signal peptide and the mature polypeptide) included in one of SEQ ID Nos. 1554-1580. In other embodiments, the nucleic acid inserted into the expression vector may encode the mature polypeptide (*i.e.* the polypeptide generated after cleavage of the signal peptide) included in one of the sequences of SEQ ID Nos. 1554-1580. In further embodiments, the nucleic acids inserted into the expression vector may encode the signal peptide included in one of the sequences of 812-1516 and 1554-1580.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767, the entire disclosure of which is incorporated herein by reference.

The following is provided as one exemplary method to express the proteins encoded by the nucleic acids described above. In some instances the nucleic acid encoding the protein or polypeptide to be expressed includes a methionine initiation codon and a polyA signal. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the nucleic acid encoding the protein or polypeptide to be expressed lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the polyA signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The nucleic acid encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the nucleic acid encoding the protein or polypeptide to be expressed and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of 3' primer, taking care to ensure that the nucleic acid encoding the protein or polypeptide to be expressed is correctly positioned with respect to the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended

with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 µg/ml G418 (Sigma, St. Louis, Missouri).

Alternatively, the nucleic acid encoding the protein or polypeptide to be expressed may be cloned into pED6dpc2. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. The expressed protein or polypeptide may be isolated, purified, or enriched as described above.

To confirm expression of the desired protein or polypeptide, the proteins or polypeptides produced by cells containing a vector with a nucleic acid insert encoding the protein or polypeptide are compared to those lacking such an insert. The expressed proteins are detected using techniques familiar to those skilled in the art such as Coomassie blue or silver staining or using antibodies against the protein or polypeptide encoded by the nucleic acid insert. Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate nucleic acid. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the nucleic acid.

If the proteins or polypeptides encoded by the nucleic acid inserts are secreted, medium prepared from the host cells or organisms containing an expression vector which contains a nucleic acid insert encoding the desired protein or polypeptide is compared to medium prepared from the control cells or organism. The presence of a band in medium from the cells containing the nucleic acid insert which is absent from preparations from the control cells indicates that the protein or polypeptide encoded by the nucleic acid insert is being expressed and secreted. Generally, the band corresponding to the protein encoded by the nucleic acid insert will have a mobility near that expected based on the number of amino acids in the open reading frame of the nucleic acid insert. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected

for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The expressed protein or polypeptide may be purified, isolated or enriched using a variety of methods. In some methods, the protein or polypeptide may be secreted into the culture medium via a native signal peptide or a heterologous signal peptide operably linked thereto. In some methods, the protein or polypeptide may be linked to a heterologous polypeptide which facilitates its isolation, purification, or enrichment such as a nickel binding polypeptide. The protein or polypeptide may also be obtained by gel electrophoresis, ion exchange chromatography, size chromatography, hplc, salt precipitation, immunoprecipitation, a combination of any of the preceding methods, or any of the isolation, purification, or enrichment techniques familiar to those skilled in the art.

The protein encoded by the nucleic acid insert may also be purified using standard immunochromatography techniques using immunoaffinity chromatography with antibodies directed against the encoded protein or polypeptide as described in more detail below. If antibody production is not possible, the nucleic acid insert encoding the desired protein or polypeptide may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies, the coding sequence of the nucleic acid insert is ligated in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β -globin or a nickel binding polypeptide. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β -globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, (*Basic Methods in Molecular Biology*, L.G. Davis, M.D. Digner, and J.F. Battey, ed., Elsevier Press, NY, 1986), the entire disclosure of which is incorporated herein by reference, and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro* translation systems such as the *In vitro Express*TM Translation Kit (Stratagene).

Following expression and purification of the proteins or polypeptides encoded by the nucleic acid inserts, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 23 below. It will be appreciated that a plurality of proteins expressed from these nucleic acid inserts may be included in a panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 23

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, fragments of positional segments of EST-related nucleic acids, nucleic acids encoding the EST-related polypeptides, nucleic acids encoding fragments of the EST-related polypeptides, nucleic acids encoding positional segments of EST-related polypeptides, or nucleic acids encoding fragments of positional segments of EST-related polypeptides are cloned into expression vectors such as those described in Example 22. The encoded proteins or polypeptides are purified, isolated, or enriched as described above. Following purification, isolation, or enrichment, the proteins or polypeptides are labeled using techniques known to those skilled in the art. The labeled proteins or polypeptides are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound proteins or polypeptides. The specifically bound labeled proteins or polypeptides are detected by autoradiography. Alternatively, unlabeled proteins or polypeptides may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein or polypeptide are incubated along with the labeled protein or polypeptide. The amount of labeled protein or polypeptide bound to the cell surface decreases as the amount of competitive unlabeled protein or polypeptide increases. As a control, various amounts of an unlabeled protein or polypeptide unrelated to the labeled protein or polypeptide is included in some binding reactions. The amount of labeled protein or polypeptide bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein or polypeptide encoded by the nucleic acid binds specifically to the cell surface.

As discussed above, human proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The human

proteins or polypeptides made as described above may be evaluated to determine their physiological activities as described below.

EXAMPLE 24

Assaying the Expressed Proteins or Polypeptides for Cytokine,

Cell Proliferation or Cell Differentiation Activity

As discussed above, some human proteins act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein or polypeptide of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M⁺ (preB M⁺), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins or polypeptides prepared as described above may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references: *Current Protocols in Immunology*, Ed. by J.E. Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al. J. Immunol.* **137**:3494-3500, 1986., Bertagnolli *et al. J. Immunol.* **145**:1706-1712, 1990., Bertagnolli *et al., Cellular Immunology* **133**:327-341, 1991. Bertagnolli, *et al. J. Immunol.* **149**:3778-3783, 1992; and Bowman *et al., J. Immunol.* **152**:1756-1761, 1994, the entire disclosures of which are incorporated herein by reference.

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology*. J.E. Coligan *et al.* Eds., **1**:3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Schreiber, R.D. In *Current Protocols in Immunology.*, *supra* **1** : 6.8.1-6.8.8, the entire disclosures of which are incorporated herein by reference

The proteins or polypeptides prepared as described above may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references: Bottomly *et al.*, In *Current Protocols in Immunology.*, *supra* **1** : 6.3.1-6.3.12.; deVries *et al., J. Exp. Med.* **173**:1205-1211, 1991; Moreau *et al., Nature* **36**:690-692, 1988; Greenberger *et al., Proc. Natl. Acad. Sci. U.S.A.* **80**:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology.*, *supra* **1** : 6.6.1-6.6.5; Smith *et al., Proc. Natl. Acad. Sci. U.S.A.* **83**:1857-1861, 1986; Bennett *et al* in *Current Protocols in Immunology supra* **1** : 6.15.1; and

Ciarletta *et al* In *Current Protocols in Immunology. supra* 1 : 6.13.1, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides prepared as described above may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references: Chapter 3 (*In vitro* Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in *Current Protocols in Immunology supra*; Weinberger *et al.*, *Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur. J. Immun.* 11:405-411, 1981; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; and Takai *et al.*, *J. Immunol.* 140:508-512, 1988, the entire disclosure of which is incorporated herein by reference.

Those proteins or polypeptides which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, nucleic acids encoding these proteins or polypeptides or nucleic acids regulating the expression of these proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

EXAMPLE 25

Assaying the Expressed Proteins or Polypeptides

for Activity as Immune System Regulators

The proteins or polypeptides prepared as described above may also be evaluated for their effects as immune regulators. For example, the proteins or polypeptides may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references: Chapter 3 (*In vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in Immunology*, J.E. Coligan *et al.* Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann *et al.*, *J. Immunol.* 128:1968-1974, 1982; Handa *et al.*, *J. Immunol.* 135:1564-1572, 1985; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988; Bowman *et al.*, *J. Virology* 61:1992-1998; Bertagnolli *et al.* *Cell. Immunol.* 133:327-341, 1991; and Brown *et al.*, *J. Immunol.* 153:3079-3092, 1994, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides prepared as described above may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the

following references: Maliszewski, *J. Immunol.* **144**:3028-3033, 1990, the entire disclosure of which is incorporated herein by reference; and Mond *et al.* in *Current Protocols in Immunology*, **1** : 3.8.1-3.8.16, *supra*.

The proteins or polypeptides prepared as described above may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 3 (*In vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in *Current Protocols in Immunology*, *supra*; Takai *et al.*, *J. Immunol.* **137**:3494-3500, 1986; Takai *et al.*, *J. Immunol.* **140**:508-512, 1988; and Bertagnolli *et al.*, *J. Immunol.* **149**:3778-3783, 1992, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides prepared as described above may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Guery *et al.*, *J. Immunol.* **134**:536-544, 1995; Inaba *et al.*, *J. Exp. Med.* **173**:549-559, 1991; Macatonia *et al.*, *J. Immunol.* **154**:5071-5079, 1995; Porgador *et al.* *J. Exp. Med.* **182**:255-260, 1995; Nair *et al.*, *J. Virol.* **67**:4062-4069, 1993; Huang *et al.*, *Science* **264**:961-965, 1994; Macatonia *et al.* *J. Exp. Med.* **169**:1255-1264, 1989; Bhardwaj *et al.*, *Journal of Clinical Investigation* **94**:797-807, 1994; and Inaba *et al.*, *J. Exp. Med.* **172**:631-640, 1990, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides prepared as described above may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Darzynkiewicz *et al.*, *Cytometry* **13**:795-808, 1992; Gorczyca *et al.*, *Leukemia* **7**:659-670, 1993; Gorczyca *et al.*, *Cancer Res.* **53**:1945-1951, 1993; Itoh *et al.*, *Cell* **66**:233-243, 1991; Zacharchuk, *J. Immunol.* **145**:4037-4045, 1990; Zamai *et al.*, *Cytometry* **14**:891-897, 1993; and Gorczyca *et al.*, *Int. J. Oncol.* **1**:639-648, 1992, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides prepared as described above may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references: Antica *et al.*, *Blood* **84**:111-117, 1994; Fine *et al.*, *Cell. Immunol.* **155**:111-122, 1994; Galy *et al.*, *Blood* **85**:2770-2778, 1995; and Toki *et al.*, *Proc. Nat. Acad. Sci. USA* **88**:7548-7551, 1991, the entire disclosures of which are incorporated herein by reference.

Those proteins or polypeptides which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation

of immune activity is beneficial. For example, the protein or polypeptide may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations.

5 These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using the protein or polypeptide including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plamodium. and various fungal infections such as candidiasis. Of course, in this

10 regard, a protein or polypeptide may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Alternatively, the proteins or polypeptides prepared as described above may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

15 inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein or polypeptide may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation),

20 may also be treatable using the protein or polypeptide.

Using the proteins or polypeptides of the invention it may also be possible to regulate immune responses either up or down. Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by

25 inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be demonstrated by the

30 lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function

35 should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants,

rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* **257**:789-792 (1992) and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, **89**:11102-11105 (1992), the entire disclosures of which are incorporated herein by reference. In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847, the entire disclosure of which is incorporated herein by reference) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples

include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/pr/pr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856, the entire disclosure of which is incorporated herein by reference).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, antiviral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing the proteins or polypeptides described above or together with a stimulatory form of the protein or polypeptide and reintroducing the *in vitro* primed T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with one of the above-described nucleic acids encoding a protein or polypeptide can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the protein or polypeptide encoded by the nucleic acids described above having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain and β_2

microglobulin or an MHC class II α chain and an MHC class II β chain to thereby express MHC class I or MHC class II proteins on the cell surface, respectively. Expression of the appropriate MHC class I or class II molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a nucleic acid encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a protein or polypeptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, nucleic acids encoding these immune system regulator proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 26

Assaying the Expressed Proteins or Polypeptides for Hematopoiesis Regulating Activity

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins or polypeptides on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Johansson *et al.*, *Cell. Biol.* **15**:141-151, 1995; Keller *et al.*, *Mol. Cell. Biol.* **13**:473-486, 1993; and McClanahan *et al.*, *Blood* **81**:2903-2915, 1993, the entire disclosures of which are incorporated herein by reference.

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Freshney, M.G. Methylcellulose Colony Forming Assays, in Culture of Hematopoietic Cells. R.I. Freshney, *et al.* Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al.*, *Proc. Natl. Acad. Sci. USA* **89**:5907-5911, 1992; McNiece, I.K. and Briddell, R.A. Primitive Hematopoietic Colony Forming Cells with High Proliferative Potential, in Culture of Hematopoietic Cells. *supra*; Neben *et al.*, *Experimental Hematology* **22**:353-359, 1994; Ploemacher, R.E. Cobblestone Area Forming Cell Assay, In Culture of Hematopoietic Cells. *supra*; Spooncer, E., Dexter, M. and Allen, T. Long Term Bone Marrow Cultures in the Presence of Stromal Cells, in Culture of Hematopoietic Cells *supra*; and Sutherland, H.J. Long Term Culture

Initiating Cell Assay, in Culture of Hematopoietic Cells. *supra*, the entire disclosure of which is incorporated herein by reference.

Those proteins or polypeptides which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoiesis is beneficial. For example, a protein or polypeptide of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, nucleic acids encoding these proteins or polypeptides or nucleic acids regulating the expression of these proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 27

Assaying the Expressed Proteins or Polypeptides for Regulation of Tissue Growth

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No.

WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491, the entire disclosures of which are incorporated herein by reference.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112 (Maibach, H1 and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978), the entire disclosure of which is incorporated herein by reference.

Those proteins or polypeptides which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein or polypeptide may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein or polypeptide encoded by the nucleic acids described above which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein or polypeptide of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein or polypeptide of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the proteins or polypeptides encoded by the nucleic acids described above is tendon/ligament formation. A protein or polypeptide encoded by the nucleic acids described above, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or

other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a protein or polypeptide of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The proteins or polypeptides of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return *in vivo* to effect tissue repair. The proteins or polypeptides of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The therapeutic compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The proteins or polypeptides of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein or polypeptide may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein or polypeptide of the invention.

Proteins or polypeptides of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein or polypeptide of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein or polypeptide of the invention may also exhibit angiogenic activity.

A protein or polypeptide of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein or polypeptide of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, nucleic acids encoding tissue growth regulating activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 28

Assaying the Expressed Proteins or Polypeptides for Regulation of Reproductive Hormones

The proteins or polypeptides of the present invention may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Vale *et al.*, *Endocrinol.* **91**:562-572, 1972; Ling *et al.*, *Nature* **321**:779-782, 1986; Vale *et al.*, *Nature* **321**:776-779, 1986; Mason *et al.*, *Nature* **318**:659-663, 1985; Forage *et al.*, *Proc. Natl. Acad. Sci. USA* **83**:3091-3095, 1986. Chapter 6.12 in *Current Protocols in Immunology*, J.E. Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Taub *et al.* *J. Clin. Invest.* **95**:1370-1376, 1995; Lind *et al.* *APMIS* **103**:140-146, 1995; Muller *et al.* *Eur. J. Immunol.* **25**:1744-1748; Gruber *et al.* *J. Immunol.* **152**:5860-5867, 1994; and Johnston *et al.*, *J. Immunol.* **153**:1762-1768, 1994, the entire disclosures of which are incorporated herein by reference.

Those proteins or polypeptides which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of reproductive hormones are beneficial. For example, a protein or polypeptide may exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of FSH. Thus, a protein or polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein or polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful

as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein or polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, nucleic acids encoding reproductive hormone regulating activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

EXAMPLE 29

Assaying the Expressed Proteins or Polypeptides For Chemotactic/Chemokinetic Activity

The proteins or polypeptides of the present invention may also be evaluated for chemotactic/chemokinetic activity. For example, a protein or polypeptide of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins or polypeptides can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins or polypeptides provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or polypeptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or polypeptide has the ability to directly stimulate directed movement of cells. Whether a particular protein or polypeptide has chemotactic activity for a population of cells can be readily determined by employing such protein or polypeptide in any known assay for cell chemotaxis.

The activity of a protein or polypeptide of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins or polypeptides that induce or prevent chemotaxis) consist of assays that measure the ability of a protein or polypeptide to induce the migration of cells across a membrane as well as the ability of a protein or polypeptide to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by

J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience, Chapter 6.12: 6.12.1-6.12.28; Taub *et al. J. Clin. Invest.* **95**:1370-1376, 1995; Lind *et al. APMIS* **103**:140-146, 1995; Mueller *et al., Eur. J. Immunol.* **25**:1744-1748; Gruber *et al. J. Immunol.* **152**:5860-5867, 1994; and Johnston *et al. J. Immunol.*, **153**:1762-1768, 1994, the entire disclosures of which are incorporated herein by reference.

EXAMPLE 30

Assaying the Expressed Proteins or Polypeptides for Regulation of Blood Clotting

The proteins or polypeptides of the present invention may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Linet *et al., J. Clin. Pharmacol.* **26**:131-140, 1986; Burdick *et al., Thrombosis Res.* **45**:413-419, 1987; Humphrey *et al., Fibrinolysis* **5**:71-79 (1991); and Schaub, *Prostaglandins* **35**:467-474, 1988, the entire disclosures of which are incorporated herein by reference.

Those proteins or polypeptides which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein or polypeptide of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein or polypeptide is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein or polypeptide of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in more detail below, nucleic acids encoding blood clotting activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

EXAMPLE 31

Assaying the Expressed Proteins or Polypeptides for Involvement in Receptor/Ligand Interactions

The proteins or polypeptides of the present invention may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 7.7.28.1-7.28.22) in *Current Protocols in Immunology*, J.E. Coligan *et al.* Eds. Greene Publishing

Associates and Wiley-Interscience; Takai *et al.*, *Proc. Natl. Acad. Sci. USA* **84**:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* **168**:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* **169**:149-160, 1989; Stoltenborg *et al.*, *J. Immunol. Methods* **175**:59-68, 1994; Stitt *et al.*, *Cell* **80**:661-670, 1995; and Gyuris *et al.*, *Cell* **75**:791-803, 1993, the entire disclosures of which are incorporated herein by reference.

For example, the proteins or polypeptides of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein or polypeptide of the present invention (including, without limitation, fragments of receptors and ligands) may be useful as inhibitors of receptor/ligand interactions. Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides involved in receptor/ligand interactions or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

EXAMPLE 32

Assaying the Proteins or Polypeptides for Anti-Inflammatory Activity

The proteins or polypeptides of the present invention may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins or polypeptides exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins or polypeptides of the invention may also be useful to treat anaphylaxis and

hypersensitivity to an antigenic substance or material. Alternatively, as described in more detail below, nucleic acids encoding anti-inflammatory activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

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EXAMPLE 33

Assaying the Expressed Proteins or Polypeptides for Tumor Inhibition Activity

10 The proteins or polypeptides of the present invention may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein or polypeptide of the invention may exhibit other anti-tumor activities. A protein or polypeptide may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein or polypeptide may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth. . Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides with tumor inhibition activity or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

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25 A protein or polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative

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disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

EXAMPLE 34

Identification of Proteins or Polypeptides which Interact with Proteins or Polypeptides of the Present Invention

Proteins or polypeptides which interact with the proteins or polypeptides of the present invention, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the kit, nucleic acids encoding the proteins or polypeptides of the present invention, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins or polypeptides which might interact with the proteins or polypeptides of the present invention are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins or polypeptides which interact with the proteins or polypeptides of the present invention.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* **283**: 83-99 (1997), the entire disclosure of which is incorporated herein by reference, may be used for identifying molecules which interact with the proteins or polypeptides of the present invention. In such systems, *in vitro* transcription reactions are performed on a pool of vectors containing nucleic acid inserts which encode the proteins or polypeptides of the present invention. The nucleic acid inserts are cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a desired activity or for interaction with a known protein or polypeptide.

Proteins, polypeptides or other molecules interacting with proteins or polypeptides of the present invention can be found by a variety of additional techniques. In one method, affinity columns containing the protein or polypeptide of the present invention can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein or polypeptide of the present invention is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Molecules interacting with the protein or polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al. Electrophoresis*, **18**, 588-598 (1997). Alternatively, the molecules retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Molecules interacting with the proteins or polypeptides of the present invention can also be screened by using an Optical Biosensor as described in Edwards & Leatherbarrow, *Analytical Biochemistry*, **246**, 1-6 (1997), the entire disclosure of which is incorporated herein by reference. The main advantage of the method is that it allows the determination of the association rate between the protein or polypeptide and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethyl dextran matrix) and a sample of test molecules is placed in contact with the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extends a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the proteins or polypeptides of the present invention and the test sample can be a collection of proteins, polypeptides or other molecules extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test molecules are extracted can originate from any species.

In other methods, a target protein or polypeptide is immobilized and the test population is a collection of unique proteins or polypeptides of the present invention.

To study the interaction of the proteins or polypeptides of the present invention with drugs, the microdialysis coupled to HPLC method described by Wang *et al.*, *Chromatographia*,

44, 205-208(1997) or the affinity capillary electrophoresis method described by Busch *et al.*, *J. Chromatogr.* 777:311-328 (1997), the entire disclosures of which are incorporated herein by reference, can be used.

5 The system described in U.S. Patent No. 5,654,150 may also be used to identify molecules which interact with the proteins or polypeptides of the present invention. In this system, pools of nucleic acids encoding the proteins or polypeptides of the present invention are transcribed and translated *in vitro* and the reaction products are assayed for interaction with a known polypeptide or antibody.

10 It will be appreciated by those skilled in the art that the proteins or polypeptides of the present invention may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins or polypeptides may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins or polypeptides may be useful as nutritional agents or cosmetic agents.

15 The proteins or polypeptides of the present invention may be used to generate antibodies capable of specifically binding to the proteins or polypeptides of the present invention. The antibodies may be monoclonal antibodies or polyclonal antibodies. As used herein, "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where a binding domain is formed from the folding of variable
20 domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an antigenic determinant of an antigen., which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as wells as fragments, including Fab, Fab', F(ab)₂, and F(ab')₂ fragments.

25 As used herein, an "antigenic determinant" is the portion of an antigen molecule, that determines the specificity of the antigen-antibody reaction. An "epitope" refers to an antigenic determinant of a polypeptide. An epitope can comprise as few as 3 amino acids in a spatial conformation which is unique to the epitope. Generally an epitope consists of at least 6 such amino acids, and more usually at least 8-10 such amino acids. Methods for determining the
30 amino acids which make up an epitope include x-ray crystallography, 2-dimensional nuclear magnetic resonance, and epitope mapping e.g. the Pepscan method described by H. Mario Geysen *et al.* 1984. Proc. Natl. Acad. Sci. U.S.A. 81:3998-4002; PCT Publication No. WO 84/03564; and PCT Publication No. WO 84/03506, the entire disclosures of which are incorporated herein by reference.

In some embodiments, the antibodies may be capable of specifically binding to a protein or polypeptide encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In some embodiments, the antibody may be capable of binding an antigenic determinant or an epitope in a protein or polypeptide encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

In other embodiments, the antibodies may be capable of specifically binding to an EST-related polypeptide, fragment of an EST-related polypeptide, positional segment of an EST-related polypeptide or fragment of a positional segment of an EST-related polypeptide. In some embodiments, the antibody may be capable of binding an antigenic determinant or an epitope in an EST-related polypeptide, fragment of an EST-related polypeptide, positional segment of an EST-related polypeptide or fragment of a positional segment of an EST-related polypeptide.

In the case of secreted proteins, the antibodies may be capable of binding a full-length protein encoded by a nucleic acid of the present invention, a mature protein (*i.e.* the protein generated by cleavage of the signal peptide) encoded by a nucleic acid of the present invention, or a signal peptide encoded by a nucleic acid of the present invention.

EXAMPLE 35

Production of an Antibody to a Human Polypeptide or Protein

The above described EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or nucleic acids encoding EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides are operably linked to promoters and introduced into cells as described above.

In the case of secreted proteins, nucleic acids encoding the full protein (*i.e.* the mature protein and the signal peptide), nucleic acids encoding the mature protein (*i.e.* the protein generated by cleavage of the signal peptide), or nucleic acids encoding the signal peptide are operably linked to promoters and introduced into cells as described above.

The encoded proteins or polypeptides are then substantially purified or isolated as described above. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few $\mu\text{g/ml}$. Monoclonal or polyclonal antibody to the protein or polypeptide can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the proteins or polypeptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* **256**:495 (1975), the entire disclosure of which is incorporated herein by reference, or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as Elisa, as originally described by Engvall, *Meth. Enzymol.* **70**:419 (1980), the entire disclosure of which is incorporated herein by reference. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* in *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2, the entire disclosure of which is incorporated herein by reference.

2. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein or polypeptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis. *et al.* *J. Clin. Endocrinol. Metab.* **33**:988-991 (1971), the entire disclosure of which is incorporated herein by reference.

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al.*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973), the entire disclosure of which is incorporated herein by reference. Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by

Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980), the entire disclosure of which is incorporated herein by reference.

Antibody preparations prepared according to either of the above protocols are useful in a variety of contexts. In particular, the antibodies may be used in immunoaffinity chromatography techniques such as those described below to facilitate large scale isolation, purification, or enrichment of the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or for the isolation, purification or enrichment of EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

In the case of secreted proteins, the antibodies may be used for the isolation, purification, or enrichment of the full protein (*i.e.* the mature protein and the signal peptide), the mature protein (*i.e.* the protein generated by cleavage of the signal peptide), or the signal peptide are operably linked to promoters and introduced into cells as described above.

Additionally, the antibodies may be used in immunoaffinity chromatography techniques such as those described below to isolate, purify, or enrich polypeptides which have been linked to the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or to isolate, purify, or enrich EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

The antibodies may also be used to determine the cellular localization of polypeptides encoded by the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the cellular localization of EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

In addition, the antibodies may also be used to determine the cellular localization of polypeptides which have been linked to the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or polypeptides which have been linked to EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

The antibodies may also be used in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they may also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample or to identify the type of tissue present in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

VI. Use of 5'ESTs or Consensus Contigated 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids, may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

1. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in isolation, diagnostic and forensic procedures

EXAMPLE 36

Preparation of PCR Primers and Amplification of DNA

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. In some embodiments, the PCR primers at least 10, 15, 18, 20, 23, 25, 28, 30, 40, or 50 nucleotides in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa 1997, the entire disclosure of which is incorporated herein by reference. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample

along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 37

Use of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids as probes

Probes derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 20 above.

PCR primers made as described in Example 36 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 38-42 below. Such analyses may utilize detectable probes or primers based on the sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

EXAMPLE 38

Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is then utilized in accordance with Example 36 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 39

Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 34. Each of these DNA segments is sequenced, using the methods set forth in Example 36. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 40

Southern Blot Forensic Identification

The procedure of Example 38 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one

or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65), the entire disclosure of which is incorporated herein by reference.

A panel of probes based on the sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*, supra). Preferably, the probe is at least 10, 12, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 nucleotides in length. Preferably, the probes are at least 10, 12, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 nucleotides in length. In some embodiments, the probes are oligonucleotides which are 40 nucleotides in length or less.

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 41

Dot Blot Identification Procedure

Another technique for identifying individuals using the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Probes are prepared that correspond to at least 10, preferably 50 sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P³² using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic

sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis *et al.*, *supra*). The ^{32}P labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al.*, *Proc. Natl. Acad. Sci. USA* **82**(6):1585-1588 (1985), the entire disclosure of which is incorporated herein by reference). A unique pattern of dots distinguishes one individual from another individual.

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids can be used as probes in the following alternative fingerprinting technique. In some embodiments, the probes are oligonucleotides which are 40 nucleotides in length or less.

Preferably, a plurality of probes having sequences from different EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are used in the alternative fingerprinting technique. Example 42 below provides a representative alternative fingerprinting procedure in which the probes are derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

EXAMPLE 42

Alternative "Fingerprint" Identification Technique

Oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids using commercially available oligonucleotide services such as Genset, Paris, France. Preferably, the oligonucleotides are at least 10, 15, 18, 20, 23, 25, 28, or 30 nucleotides in length. However, in some embodiments, the oligonucleotides may be more than 40, 50, 60 or 70 nucleotides in length.

Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with P^{32} . The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes.

Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

5 In addition to their applications in forensics and identification, EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be mapped to their chromosomal locations. Example 41 below describes radiation hybrid (RH) mapping of human chromosomal regions using EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Example 42 below describes a representative procedure for mapping EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to their locations on human chromosomes. Example 43 below describes mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH).

2. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in Chromosome Mapping

EXAMPLE 43

Radiation hybrid mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to the human genome

20 Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human genome. This technique is described by Benham *et al.* (*Genomics* 4:509-517, 1989) and Cox *et al.*, (*Science* 250:245-250, 1990), the entire disclosures of which are incorporated herein by reference. The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using

conventional ESTs (Schuler *et al.*, *Science* **274**:540-546, 1996), the entire disclosure of which is incorporated herein by reference.

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) (Foster *et al.*, *Genomics* **33**:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* **4**:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* **29**:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* **14**:574-584, 1992) and 13 loci on the long arm of chromosome 5 (Warrington *et al.*, *Genomics* **11**:701-708, 1991), the entire disclosures of which are incorporated herein by reference.

EXAMPLE 44

Mapping of EST-related nucleic acids, positional segments of

EST-related nucleic acids or fragments of positional segments of

EST-related nucleic acids to Human Chromosomes using PCR techniques

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich. in PCR Technology; Principles and Applications for DNA Amplification. 1992. W.H. Freeman and Co., New York, the entire disclosure of which is incorporated herein by reference.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 μ Cu of a ³²P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the 5'EST from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation)

and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given 5'EST. DNA is isolated from the somatic hybrids and used as starting templates for PCR_reactions using the primer pairs from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids will yield an amplified fragment. The 5'ESTs are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. For a review of techniques and analysis of results from somatic cell gene mapping experiments. (See Ledbetter *et al.*, Genomics 6:475-481 (1990), the entire disclosure of which is incorporated herein by reference).

Alternatively, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be mapped to individual chromosomes using FISH as described in Example 45 below.

EXAMPLE 45

Mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Chromosomes Using

Fluorescence In Situ Hybridization

Fluorescence in situ hybridization allows the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are obtained by FISH as described by Cherif *et al.* (*Proc. Natl. Acad. Sci. U.S.A.*, **87**:6639-6643, 1990, the entire disclosure of which is incorporated herein by reference). Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell

donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μ M) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1 μ g/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μ g/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 μ g/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be localized to a particular cytogenetic R-band on a given chromosome.

Once the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids have been assigned to particular chromosomes using the techniques described in Examples 42-44 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 46

Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are obtained. This approach is described in Ramaiah Nagaraja *et al.*, *Genome Research* 7:210-222, March 1997, the entire disclosure of which is incorporated herein by reference. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids whose position is to be determined. Once an insert has been found which includes the 5'EST, the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be obtained.

As described in Example 47 below EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

3. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids Gene Identification

EXAMPLE 47

Identification of genes associated with hereditary diseases or drug response

This example illustrates an approach useful for the association of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with particular phenotypic characteristics. In this example, a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is used as a test probe to associate that EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with a particular phenotypic characteristic.

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are mapped to a particular location on a human chromosome using techniques such as those described in Examples 41 and 42 or other techniques known in the art. A search of Mendelian Inheritance in Man (V. McKusick, *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to be a very gene rich region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids thus becomes an immediate candidate for each of these genetic diseases.

Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are used to screen genomic DNA, mRNA or cDNA obtained from the patients. EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be responsible for the genetic disease.

VII. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Construct Vectors

The present EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 48 below.

1. Construction of secretion vectors

EXAMPLE 48

Construction of Secretion Vectors

The secretion vectors of the present invention include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from one of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. Preferably, the signal sequence is from one of the nucleic acids of SEQ ID NOs. 24-811. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Preferably, the secretion vector is maintained in multiple copies in each host cell. As used herein, multiple copies means at least 2, 5, 10, 20, 25, 50 or more than 50 copies per cell. In some embodiments, the multiple copies are maintained

extrachromosomally. In other embodiments, the multiple copies result from amplification of a chromosomal sequence.

Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunoaffinitychromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

EXAMPLE 49

Fusion Vectors

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to construct fusion vectors for the expression of chimeric polypeptides. The chimeric polypeptides comprise a first polypeptide portion and a second polypeptide portion. In the fusion vectors of the present invention, nucleic acids encoding the first polypeptide portion and the second polypeptide portion are joined in frame with one another so as to generate a nucleic acid encoding the chimeric polypeptide. The nucleic acid encoding the chimeric polypeptide is operably linked to a promoter

which directs the expression of an mRNA encoding the chimeric polypeptide. The promoter may be in any of the expression vectors described herein including those described in Examples 21 and 48.

Preferably, the fusion vector is maintained in multiple copies in each host cell. In some embodiments, the multiple copies are maintained extrachromosomally. In other embodiments, the multiple copies result from amplification of a chromosomal sequence.

The first polypeptide portion may comprise any of the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In some embodiments, the first polypeptide portion may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides.

The second polypeptide portion may comprise any polypeptide of interest. In some embodiments, the second polypeptide portion may comprise a polypeptide having a detectable enzymatic activity such as green fluorescent protein or β galactosidase. Chimeric polypeptides in which the second polypeptide portion comprises a detectable polypeptide may be used to determine the intracellular localization of the first polypeptide portion. In such procedures, the fusion vector encoding the chimeric polypeptide is introduced into a host cell under conditions which facilitate the expression of the chimeric polypeptide. Where appropriate, the cells are treated with a detection reagent which is visible under the microscope following a catalytic reaction with the detectable polypeptide and the cellular location of the detection reagent is determined. For example, if the polypeptide having a detectable enzymatic activity is β galactosidase, the cells may be treated with Xgal. Alternatively, where the detectable polypeptide is directly detectable without the addition of a detection reagent, the intracellular location of the chimeric polypeptide is determined by performing microscopy under conditions in which the detectable polypeptide is visible. For example, if the detectable polypeptide is green fluorescent protein or a modified version thereof, microscopy is performed by exposing the host cells to light having an appropriate wavelength to cause the green fluorescent protein or modified version thereof to fluoresce.

Alternatively, the second polypeptide portion may comprise a polypeptide whose isolation, purification, or enrichment is desired. In such embodiments, the isolation, purification, or enrichment of the second polypeptide portion may be achieved by performing the immunoaffinity chromatography procedures described below using an immunoaffinity column having an antibody directed against the first polypeptide portion coupled thereto.

The proteins encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related

polypeptides, or fragments of positional segments of EST-related polypeptides may also be used to generate antibodies as explained herein in order to identify the tissue type or cell species from which a sample is derived as described in Example 50.

EXAMPLE 50

Identification of Tissue Types or Cell Species by Means of Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations as described herein which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

1. Immunohistochemical Techniques

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, H., Chap. 26 in: *Basic 503 Clinical Immunology*, 3rd Ed. Lange, Los Altos, California (1980) or Rose, *et al.*, Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980), the entire disclosures of which are incorporated herein by reference.

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ¹²⁵I, and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or

antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μ m, unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

2. Identification of Tissue Specific Soluble Proteins

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, L. *et al.*, Section 19-2 in: *Basic Methods in Molecular Biology* (P. Leder, ed), Elsevier, New York (1986), using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient

volume of from 5 to 55 μ l, and containing from about 1 to 100 μ g protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al.*, *supra* Section 19-3, the entire disclosure of which is incorporated herein by reference. One set of nitrocellulose blots is stained with Coomassie Blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 20 and 33. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure described above a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

EXAMPLE 51

Immunohistochemical Localization of Polypeptides

The antibodies prepared as described herein above may be utilized to determine the cellular location of a polypeptide. The polypeptide may be any of the polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the polypeptide may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In some embodiments, the polypeptide may be a chimeric polypeptide such as those encoded by the fusion vectors of Example 49.

Cells expressing the polypeptide to be localized are applied to a microscope slide and fixed using any of the procedures typically employed in immunohistochemical localization techniques, including the methods described in *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997. Following a washing step, the cells are contacted with the antibody. In some embodiments, the antibody is conjugated to a detectable marker as described above to facilitate detection. Alternatively, in some embodiments, after the cells have been contacted with an

whose isolation, purification or enrichment is desired. The target polypeptide may be a polypeptide encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the target polypeptide may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. The target polypeptides may also be polypeptides which have been linked to the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the target polypeptides may be polypeptides which have been linked to EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides using the fusion vectors described above.

Preferably, the sample is placed in contact with the support for a sufficient amount of time and under appropriate conditions to allow at least 50% of the target polypeptide to specifically bind to the antibody coupled to the support.

Thereafter, the support is washed with an appropriate wash solution to remove polypeptides which have non-specifically adhered to the support. The wash solution may be any of those typically employed in immunoaffinity chromatography, including PBS, Tris-lithium chloride buffer (0.1M lysine base and 0.5M lithium chloride, pH 8.0), Tris-hydrochloride buffer (0.05M Tris-hydrochloride, pH 8.0), or Tris/Triton/NaCl buffer (50mM Tris.cl, pH 8.0 or 9.0, 0.1% Triton X-100, and 0.5MNaCl).

After washing, the specifically bound target polypeptide is eluted from the support using the high pH or low pH elution solutions typically employed in immunoaffinity chromatography. In particular, the elution solutions may contain an eluant such as triethanolamine, diethylamine, calcium chloride, sodium thiocyanate, potassium bromide, acetic acid, or glycine. In some embodiments, the elution solution may also contain a detergent such as Triton X-100 or octyl- β -D-glucoside.

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to clone sequences located upstream of the 5'ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 51 describes a method for cloning sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

2. Identification of upstream sequences with promoting or regulatory activities

EXAMPLE 53

Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Clone Upstream Sequences from Genomic DNA

Sequences derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions using an outer adapter primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for 5' EST of interest and should have a melting temperature, length, and location in the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids which is consistent with its use in PCR reactions. Each first PCR reaction contains 5ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adapter primer and outer gene specific primer, 1.1 mM of Mg(OAc)₂, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min at 94°C / 2 sec at 94°C, 3 min at 72°C (7 cycles) / 2 sec at 94°C, 3 min at 67°C (32 cycles) / 5 min at 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adapter, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids for which the promoter is to be cloned and should have a melting temperature, length, and location in the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-

related nucleic acids which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min at 94°C / 2 sec at 94°C, 3 min at 72°C (6 cycles) / 2 sec at 94°C, 3 min at 67°C (25 cycles) / 5 min at 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 10, 12, 15, 18, 20, 23, 25, 27, 30, 35, 40, or 50 nucleotides from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are isolated as described above. Thereafter, the single stranded DNA containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is released from the beads and converted into double stranded DNA using a primer specific for the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. cDNAs containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example 54.

EXAMPLE 54

Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are cloned into a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβ-

gal-Basic, p β -gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β -galactosidase, or green fluorescent protein. The sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for augmenting transcription levels from weak promoter sequences. A significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 55

Cloning and Identification of Promoters

Using the method described in Example 54 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT

G (SEQ ID NO:15) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:16), the promoter having the internal designation P13H2 (SEQ ID NO:17) was obtained.

Using the primer pairs GTA CCA GGG ACT GTG ACC ATT GC (SEQ ID NO:18) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:19), the promoter having the internal designation P15B4 (SEQ ID NO:20) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:21) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:22), the promoter having the internal designation P29B6 (SEQ ID NO:23) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Figure 5 describes the transcription factor binding sites present in each of these promoters. The columns labeled *matrice* provides the name of the MatInspector matrix used. The column labeled *position* provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the inserted EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The PCR product which corresponds to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments

of EST-related nucleic acids can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The promoters and other regulatory sequences located upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described above. For example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids derived from an mRNA which are expressed at a high level in muscle, as determined by the methods above, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences, proteins which interact with the promoter may be identified as described in Example 56 below.

EXAMPLE 56

Identification of Proteins Which Interact with

Promoter Sequences, Upstream Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the

deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1). Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNase protection analysis.

VIII. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in Gene Therapy

The present invention also comprises the use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in gene therapy strategies, including antisense and triple helix strategies as described in Examples 57 and 58 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

EXAMPLE 57

Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et al.*, *Ann. Rev. Biochem.* 55:569-597 (1986) and Izant and Weintraub, *Cell* 36:1007-1015 (1984), the entire disclosures of which are incorporated herein by reference.

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, (1991), the entire disclosure of which is incorporated herein by reference.

Various types of antisense oligonucleotides complementary to the sequence of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026, the entire disclosure of which is incorporated herein by reference, are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, the entire disclosure of which is incorporated herein by reference, are used.

5 In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, the entire disclosure of which is incorporated herein by reference, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary
10 amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, the entire disclosure of which is incorporated herein by reference,
15 may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefor. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2, the entire disclosure of which is incorporated
20 herein by reference. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732 is also contemplated. Because these molecules have no free ends, they are more
25 resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be
30 determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection or transfection using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression
35 vector. The expression vector may be any of a variety of expression vectors known in the art,

including retroviral or viral vectors, vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between $1 \times 10^{-10} \text{M}$ to $1 \times 10^{-4} \text{M}$. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al.*, *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are contemplated within the scope of this invention.

EXAMPLE 58

Preparation and use of Triple Helix Probes

The sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target genes corresponding to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids from which the oligonucleotide were derived with known gene sequences that have been associated with a particular function. The cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are associated with the disease using techniques described herein.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 56 at a dosage calculated based on the *in vitro* results, as described in Example 57.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin *et al.* (*Science* **245**:967-971 (1989), the entire disclosure of which is incorporated herein by reference).

EXAMPLE 59

Use of EST-related nucleic acids, positional segments of
EST-related nucleic acids or fragments of positional segments of
EST-related nucleic acids to express an Encoded Protein in a Host Organism

5 The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to express an encoded protein or polypeptide in a host organism to produce a beneficial effect. In addition, nucleic acids encoding the EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides may be used to
10 express the encoded protein or polypeptide in a host organism to produce a beneficial effect.

 In such procedures, the encoded protein or polypeptide may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein or polypeptide may have any of the activities described above. The encoded protein or polypeptide may be a protein or polypeptide which the host organism lacks or, alternatively, the encoded protein may augment the
15 existing levels of the protein in the host organism.

 In some embodiments in which the protein or polypeptide is secreted, nucleic acids encoding the full length protein (*i.e.* the signal peptide and the mature protein), or nucleic acids encoding only the mature protein (*i.e.* the protein generated when the signal peptide is cleaved off) is introduced into the host organism.

20 The nucleic acids encoding the proteins or polypeptides may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

 Alternatively, the nucleic acids encoding the protein or polypeptide may be cloned into an
25 expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the
30 expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein or polypeptide to produce a beneficial effect.

EXAMPLE 60

Use of Signal Peptides To Import Proteins Into Cells

5 The short core hydrophobic region (h) of signal peptides encoded by the sequences of SEQ ID NOs. 24-728 and 766-792 may also be used as a carrier to import a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol. Chem.*, **270**: 14225-14258 (1995); Du *et al.*, *J. Peptide Res.*, **51**: 235-243 (1998); and Rojas *et al.*, *Nature Biotech.*, **16**: 370-375 (1998), the entire disclosures of which are incorporated herein by reference).

10 When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

15 This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, **271**: 5305-5308 (1996); Rojas *et al.*, *J. Biol. Chem.*, **271**: 27456-27461 (1996); Liu *et al.*, *Proc. Natl. Acad. Sci. USA*, **93**: 11819-11824 (1996); Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, **234**: 675-680 (1997), the entire disclosure of which is incorporated herein by reference).

25 Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

30 Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form triple helixes, as described above, in order to inhibit processing and maturation of a target cellular RNA.

EXAMPLE 61

Computer Embodiments

As used herein the term “nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 encompasses the nucleotide sequences of SEQ ID NOs. 24-811 and 1600-1622, fragments of
5 SEQ ID NOs. 24-811 and 1600-1622, nucleotide sequences homologous to SEQ ID NOs. 24-811 and 1600-1622 or homologous to fragments of SEQ ID NOs. 24-811 and 1600-1622, and sequences complementary to all of the preceding sequences. The fragments include portions of SEQ ID NOs. 24-811 and 1600-1622 comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of SEQ ID NOs. 24-811 and 1600-1622.
10 Preferably, the fragments are novel fragments. Preferably the fragments include polynucleotides described in Table II, polynucleotides described in Table III, polynucleotides described in Table IV or portions thereof comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the polynucleotides described in Tables II, III, or IV. Homologous sequences and fragments of SEQ ID NOs. 24-811 and 1600-1622 refer to a sequence having at
15 least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, or 75% homology to these sequences. Homology may be determined using any of the computer programs and parameters described in Example 18, including BLAST2N with the default parameters or with any modified parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622. The homologous sequences may be
20 obtained using any of the procedures described herein or may result from the correction of a sequencing error as described above. Preferably the homologous sequences and fragments of SEQ ID NOs. 24-811 and 1600-1622 include polynucleotides described in Table II, polynucleotides described in Table III, polynucleotides described in Table IV or portions thereof comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the
25 polynucleotides described in Tables II, III, or IV. It will be appreciated that the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. *Biochemistry*, 3rd edition. W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

As used herein the term “polypeptide codes of SEQ ID NOS. 812-1599” encompasses
30 the polypeptide sequence of SEQ ID NOS. 812-1599 which are encoded by the 5' EST s of SEQ ID NOs. 24-811 and 1600-1622, polypeptide sequences homologous to the polypeptides of SEQ ID NOS. 812-1599, or fragments of any of the preceding sequences. Homologous polypeptide sequences refer to a polypeptide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, 75% homology to one of the polypeptide sequences of SEQ ID NOS. 812-1599. Homology
35 may be determined using any of the computer programs and parameters described herein, including

FASTA with the default parameters or with any modified parameters. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error as described above. The polypeptide fragments comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of the polypeptides of SEQ ID NOS. 812-1599. Preferably, the fragments are novel fragments. Preferably, the fragments include polypeptides encoded by the polynucleotides described in Table II, or portions thereof comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of the polypeptides encoded by the polynucleotides described in Table II. It will be appreciated that the polypeptide codes of the SEQ ID NOS. 812-1599 can be represented in the traditional single character format or three letter format (See the inside back cover of Stryer, Lubert. *Biochemistry*, 3rd edition. W. H Freeman & Co., New York.) or in any other format which relates the identity of the polypeptides in a sequence.

It will be appreciated by those skilled in the art that the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 and polypeptide codes of SEQ ID NOS. 812-1599 can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622, one or more of the polypeptide codes of SEQ ID NOS. 812-1599. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 polypeptide codes of SEQ ID NOS. 812-1599.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Embodiments of the present invention include systems, particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 6. As used herein, "a computer system" refers to the hardware components, software components, and data storage components used to analyze the nucleotide sequences of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599. In

one embodiment, the computer system 100 is a Sun Enterprise 1000 server (Sun Microsystems, Palo Alto, CA). The computer system 100 preferably includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq or International Business Machines.

Preferably, the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable.

In one particular embodiment, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (preferably implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some embodiments, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, etc. In some embodiments, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599 (such as search tools, compare tools, and modeling tools etc.) may reside in main memory 115 during execution.

In some embodiments, the computer system 100 may further comprise a sequence comparer for comparing the above-described nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide codes of SEQ ID NOS. 812-1599 stored on a computer readable medium to reference nucleotide or polypeptide sequences stored on a computer readable medium. A "sequence comparer" refers to one or more programs which are implemented on the computer

system 100 to compare a nucleotide or polypeptide sequence with other nucleotide or polypeptide sequences and/or compounds including but not limited to peptides, peptidomimetics, and chemicals stored within the data storage means. For example, the sequence comparer may compare the nucleotide sequences of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599 stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies, motifs implicated in biological function, or structural motifs. The various sequence comparer programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention.

Figure 7 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK, PIR OR SWISSPROT that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200.

If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200

moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the present invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 or a polypeptide code of SEQ ID NOS. 812-1599, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide code of SEQ ID NOS. 812-1599 and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and polypeptide codes of SEQ ID NOS. 812-1599 or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some embodiments, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide codes of SEQ ID NOS. 812-1599.

Another aspect of the present invention is a method for determining the level of homology between a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a reference nucleotide sequence, comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through the use of a computer program which determines homology levels and determining homology between the nucleic acid code and the reference nucleotide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, including BLAST2N with the default parameters or with any modified parameters. The method may be implemented using the computer systems described above. The method may also be performed by reading 2, 5, 10, 15, 20, 25, 30, or 50 of the above described nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 through use of the computer program and determining homology between the nucleic acid codes and reference nucleotide sequences .

Figure 8 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it should be in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

If there are no more more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

Alternatively, the computer program may be a computer program which compares the nucleotide sequences of the nucleic acid codes of the present invention, to reference nucleotide sequences in order to determine whether the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622. In one embodiment, the computer program may be a program which determines whether the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 contain a biallelic marker or single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence. This single nucleotide polymorphism may comprise a single base substitution, insertion, or deletion, while this biallelic marker may comprise about one to ten consecutive bases substituted, inserted or deleted.

Another aspect of the present invention is a method for determining the level of homology between a polypeptide code of SEQ ID NOS. 812-1599 and a reference polypeptide sequence, comprising the steps of reading the polypeptide code of SEQ ID NOS. 812-1599 and the reference polypeptide sequence through use of a computer program which determines homology levels and determining homology between the polypeptide code and the reference polypeptide sequence using the computer program.

Accordingly, another aspect of the present invention is a method for determining whether a nucleic acid code of SEQ ID NOS. 24-811 and 1600-1622 differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some embodiments, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 8. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other embodiments the computer based system may further comprise an identifier for identifying features within the nucleotide sequences of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599.

An “identifier” refers to one or more programs which identifies certain features within the above-described nucleotide sequences of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599. In one embodiment, the identifier may comprise a program which identifies an open reading frame in the cDNAs codes of SEQ ID NOS. 24-811 and 1600-1622.

Figure 9 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature’s attributes along with the name of the feature. For example, a feature name could be “Initiation Codon” and the attribute would be “ATG”. Another example would be the feature name “TAATAA Box” and the feature attribute would be “TAATAA”. An example of such a

database is produced by the University of Wisconsin Genetics Computer Group (www.gcg.com).

Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature is found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether move features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence.

It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

In another embodiment, the identifier may comprise a molecular modeling program which determines the 3-dimensional structure of the polypeptides codes of SEQ ID NOS. 812-1599. In some embodiments, the molecular modeling program identifies target sequences that are most compatible with profiles representing the structural environments of the residues in known three-dimensional protein structures. (See, *e.g.*, Eisenberg *et al.*, U.S. Patent No. 5,436,850 issued July 25, 1995, the entire disclosure of which is incorporated herein by reference). In another technique, the known three-dimensional structures of proteins in a given family are superimposed to define the structurally conserved regions in that family. This protein modeling technique also uses the known three-dimensional structure of a homologous protein to approximate the structure of the polypeptide codes of SEQ ID NOS. 812-1599. (See *e.g.*, Srinivasan, *et al.*, U.S. Patent No. 5,557,535 issued September 17, 1996, the entire disclosure of which is incorporated herein by reference). Conventional homology modeling techniques have been used routinely to build models of proteases and antibodies. (Sowdhamini *et al.*, Protein Engineering **10**:207, 215 (1997), the entire disclosure of which is incorporated herein by reference). Comparative approaches can also be used to develop three-dimensional protein models when the protein of interest has poor sequence identity to template proteins. In some cases, proteins fold into similar three-dimensional structures despite having very weak sequence identities. For example, the three-dimensional structures of a number of helical cytokines fold in similar three-dimensional topology in spite of weak sequence homology.

The recent development of threading methods now enables the identification of likely folding patterns in a number of situations where the structural relatedness between target and template(s) is not detectable at the sequence level. Hybrid methods, in which fold recognition is performed using Multiple Sequence Threading (MST), structural equivalencies are deduced from the threading output using a distance geometry program DRAGON to construct a low resolution model, and a full-atom representation is constructed using a molecular modeling package such as QUANTA.

According to this 3-step approach, candidate templates are first identified by using the novel fold recognition algorithm MST, which is capable of performing simultaneous threading of multiple aligned sequences onto one or more 3-D structures. In a second step, the structural equivalencies obtained from the MST output are converted into interresidue distance restraints and fed into the distance geometry program DRAGON, together with auxiliary information obtained from secondary structure predictions. The program combines the restraints in an unbiased manner and rapidly generates a large number of low resolution model confirmations. In a third step, these low resolution model confirmations are converted into full-atom models and subjected to energy minimization using the molecular modeling package QUANTA. (See e.g., Aszodi et al., Proteins:Structure, Function, and Genetics, Supplement 1:38-42 (1997), the entire disclosure of which is incorporated herein by reference).

The results of the molecular modeling analysis may then be used in rational drug design techniques to identify agents which modulate the activity of the polypeptide codes of SEQ ID NOS. 812-1599.

Accordingly, another aspect of the present invention is a method of identifying a feature within the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 comprising reading the nucleic acid code(s) or the polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) or polypeptide code(s) with the computer program. In one embodiment, computer program comprises a computer program which identifies open reading frames. In a further embodiment, the computer program identifies structural motifs in a polypeptide sequence. In another embodiment, the computer program comprises a molecular modeling program. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

The nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 may be stored as text in a word processing file, such as MicrosoftWORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE. In addition, many computer programs and databases may be used as sequence comparers, identifiers, or sources of reference nucleotide or polypeptide sequences to be compared to the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid codes of SEQ ID NOS. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599. The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul *et al*, *J. Mol. Biol.* **215**: 403 (1990)), FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, **85**: 2444 (1988)), FASTDB (Brutlag *et al*. *Comp. App. Biosci.* **6**:237-245, 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE (Molecular Simulations Inc.), Cerius².DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMM (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the EMBL/Swissprotein database, the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwent's World Drug Index database, the BioByteMasterFile database, the Genbank database, and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

EXAMPLE 62

Methods of Making Nucleic Acids

The present invention also comprises methods of making the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids. The methods comprise sequentially linking together nucleotides to produce the nucleic acids having the preceding sequences. A variety of methods of synthesizing nucleic acids are known to those skilled in the art.

In many of these methods, synthesis is conducted on a solid support. These included the 3' phosphoramidite methods in which the 3' terminal base of the desired oligonucleotide is immobilized on an insoluble carrier. The nucleotide base to be added is blocked at the 5' hydroxyl and activated at the 3' hydroxyl so as to cause coupling with the immobilized nucleotide base. Deblocking of the new immobilized nucleotide compound and repetition of the cycle will produce the desired polynucleotide. Alternatively, polynucleotides may be prepared as described in U.S. Patent No. 5,049,656. In some embodiments, several polynucleotides prepared as described above are ligated together to generate longer polynucleotides having a desired sequence.

EXAMPLE 63

Methods of Making Polypeptides

The present invention also comprises methods of making the polynucleotides encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids and methods of making the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of EST-related polypeptides. The methods comprise sequentially linking together amino acids to produce the nucleic polypeptides having the preceding sequences. In some embodiments, the polypeptides made by these methods are 150 amino acid or less in length. In other embodiments, the polypeptides made by these methods are 120 amino acids or less in length.

A variety of methods of making polypeptides are known to those skilled in the art, including methods in which the carboxyl terminal amino acid is bound to polyvinyl benzene or another suitable resin. The amino acid to be added possesses blocking groups on its amino moiety and any side chain reactive groups so that only its carboxyl moiety can react. The carboxyl group is activated with carbodiimide or another activating agent and allowed to couple

to the immobilized amino acid. After removal of the blocking group, the cycle is repeated to generate a polypeptide having the desired sequence. Alternatively, the methods described in U.S. Patent No. 5,049,656, the entire disclosure of which is incorporated herein by reference, may be used.

5 As discussed above, the EST-related nucleic acids, fragments of the EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; production of secreted polypeptides or chimeric polypeptides, antibody production, as markers for tissues in
10 which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences;
15 as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein or polypeptide which binds or potentially binds to another protein or polypeptide
20 (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* 75:791-803 (1993), the entire disclosure of which is incorporated herein by reference) to identify polynucleotides encoding the other protein or polypeptide with which binding occurs or to identify inhibitors of the binding interaction.

25 The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including as a labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is
30 preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein or polypeptide binds or potentially binds to another protein or polypeptide (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins or polypeptides

involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning; A Laboratory Manual," 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology; Guide to Molecular Cloning Techniques," Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987, the entire disclosures of which are incorporated
10 herein by reference.

Polynucleotides and proteins or polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed
15 of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Although this invention has been described in terms of certain preferred embodiments,
20 other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be limited only by reference to the appended claims.

CLAIMS

1. A purified nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

2. A purified nucleic acid comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

3. A purified or isolated polypeptide comprising a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

4. A method of making a cDNA comprising the steps of:

a) contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622;

b) hybridizing said primer to an mRNA in said collection that encodes said protein;

c) reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA;

d) making a second cDNA strand complementary to said first cDNA strand; and

e) isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

5. A method of making a cDNA comprising the steps of:

a) obtaining a cDNA comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622;

b) contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 under conditions which permit said probe to hybridize to said cDNA;

c) identifying a cDNA which hybridizes to said detectable probe; and

d) isolating said cDNA which hybridizes to said probe.

6. A method of making a cDNA comprising the steps of:

a) contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

b) hybridizing said first primer to said polyA tail;

c) reverse transcribing said mRNA to make a first cDNA strand;

d) making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622; and

e) isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

7. A method of making a polypeptide comprising the steps of:

a) obtaining a cDNA which encodes a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 or a cDNA which encodes a polypeptide comprising at least 10 consecutive amino acids of a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NOs. 24-811;

b) inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

c) introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

d) isolating said protein.

8. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequence.

9. The array of Claim 8 including therein at least five sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequences.

10. An enriched population of recombinant nucleic acids, said recombinant nucleic acids comprising an insert nucleic acid and a backbone nucleic acid, wherein at least 5% of said insert nucleic acids in said population comprise a sequence selected from the group consisting

of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequences.

11. An antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide comprising a contiguous span of at least 8 amino acids of any of SEQ ID NOs. 812-1599, wherein said antibody is polyclonal or monoclonal.

12. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

13. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

14. The computer system of Claim 13 further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

15. The computer system of Claim 14 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

16. The computer system of Claim 13 further comprising an identifier which identifies features in said sequence.

17. A method for comparing a first sequence to a reference sequence wherein said first sequence is selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of:

a) reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program.

18. The method of Claim 17, wherein said step of determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

19. A method for identifying a feature in a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of:

- 5 a) reading said sequence through the use of a computer program which identifies features in sequences; and
- b) identifying features in said sequence with said computer program.

20. A vector comprising a nucleic acid according to either Claims 1 or 2.

10 21. A host cell containing a nucleic acid of Claim 20.

11

ESTs AND ENCODED HUMAN PROTEINS

Abstract of the Disclosure

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed.

5 The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

10

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121499

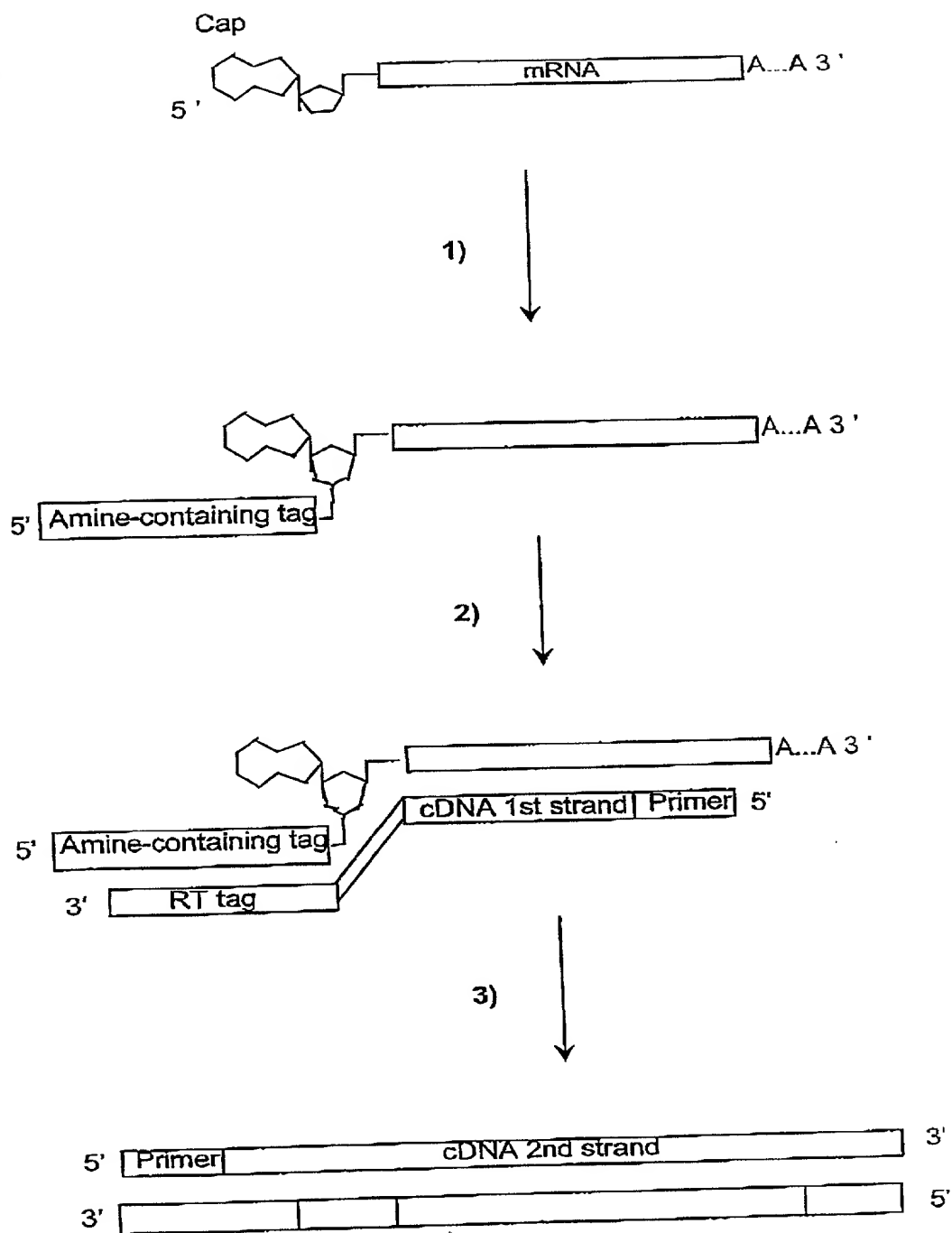


Figure 1

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3,5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,519	0,708
4,5	0,078	0,079	0,565	0,745
5	0,062	0,098	0,615	0,782
5,5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,694	0,836
6,5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7,5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8,5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9,5	0,007	0,581	0,863	0,934
10	0,006	0,679	0,835	0,919

Figure 2

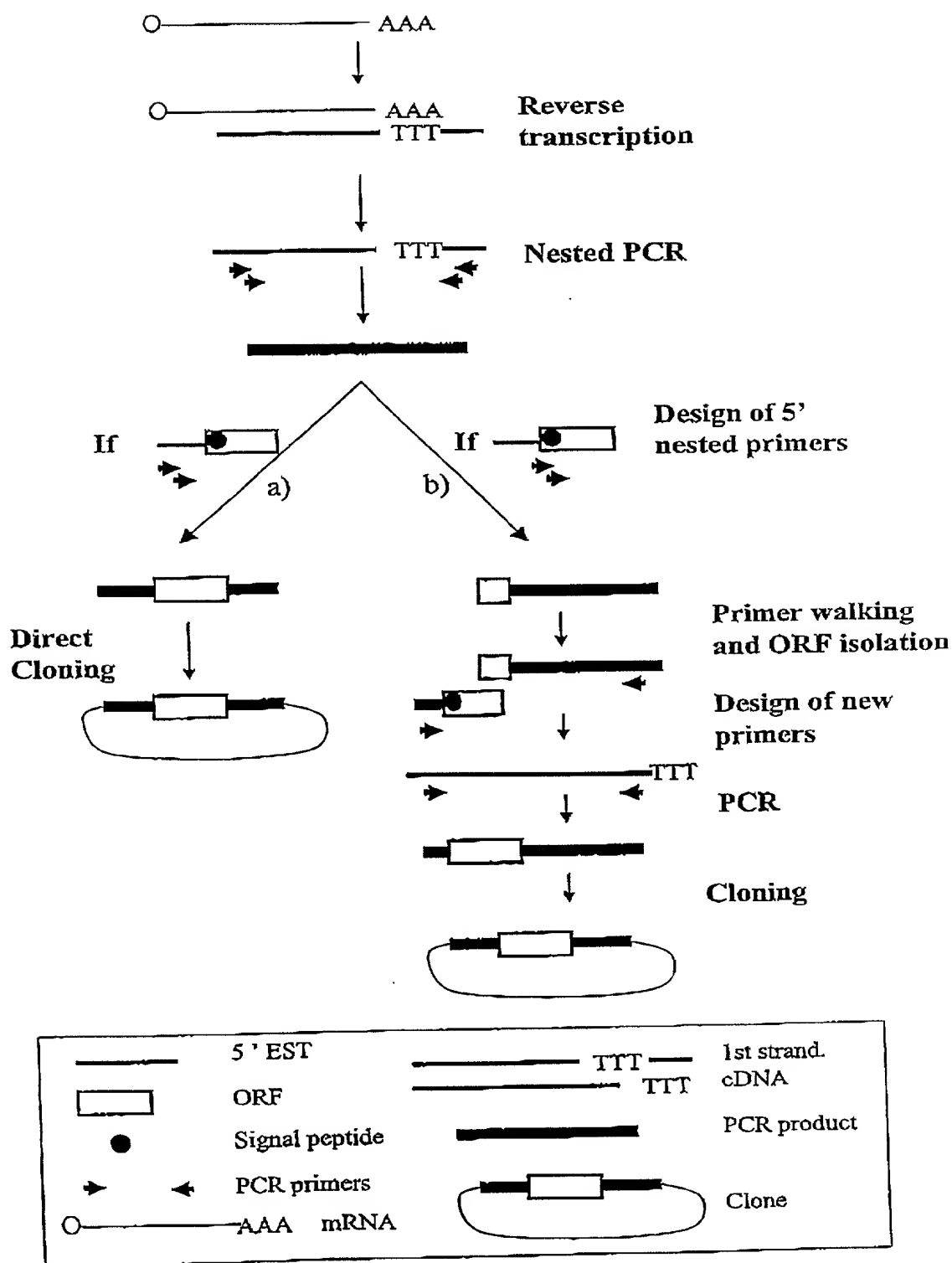


Figure 3

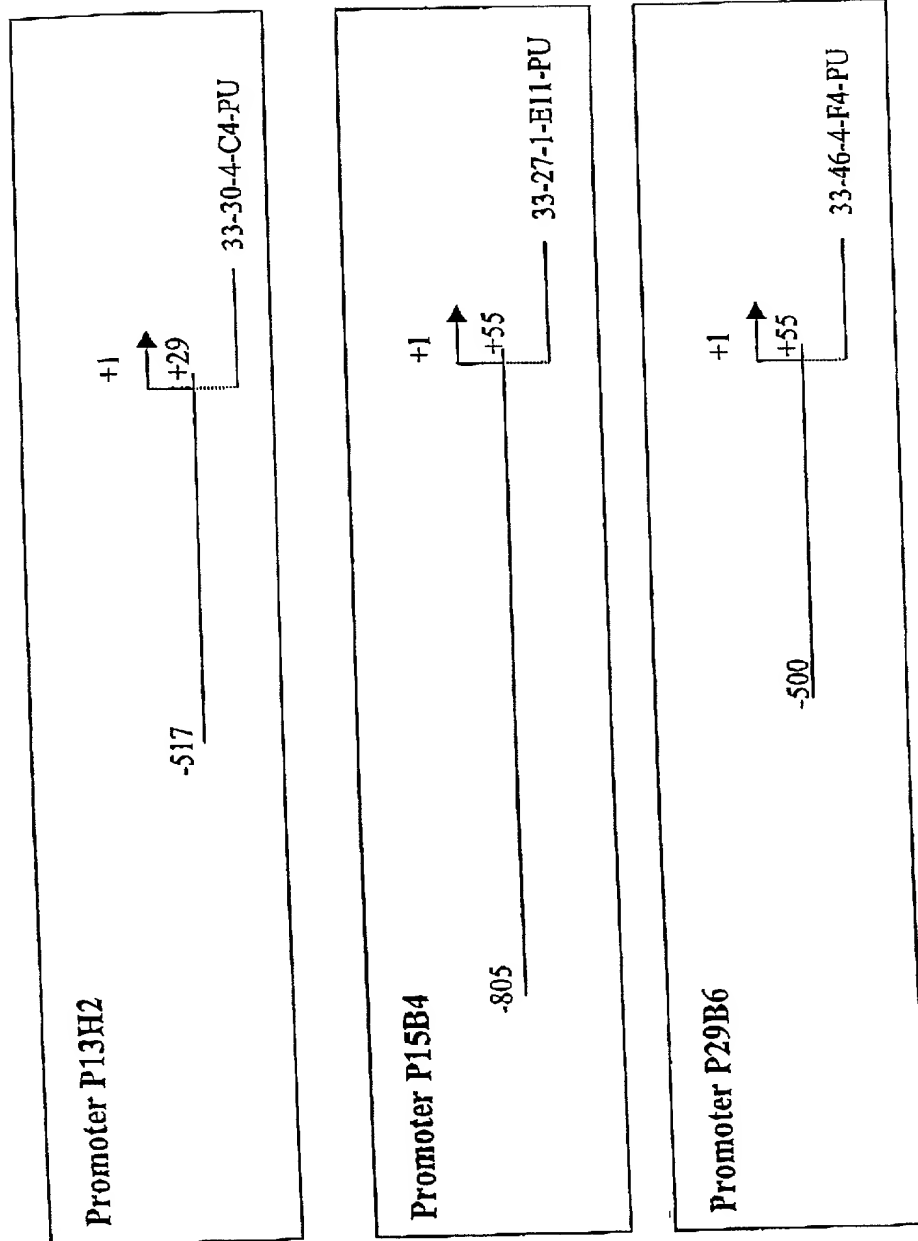


Figure 4

Promoter sequence P13H2 (546 bp):

Matrix	Orient		Score	Length	Sequence
	Position	ation			
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRY_02	-41	-	0.951	12	TAAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P15B4 (861bp) :

Matrix	Orient		Score	Length	Sequence
	Position	ation			
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTTGGA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P29B6 (555 bp) :

Matrix	Orient		Score	Length	Sequence
	Position	ation			
ARNT_01	-311	+	0.964	16	GGA CTCACGTGCTGCT
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NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
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Figure 5

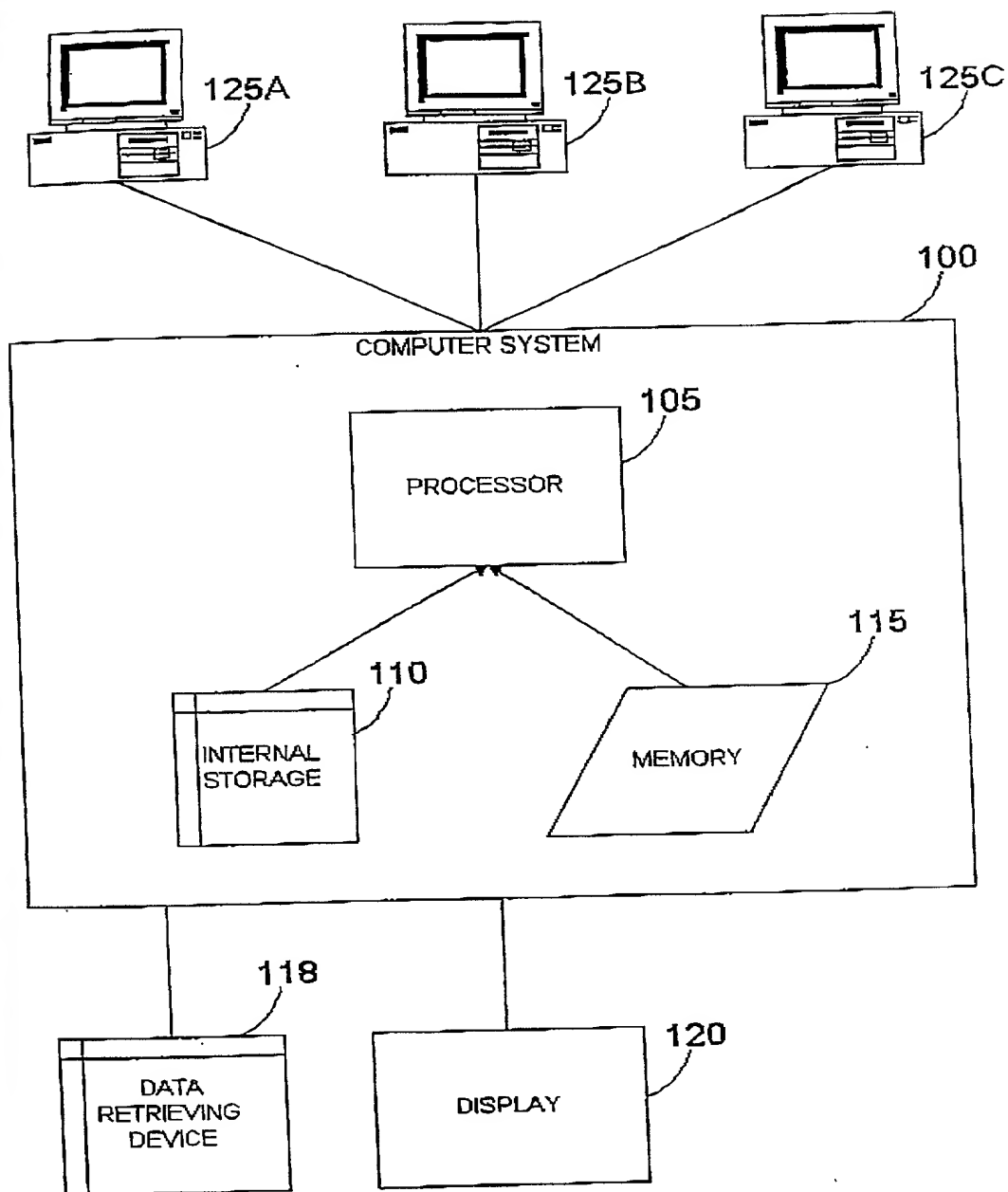


FIGURE 6

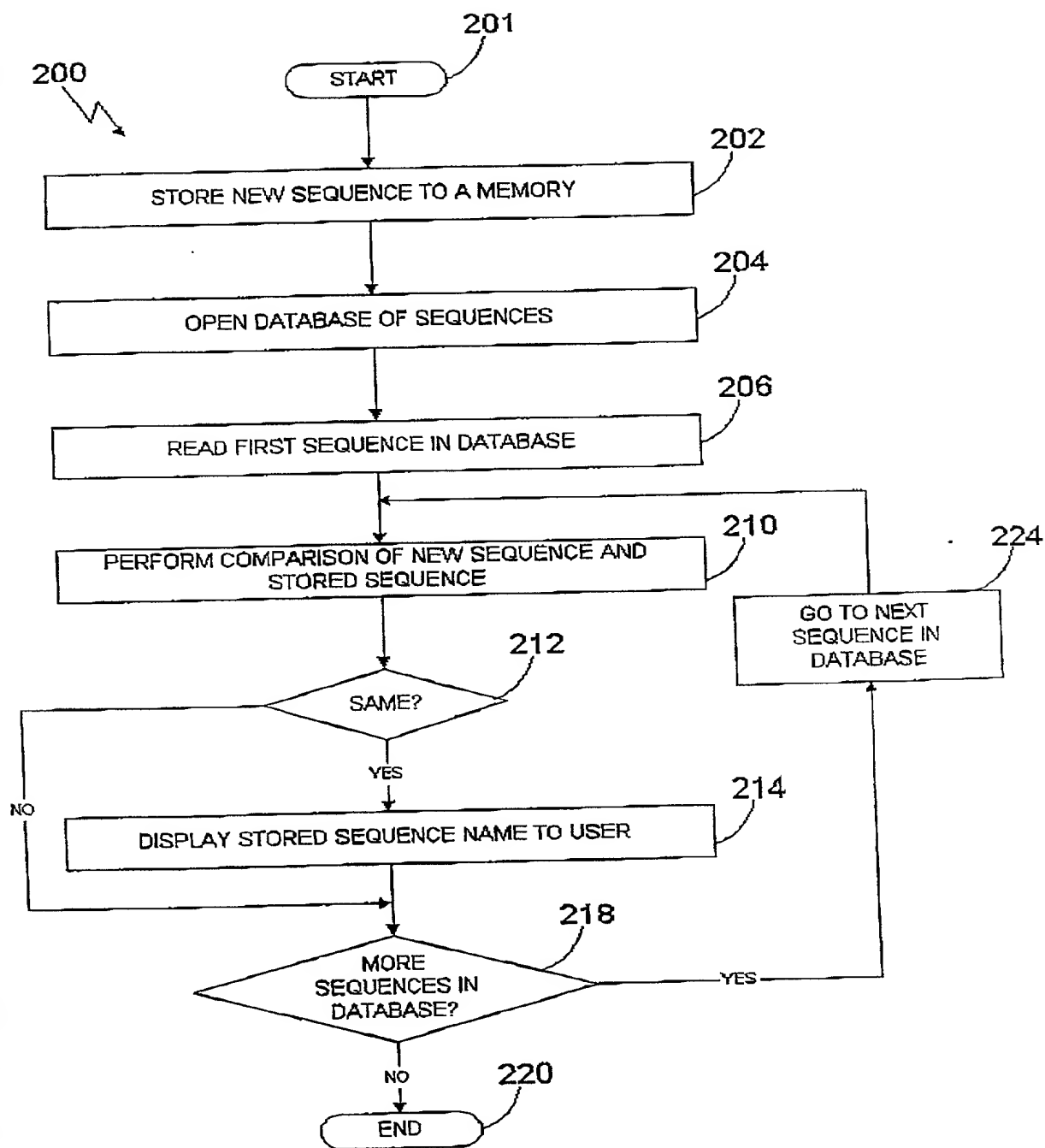


FIGURE 7

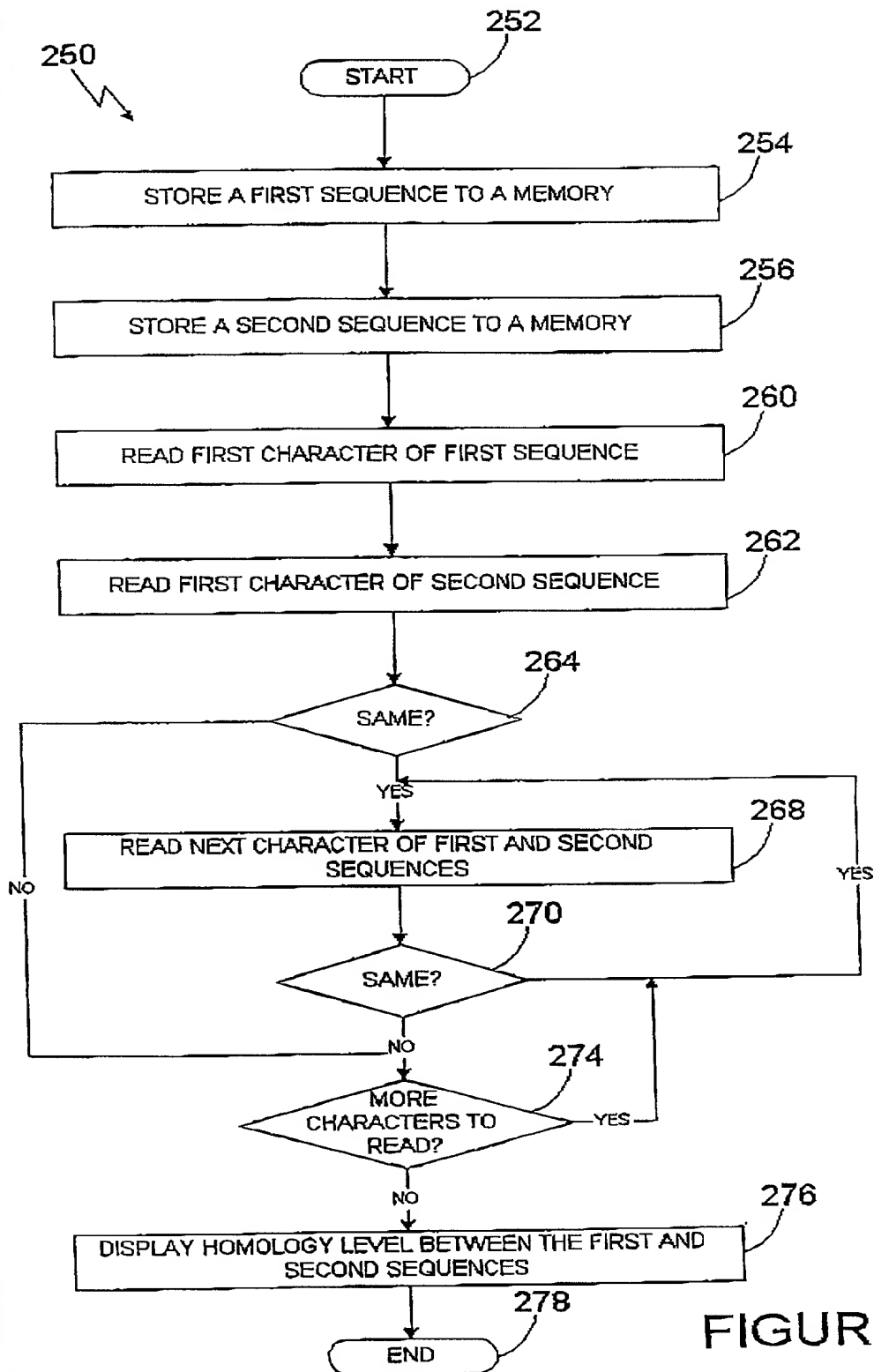


FIGURE 8

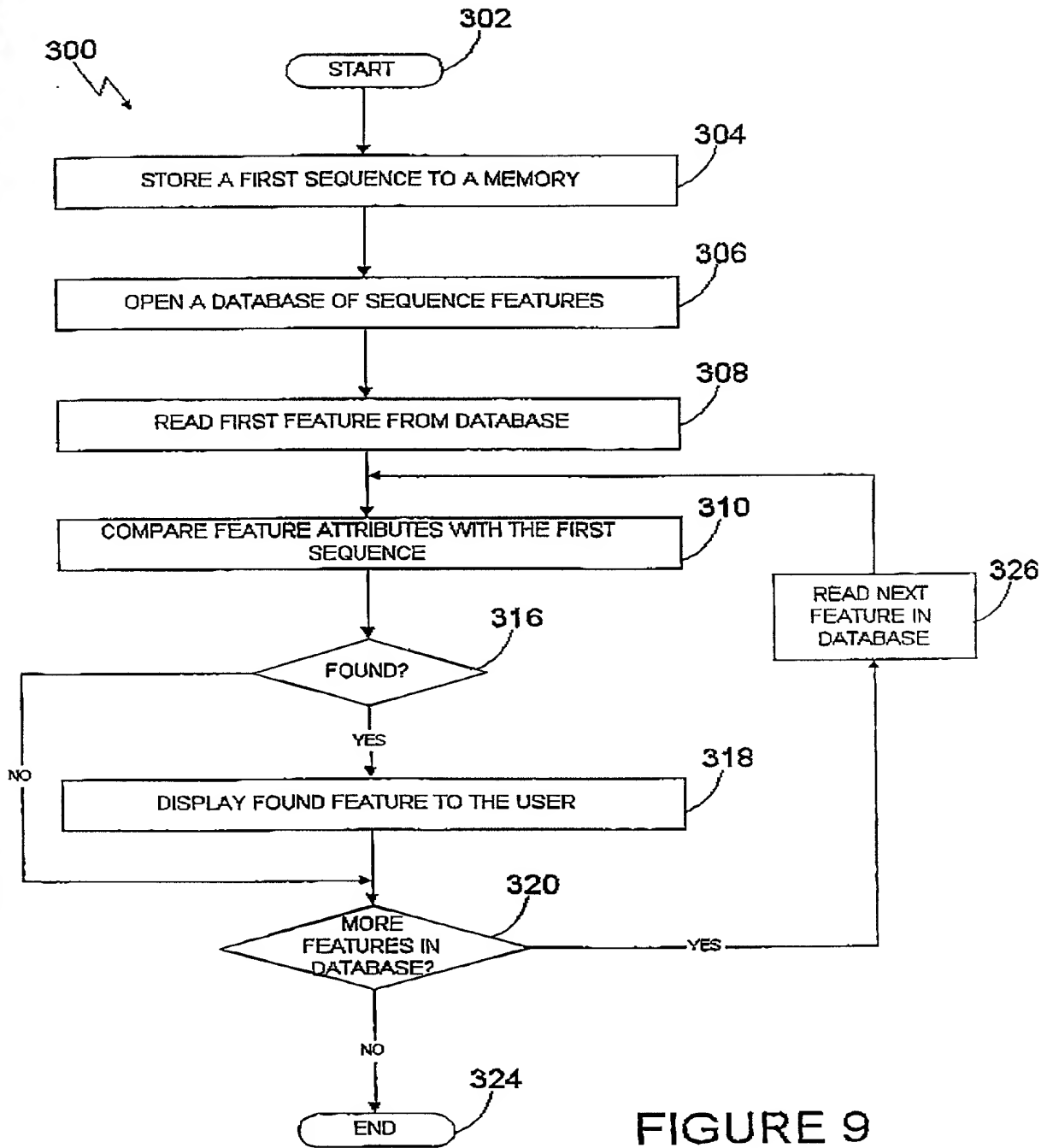


FIGURE 9

Search characteristic		Selection Characteristics		
Step	Program	Strand	Parameters	Identity (%) Length (bp) Comments
miscellaneous	FASTA	both	-	90 15
tRNA	FASTA	both	-	80 60
rRNA	BLASTN	both	S=108	80 40
miRNA	BLASTN	both	S=108	80 40
Prokaryotic	BLASTN	both	S=144	90 40
Fungal	BLASTN	both	S=144	90 40
Alu	BLASTN	both	S=72, B=5	70 40 max 5 matches, masking
L1	BLASTN	both	S=72, B=5	70 40 max 5 matches, masking
Repeats	BLASTN	both	S=72	70 40 masking
PolyA	BLAST2N	top	W=6, S=10, E=1000, N=12	90 10 in the last 100 nucleotides
Polyadenylation signal	-	top	AATAAA allowing 1 mismatch	in the 50 nucleotides before the 5' end of the polyA
Vertebrate	BLASTN then FASTA	both	-	90 then 70 30 first BLASTN, then FASTA on matching sequences
ESTs	BLAST2N	both	-	90 30
Geneseq	BLASTN	both	W=8, B=10	90 30
ORF	BLASTP	top	W=8, B=10	- - on ORF proteins, max 10 matches
Proteins	BLASTX	top	E = 0.001	70 30

Figure 10

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 Giordano, J.Y.

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Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg	
135 140 145 150	
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa	578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu	
155 160 165	
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca	626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro	
170 175 180	
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac	674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn	
185 190 195	
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt	725
Gln Ala Glu Ile Ala Ala Cys	
200 205	
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccctt	785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a	826

<210> 8

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<223> score 8.5

seq AALLLGLMMVVTG/DE

<400> 8

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu	
-20 -15 -10	
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His	
-5 1 5 10	
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val	
15 20 25	
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys	
30 35 40	
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys	
45 50 55	
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp	
60 65 70	
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His	
75 80 85 90	
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile	
95 100 105	
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His	
110 115 120	
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys	
125 130 135	
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys	
140 145 150	
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser	
155 160 165 170	

Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
 175 180 185
 Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
 190 195 200
 Ala Ala Cys
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<210> 9
 <211> 852
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 229..735

<221> sig_peptide
 <222> 229..492
 <223> score 6.7
 seq VFALSSFLNKASA/VY

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 aatgactggc agtggcatca gcgatggcgg ctgcgtcggg gtcggttctg cagcgctgta 60
 tcgtgtcgcc ggcagggagg catagcgctt ctctgatctt cctgcatggc tcaggtgatt 120
 ctggacaagg attaagaatg tggatcaagc aggtttttta atcaagattt aacattccaa 180
 cacataaaaa ttatttatcc aacagctcct cccagatcat atactcct atg aaa gga 237
 Met Lys Gly
 gga atc tcc aat gta tgg ttt gac aga ttt aaa ata acc aat gac tgc 285
 Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr Asn Asp Cys
 -85 -80 -75 -70
 cca gaa cac ctt gaa tca att gat gtc atg tgt caa gtg ctt act gat 333
 Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val Leu Thr Asp
 -65 -60 -55
 ttg att gat gaa gaa gta aaa agt ggc atc aag aag aac agg ata tta 381
 Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn Arg Ile Leu
 -50 -45 -40
 ata gga gga ttc tct atg gga gga tgc atg gca atg cat tta gca tat 429
 Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His Leu Ala Tyr
 -35 -30 -25
 aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg 477
 Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu
 -20 -15 -10
 aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta 525
 Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val
 -5 1 5 10
 ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt 573
 Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu
 15 20 25
 cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg 621
 His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val
 30 35 40
 acc acg aag ttt cat agt ttt cca aat gtt tac cat gag cta agc aaa 669
 Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys
 45 50 55

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act gag tta gac ata ttg aag tta tgg att ott aca aag ctg cca gga      717
Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys Leu Pro Gly
60          65          70          75
gaa atg gaa aaa caa aaa tgaatgaatc aagagtgatt tgttaatgta      765
Glu Met Glu Lys Gln Lys
80
agtgtaatgt ctttgtgaaa agtgattttt actgccaaat tataatgata attaaaaatat      825
taagaaatag caaaaaaaaa aaaaaaa      852

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<210> 10
<211> 169
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -88..-1
<223> score 6.7
      seq VFALSSFLNKASA/VY

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Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
      -85          -80          -75
Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
      -70          -65          -60
Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
      -55          -50          -45
Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
-40          -35          -30          -25
Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
      -20          -15          -10
Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
      -5          1          5
Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
10          15          20
Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
25          30          35          40
Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
      45          50          55
Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
      60          65          70
Leu Pro Gly Glu Met Glu Lys Gln Lys
      75          80

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<210> 11
<211> 1602
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 24..1004

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<221> sig_peptide

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<222> 24..170

<223> score 5.6

seq ACLSLGFFSLLWL/QL

<400> 11

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                               Met Phe Pro Ser Arg Arg Lys Ala Ala Gln
                               -45                               -40

ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc tcc ggc ggc ctc cct      101
Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro
                               -35                               -30                               -25

cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc tgc ctc tcg ctg ggc      149
Arg Lys Cys Ser Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly
                               -20                               -15                               -10

ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc tct ggg gac gtg gcc      197
Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala
                               -5                               1                               5

cgg gca gtc agg gga caa ggg cag gag acc tcg ggc cct ccc cgt gcc      245
Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala
10                               15                               20                               25

tgc ccc cca gag ccg ccc cct gag cac tgg gaa gaa gac gca tcc tgg      293
Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
                               30                               35                               40

ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc cgc gaa cgc ttc gag      341
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe Glu
                               45                               50                               55

gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc ttc ctg agc agg aag      389
Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser Arg Lys
60                               65                               70

aag atc cgg cac cac atc tac gtg ctc aac cag gtg gac cac ttc agg      437
Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp His Phe Arg
75                               80                               85

ttc aac cgg gca gcg ctc atc aac gtg ggc ttc ctg gag agc agc aac      485
Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu Glu Ser Ser Asn
90                               95                               100                               105

agc acg gac tac att gcc atg cac gac gtt gac ctg ctc cct ctc aac      533
Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp Leu Leu Pro Leu Asn
110                               115                               120

gag gag ctg gac tat ggc ttt cct gag gct ggg ccc ttc cac gtg gcc      581
Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly Pro Phe His Val Ala
125                               130                               135

tcc ccg gag ctc cac cct ctc tac cac tac aag acc tat gtc ggc ggc      629
Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly
140                               145                               150

atc ctg ctg ctc tcc aag cag cac tac cgg ctg tgc aat ggg atg tcc      677
Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu Cys Asn Gly Met Ser
155                               160                               165

aac cgc ttc tgg ggc tgg ggc cgc gag gac gag ttc tac cgg cgc      725
Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg
170                               175                               180                               185

att aag gga gct ggg ctc cag ctt ttc cgc ccc tcg gga atc aca act      773
Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr
190                               195                               200

ggg tac aag aca ttt cgc cac ctg cat gac cca gcc tgg cgg aag agg      821
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Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro Ala Trp Arg Lys Arg	
205 210 215	
gac cag aag cgc atc gca gct caa aaa cag gag cag ttc aag gtg gac	869
Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp	
220 225 230	
agg gag gga ggc ctg aac act gtg aag tac cat gtg gct tcc cgc act	917
Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr	
235 240 245	
gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc ctc aac atc atg ttg	965
Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu	
250 255 260 265	
gac tgt gac aag acc gcc aca ccc tgg tgc aca ttc agc tgagctggat	1014
Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser	
270 275	
ggacagtgag gaagcctgta cctacaggcc atattgctca ggctcaggac aaggcctcag	1074
gtcgtggggc cagctctgac aggatgtgga gtggccagga ccaagacagc aagctacgca	1134
attgcagcca cccggccgcc aaggcaggct tgggctgggc caggacacgt ggggtgcctg	1194
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ccccctgcct tcctgtctac cctactctga cctccttcac gtgccaggc ctgtgggtag	1314
tggggagggc tgaacaggac aacctctcat cccccccact tttgttcctt cctgctgggc	1374
tgctctgtgc agagacacag tgtagggggc atgcagctgg cgtaggtggc agttgggcct	1434
ggtgaggggt aggacttcag aaaccagagc acaagcccca cagaggggga acagccagca	1494
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<210> 12

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -49..-1

<223> score 5.6

seq ACLSLGFFSLLWL/QL

<400> 12

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Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe	
-30 -25 -20	
His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp	
-15 -10 -5	
Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln	
1 5 10 15	
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro	
20 25 30	
Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala	
35 40 45	
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val	
50 55 60	
Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile	
65 70 75	
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu	

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80      85      90      95
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
      100      105      110
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
      115      120      125
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
      130      135      140
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
      145      150      155
Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
160      165      170      175
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
      180      185      190
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
      195      200      205
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
      210      215      220
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
      225      230      235
Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
240      245      250      255
Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
      260      265      270
Thr Pro Trp Cys Thr Phe Ser
      275

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<210> 13
<211> 1568
<212> DNA
<213> Homo sapiens

<220>
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<222> 75..1259

<221> sig_peptide
<222> 75..1004
<223> score 4.4
      seq VLILLFSLALIIL/PS

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ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac gcg tgg      110
      Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp
      -310      -305      -300
ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc ctg gag ctg      158
Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu
      -295      -290      -285
gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg cta cag gaa      206
Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu
      -280      -275      -270
cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt      254
Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu
      -265      -260      -255

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caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat	302
Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn	
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gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt ggc atc tct	350
Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser	
-230 -225 -220	
gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt	398
Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser	
-215 -210 -205	
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Ser Pro Met Leu Tyr Glu Val Tyr Glu Ala Gly Ala Leu Glu Arg	
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Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu	
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Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser	
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Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe	
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Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu	
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ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc ctc aag aag	734
Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys	
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gtc agg agg aaa atc cgt aac aag cag tca gct cag gac agt cgg cgg	782
Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg	
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cgg aag aag gag tac att gat ggg ctg gag agc agg gtg gca gcc tgt	830
Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys	
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Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg	
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His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile	
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Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile	
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Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe	
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Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val	
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act tcc aga aat atc ctg acc cac aag gac gta aca gaa aat ctg gag	1118
Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu	
25 30 35	

acc caa gtg gta gag tcc aga ctg agg gag cca cct gga gcc aag gat	1166
Thr Gln Val Val Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp	
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Ala Asn Gly Ser Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro	
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Arg Pro Ser Gly Arg Ile Arg Ser Val Leu His Ala Asp Glu Met	
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caggacaccc caagagatgt ccttttagtct ctgcctgagg cctagtctgc atttgtttgc	1439
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 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
 -150 -145 -140 -135
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
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 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
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Gln	Glu	Leu	Gln	Lys	Lys	Val	Gln	Glu	Leu	Glu	Arg	His	Asn	Ile	Ser	
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Asn	Lys	Ala	Ala	Gln	Thr	Ser	Thr	Cys	Val	Leu	Ile	Leu	Leu	Phe	Ser	
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Glu	Ala	Gly	Ser	Glu	Asp	Tyr	Gln	Pro	His	Gly	Val	Thr	Ser	Arg	Asn	
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Ile	Leu	Thr	His	Lys	Asp	Val	Thr	Glu	Asn	Leu	Glu	Thr	Gln	Val	Val	
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Glu	Ser	Arg	Leu	Arg	Glu	Pro	Pro	Gly	Ala	Lys	Asp	Ala	Asn	Gly	Ser	
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Thr	Arg	Thr	Leu	Leu	Glu	Lys	Met	Gly	Gly	Lys	Pro	Arg	Pro	Ser	Gly	
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score 0.986
sequence agagggga

<221> protein_bind
<222> complement(410..421)
<223> matinspector prediction
name SRY_02
score 0.955
sequence gaaaacaaaaca

<221> protein_bind
<222> 592..599
<223> matinspector prediction
name MZF1_01
score 0.960
sequence gaagggga

<221> protein_bind
<222> 618..627
<223> matinspector prediction
name MYOD_Q6
score 0.981
sequence agcatctgcc

<221> protein_bind
<222> 632..642
<223> matinspector prediction
name DELTAEF1_01

score 0.958
sequence tcccaccttcc

<221> protein_bind
<222> complement(813..823)
<223> matinspector prediction
name S8_01
score 0.992
sequence gaggcaattat

<221> protein_bind
<222> complement(824..831)
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga

<221> misc_feature
<222> 335,376
<223> n=a, g, c or t
Oligonucleotide

<400> 20
tactataggg cacgcgtggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa 60
tgattggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct 120
cgttgaccgt tggattcctg gaagcagtag ctgttctggt tggatctggt agggacaggg 180
ctcagagggc taggcacgag ggaaggctcag aggagaaggs aggsarggcc cagtgagarg 240
ggagcatgcc ttcccccaac cctggccttc ycttggymam agggcgkty tgggmacttr 300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacia tagcctgaat 360
gggatttcag gttagnccagg gtgagagggg aggcctctctg gcttagtttt gttttgtttt 420
ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggtt gtcctcacc 480
agtcggaact ccctaccact ttcaggagag tggttttagg cccgtggggc tgttctgttc 540
caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcggggc tgaaggggag 600
tgggttctcg cccaaagagc atctgcccac ttcccacctt cccttctccc accagaagct 660
tgcttgagct gtttgacaaa aaatccaaac cccacttggc tactctggcc tggcttcagc 720
ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct 780
tcctgatggt ccttttaggtt tgggcacaaa atataattgc ctctccctc tcccattttc 840
totcttggga gcaatggtca c 861

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 21
ctgggatgga aggcacggta 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 22
gagaccacac agctagacaa 20

<210> 23

<211> 555
 <212> DNA
 <213> Homo Sapiens

 <220>
 <221> promoter
 <222> 1..500

 <221> transcription start site
 <222> 501

 <221> protein_bind
 <222> 191..206
 <223> matinspector prediction
 name ARNT_01
 score 0.964
 sequence ggactcacgtgctgct

 <221> protein_bind
 <222> 193..204
 <223> matinspector prediction
 name NMYC_01
 score 0.965
 sequence actcacgtgctg

 <221> protein_bind
 <222> 193..204
 <223> matinspector prediction
 name USF_01
 score 0.985
 sequence actcacgtgctg

 <221> protein_bind
 <222> complement(193..204)
 <223> matinspector prediction
 name USF_01
 score 0.985
 sequence cagcacgtgagt

 <221> protein_bind
 <222> complement(193..204)
 <223> matinspector prediction
 name NMYC_01
 score 0.956
 sequence cagcacgtgagt

 <221> protein_bind
 <222> complement(193..204)
 <223> matinspector prediction
 name MYCMAX_02
 score 0.972
 sequence cagcacgtgagt

 <221> protein_bind

<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgtggtctc

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<220>
<221> CDS
<222> 266..535

<221> sig_peptide
<222> 266..307
<223> Von Heijne matrix
      score 15
      seq LLPLLLLLLPMCWA/VE
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23

<210> 25
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..274

<221> sig_peptide
 <222> 35..82
 <223> Von Heijne matrix
 score 14.8000001907349
 seq SLPLLLLLLGAWA/IP

<400> 25
 acagactaca cttgctgaac tggctcctgg ggcc atg agg ctg tca ctg cca ctg 55
 Met Arg Leu Ser Leu Pro Leu
 -15 -10
 ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc ggg gac 103
 Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu Gly Asp
 -5 1 5
 agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag gag atg 151
 Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu Glu Met
 10 15 20
 tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc aga gct 199
 Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys Arg Ala
 25 30 35
 gtg gct tac cag gtg agt cct tca cca ctg tca cct gcc ctg ctc aca 247
 Val Ala Tyr Gln Val Ser Pro Ser Pro Leu Ser Pro Ala Leu Leu Thr
 40 45 50 55
 ccc ctt ctc aag cca gcc ccc acc ggg 274
 Pro Leu Leu Lys Pro Ala Pro Thr Gly
 60

<210> 26
 <211> 230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..229

<221> sig_peptide
 <222> 29..94
 <223> Von Heijne matrix
 score 13.8000001907349
 seq LGLLLLWLRGARC/GV

<400> 26
 aaggagtcag tctcagtcag gacacagc atg gac atg agg gtc ccc gct cag 52
 Met Asp Met Arg Val Pro Ala Gln
 -20 -15

ctc	ctg	ggg	ctc	ctg	cta	ctc	tgg	ctc	cga	ggg	gcc	aga	tgt	ggc	gtc	100
Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Arg	Gly	Ala	Arg	Cys	Gly	Val	
			-10						-5					1		
cag	atg	acc	cag	ttt	cca	ctg	tcc	ctg	tct	gca	tcg	gta	gga	gac	aga	148
Gln	Met	Thr	Gln	Phe	Pro	Leu	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
	5						10					15				
gtc	acc	atc	act	tgc	cgg	aca	agc	cat	ata	att	aac	atc	ttt	tta	aat	196
Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	His	Ile	Ile	Asn	Ile	Phe	Leu	Asn	
	20					25					30					
tgg	tat	cag	cag	aaa	cca	ggc	aaa	gcc	cct	tgg	g					230
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Trp						
35					40					45						

<210> 27
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..193

<221> sig_peptide
 <222> 44..112
 <223> Von Heijne matrix
 score 13.8000001907349
 seq VLLLLLLSGDVQS/SE

<400> 27																
agaggggcttc	cggggctgcc	gggtctgagtg	cagagctgct	gtc	atg	gcg	gcc	gct								55
					Met	Ala	Ala	Ala								
									-20							
ctg	tgg	ggc	ttc	ttt	ccc	gtc	ctg	ctg	ctg	ctg	cta	tcg	ggg	gat		103
Leu	Trp	Gly	Phe	Phe	Pro	Val	Leu	Leu	Leu	Leu	Leu	Ser	Gly	Asp		
			-15						-10				-5			
gtc	cag	agc	tcg	gag	gtg	ccc	ggg	gct	gct	gct	gag	gga	tcg	gga	ggg	151
Val	Gln	Ser	Ser	Glu	Val	Pro	Gly	Ala	Ala	Ala	Glu	Gly	Ser	Gly	Gly	
		1				5						10				
agt	ggg	gtc	ggc	ata	gga	gak	cgc	ttc	aag	att	gag	gga	ctg	gg		195
Ser	Gly	Val	Gly	Ile	Gly	Xaa	Arg	Phe	Lys	Ile	Glu	Gly	Leu			
	15					20					25					

<210> 28
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..276

<221> sig_peptide
 <222> 25..90
 <223> Von Heijne matrix

score 13.5
seq LGLLLLWLXGARC/DI

<400> 28
agtcagtctc agacaggaca cagc atg gac atg agg gtc ccc gct cag ctc 51
Met Asp Met Arg Val Pro Ala Gln Leu
-20 -15
ctg ggg ctc ctg cta ctc tgg ctc yka ggt gcc aga tgt gac atc cag 99
Leu Gly Leu Leu Leu Leu Trp Leu Xaa Gly Ala Arg Cys Asp Ile Gln
-10 -5 1
atg aca cag tct cca gtc ctg cct gca tct gta gga gac aga gtc acc 147
Met Thr Gln Ser Pro Val Leu Pro Ala Ser Val Gly Asp Arg Val Thr
5 10 15
atc act tgc cgg gca agt cag agc att ggc agc tat tta aac tgg tat 195
Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Tyr Leu Asn Trp Tyr
20 25 30 35
cag cat aaa cca ggg cat gcc cct cgc ctc ctg atc tat gct gca act 243
Gln His Lys Pro Gly His Ala Pro Arg Leu Leu Ile Tyr Ala Ala Thr
40 45 50
act ttg tgc agg ggc ggc ccg gcc aga ttc agt 276
Thr Leu Ser Arg Gly Gly Pro Ala Arg Phe Ser
55 60

<210> 29
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..240

<221> sig_peptide
<222> 25..120
<223> Von Heijne matrix
score 13.5
seq LLLLLLLPPPGSC/AG

<400> 29
agggcgctgc gcggcgccagc gaaa atg gcg gct tcc agg tgg gcg cgc aag 51
Met Ala Ala Ser Arg Trp Ala Arg Lys
-30 -25
gcc gtg gtc ctg ctt tgt gcc tct gac ctg ctg ctg ctg ctg cta ctg 99
Ala Val Val Leu Leu Cys Ala Ser Asp Leu Leu Leu Leu Leu Leu Leu
-20 -15 -10
cta cca ccg cct ggg tcc tgc gcc ggc cga agg tgc ccy dgg acg ccc 147
Leu Pro Pro Pro Gly Ser Cys Ala Gly Arg Arg Ser Pro Xaa Thr Pro
-5 1 5
gac gag tct acc cca cct ccc cgg aag aag aag aag gat att cgc gat 195
Asp Glu Ser Thr Pro Pro Arg Lys Lys Lys Lys Asp Ile Arg Asp
10 15 20 25
tac aat gat gca gac atg gcg cgt ctt ctg gag caa ggg gag ggg 240
Tyr Asn Asp Ala Asp Met Ala Arg Leu Leu Glu Gln Gly Glu Gly
30 35 40

<210> 30
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..460

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 13.5
 seq WVLLLALLEGVQC/DV

<221> misc_feature
 <222> 280..281,311..313
 <223> n=a, g, c or t
 Oligonucleotide

<400> 30
 agctctcaga gaggtgcctt agccctggat tccaaggcat ttccacttgg tgatcagcac 60
 tgaacacaga ggactcacc atg gag ttg ggg ctg tgc tgg gtt ctc ctt tta 112
 Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu
 -15 -10
 gct ctt tta gaa ggt gtc caa tgt gac gtg gaa tta gtg gag tct ggg 160
 Ala Leu Leu Glu Gly Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly
 -5 1 5
 ggc ggc ttg gtg cag cct gga ggg tct ctg aga ctt tcc tgt gca gcc 208
 Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 10 15 20
 tct gga ttc aat ttt agc act tat gag atg cat tgg atc cgc cag gct 256
 Ser Gly Phe Asn Phe Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala
 25 30 35 40
 cca ggc aag ggc ccg gag tgg gtn nca tat gtc agt ggt gga ggt gga 304
 Pro Gly Lys Gly Pro Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly
 45 50 55
 acc agh nnn aac gcv sac tct gtg aag ggc cga ttc acc atc tcc aga 352
 Thr Xaa Xaa Asn Ala Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 60 65 70
 gac aat gcc aac agt ttt gtg tat cta caa atg gac agt ctg cga gtc 400
 Asp Asn Ala Asn Ser Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val
 75 80 85
 gag gac acc gct ctc tat tac tgt gcg aga rgg gat tac gac ttc tgg 448
 Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp
 90 95 100
 agt ggt tat tat a 461
 Ser Gly Tyr Tyr
 105

<210> 31
 <211> 112
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 28..111

<221> sig_peptide

<222> 28..84

<223> Von Heijne matrix

score 13.3999996185303

seq LLLLLSHCTGSLS/QP

<400> 31

aactgtgcat gtcaggctgt gtccacc atg gcc tgg act cct ctt ctt ctc ttg 54
Met Ala Trp Thr Pro Leu Leu Leu Leu

-15

ctc ctc tct cac tgc aca ggt tcc ctc tcc cag cct gtg ctg act cag 102
Leu Leu Ser His Cys Thr Gly Ser Leu Ser Gln Pro Val Leu Thr Gln

-10

-5

1

5

cca cgc ggg g 112
Pro Arg Gly

<210> 32

<211> 445

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 80..445

<221> sig_peptide

<222> 80..136

<223> Von Heijne matrix

score 12.8000001907349

seq WVFLVALLRGVQC/QV

<221> misc_feature

<222> 2,7

<223> n=a, g, c or t

Oligonucleotide

<400> 32

anctctngga gaggagccca gcactagaag tcggcggtgt ttccattcgg tgatcagcac 60
tgaacacaga ggactcacc atg gag ttt ggg ctg aat tgg gtt ttc ctc gtt 112
Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val

-15

-10

gct ctt tta aga ggt gtc cag tgt cag gtt cag ttg gtg gag tct ggg 160
Ala Leu Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly

-5

1

5

gga ggc gtg gtc cag cct ggg acg tcc ctg aca ctt tcc tgt gca ggc 208
Gly Gly Val Val Gln Pro Gly Thr Ser Leu Thr Leu Ser Cys Ala Gly

10

15

20

tcg gga ttc agt ttc agt gat tat ggc atc cac tgg gtc cgc cag gct 256

Ser	Gly	Phe	Ser	Phe	Ser	Asp	Tyr	Gly	Ile	His	Trp	Val	Arg	Gln	Ala	
25					30					35					40	
cca	ggc	aag	ggg	ctg	gaa	tgg	gtg	gcg	gtt	att	tca	cac	gat	gga	aat	304
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Ser	His	Asp	Gly	Asn	
			45						50					55		
aac	aaa	tat	tat	gga	ggc	tcc	atg	aag	ggc	cga	gtc	acc	atc	tcc	aga	352
Asn	Lys	Tyr	Tyr	Gly	Gly	Ser	Met	Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	
		60					65					70				
gac	aac	tcc	agg	cat	acc	gtg	tct	ttg	caa	atg	agc	agc	ttg	gga	cct	400
Asp	Asn	Ser	Arg	His	Thr	Val	Ser	Leu	Gln	Met	Ser	Ser	Leu	Gly	Pro	
		75				80					85					
gag	gac	acg	gca	gtg	tat	tac	tgt	gcg	aaa	gat	cga	acc	ggg	ggg		445
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Asp	Arg	Thr	Gly	Gly		
	90					95					100					

<210> 33
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..319

<221> sig_peptide
 <222> 41..97
 <223> Von Heijne matrix
 score 12.6000003814697
 seq FLLLLAAPRWVLS/QV

<400> 33																
aaatacttts	kgcagagtc	ctc	tggac	ctc	ctg	caaga	aac	atg	aaa	ctt	ctg	tgg				55
								Met	Lys	Leu	Leu	Trp				
												-15				
ttc	ttc	ctt	ctc	ctg	ctg	gca	gct	ccc	aga	tgg	gtc	ctg	tcc	cag	gtg	103
Phe	Phe	Leu	Leu	Leu	Leu	Ala	Ala	Pro	Arg	Trp	Val	Leu	Ser	Gln	Val	
			-10					-5						1		
cag	ctg	gtg	smg	tgc	ggc	cca	gga	ctg	gtg	aag	cct	tgc	ggg	acc	ctg	151
Gln	Leu	Val	Xaa	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gly	Thr	Leu	
		5				10					15					
tcc	cta	acg	tgc	act	gts	ksb	ggk	grs	ksc	ata	act	aat	tac	tac	tgg	199
Ser	Leu	Thr	Cys	Thr	Val	Xaa	Gly	Xaa	Xaa	Ile	Thr	Asn	Tyr	Tyr	Trp	
	20				25				30							
agt	bgg	atc	cgg	cag	tcc	cca	ggg	aag	gga	ctg	gag	tgg	att	ggg	act	247
Ser	Xaa	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Thr	
	35				40				45					50		
atc	tac	tac	agt	ggg	agc	gcc	gac	cac	aac	ccc	tcc	ctc	agg	agt	mga	295
Ile	Tyr	Tyr	Ser	Gly	Ser	Ala	Asp	His	Asn	Pro	Ser	Leu	Arg	Ser	Arg	
			55					60					65			
gcc	act	att	tca	tta	gac	acg	cgc	gg								321
Ala	Thr	Ile	Ser	Leu	Asp	Thr	Arg									
			70													

<210> 34

[illegible]

<221> CDS

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<221> sig peptide
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<223> Von Heijne matrix

seq LLXLLTALPPLWS/SS

agagctcagg gtgckgagcg tgtgaccagc agtgagcaga ggccggcc atg gcc agc 57
Met Ala Ser
-20

ctg ggg ctg ctg ctc ctg ckc tta ctg aca gca ctg cca ccg ctg tgg 105
Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro Pro Leu Trp
-15 -10 -5

tcc tcc tca ctg cct ggg ctg gac ack gct gaa agt aaa gcc acc akt 153
Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys Ala Thr Xaa
1 5 10 15

gca gac ctg atc ctg tct gcg ctg gag aga gcc acc ggg g 193
Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly
20 25

<211> 438

<213> Homo sapiens

<221> CDS

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<221> sig peptide
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<223> Von Heijne matrix

seq LLLLLLLPLRGQA/NT

acgagaaggg	gagggggccc	agccctgctt	tgggcaatcc	ttgctctgac	cactcagaca	60
ccgtgtcctc	ttgcctggga	gaggggaagc	agatctgagg	acatctctgt	gccaggccag	120
aaaccgcccc	cctgcagttc	cttctccggg	atg gac gtg ggg ccc agc tcc ctg			174
			Met Asp Val Gly Pro Ser Ser Leu			
			-25			

ccc cac ctt ggg ctg aag ctg ctg ctg ctc ctg ctg ctg ctg ccc ctc 222
Pro His Leu Gly Leu Lys Leu Leu Leu Leu Leu Leu Leu Leu Pro Leu
-20 -15 -10 -5

agg ggc caa gcc aac aca ggc tgc tac ggg atc cca ggg atg ccc ggc 270
Arg Gly Gln Ala Asn Thr Gly Cys Tyr Gly Ile Pro Gly Met Pro Gly

	1	5	10	
ctg ccc ggg gca cca ggg aag gat ggg tac gac gga ctg ccg ggg ccc				318
Leu Pro Gly Ala Pro Gly Lys Asp Gly Tyr Asp Gly Leu Pro Gly Pro				
15	20	25		
aag ggg gag cca gga atc cca gcc att ccc ggg atc cga gga ccc aaa				366
Lys Gly Glu Pro Gly Ile Pro Ala Ile Pro Gly Ile Arg Gly Pro Lys				
30	35	40		
ggg cag aag gga gaa ccc ggc tta ccc ggc cat cct ggg aaa aat ggc				414
Gly Gln Lys Gly Glu Pro Gly Leu Pro Gly His Pro Gly Lys Asn Gly				
45	50	55	60	
ccc atg gga ccc cct ggg atg cca				438
Pro Met Gly Pro Pro Gly Met Pro				
65				

<210> 36
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..487

 <221> sig_peptide
 <222> 59..115
 <223> Von Heijne matrix
 score 12.3999996185303
 seq ILLLVAAATGTHA/QV

<221> misc_feature
 <222> 26..28
 <223> n=a, g, c or t
 Oligonucleotide

<400> 36	
atcacacaac agmcacatcs swmvsnnnmc agaagcccc agagtgcagc acctcacc	58
atg gac tgc acc tgg agg atc ctc ctc ttg gtg gca gca gct aca ggc	106
Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly	
-15	-10
acc cac gcc cag gtc cag ttg gta cag tct ggg cct gag gtg aaa aag	154
Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys	
1	5
cct ggg gcc tca gtg aag gtc tcc tgc cag gtt tcc gga tac aac gtc	202
Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val	
15	20
gtg gaa tta tcc atc cac tgg gtg cgt cag tgc cct gga aaa ggg ctt	250
Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu	
30	35
gag tgg atg gga ggt ttt gac ctt gaa agt ggt gaa aca atc tac gca	298
Glu Trp Met Gly Gly Phe Asp Leu Glu Ser Gly Glu Thr Ile Tyr Ala	
50	55
cag agg ttc cag ggc aga atc acc atg acc gag gac tca tct tca gac	346
Gln Arg Phe Gln Gly Arg Ile Thr Met Thr Glu Asp Ser Ser Ser Asp	
65	70
	75

aca gcc ttc atg gag ctg atc agc ctg aga cct gaa gat gcg gcc gtc	394
Thr Ala Phe Met Glu Leu Ile Ser Leu Arg Pro Glu Asp Ala Ala Val	
80 85 90	
tac tac tgt gca acg atc cgg ctg cca gta gtg ctt ttt ttc gcg gct	442
Tyr Tyr Cys Ala Thr Ile Arg Leu Pro Val Val Leu Phe Phe Ala Ala	
95 100 105	
tct ggg gcc agg gaa ccc tgg tcg ccg tct cct cag cmt cca cgg g	488
Ser Gly Ala Arg Glu Pro Trp Ser Pro Ser Pro Gln Xaa Pro Arg	
110 115 120	

<210> 37
 <211> 138
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..136

<221> sig_peptide
 <222> 26..79
 <223> Von Heijne matrix
 score 12.1000003814697
 seq VLLLVAVLLVAVLC/KV

<400> 37	
ttttaccoga ccgacgccg gcgtg atg tgg ctt ccg ctg gtg ctg ctc ctg	52
Met Trp Leu Pro Leu Val Leu Leu Leu	
-15 -10	
gct gtg ctg ctg ctg gcc gtc ctc tgc aaa gtt tac ttg gga cta ttc	100
Ala Val Leu Leu Ala Val Leu Cys Lys Val Tyr Leu Gly Leu Phe	
-5 1 5	
tct ggc agc tcc ccg aat cct ttc tcc gaa gaa agg gg	138
Ser Gly Ser Ser Pro Asn Pro Phe Ser Glu Glu Arg	
10 15	

<210> 38
 <211> 163
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..161

<221> sig_peptide
 <222> 9..83
 <223> Von Heijne matrix
 score 11.8999996185303
 seq WLLLLPLLLLGLNA/GA

<400> 38	
aacttgtc atg gag ctg gca ctg cgg cgc tct ccc gtc ccg cgg tgg ttg	50
Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu	

	-25		-20		-15	
ctg	ctg	ctg	ccg	ctg	ctg	ctg
Leu	Leu	Leu	Pro	Leu	Leu	Leu
	-10		-5		1	5
tgg	ccc	aca	gag	gag	ggc	aag
Trp	Pro	Thr	Glu	Glu	Gly	Lys
			10		15	20
aag	gat	gcc	tac	atg	gg	
Lys	Asp	Ala	Tyr	Met		
		25				

98

146

163

<210> 39
 <211> 427
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..427
 <221> sig_peptide
 <222> 35..91
 <223> Von Heijne matrix
 score 11.8999996185303
 seq FLFLLTCCPGSNS/QA

<221> misc_feature
 <222> 138..139
 <223> n=a, g, c or t
 Oligonucleotide

<400> 39	
tctggcacca ggggtccctt ccaatatcag cacc atg gcc tgg act cct ctc ttt	55
	Met Ala Trp Thr Pro Leu Phe

	-15	
ctg ttc ctc ctc act tgc tgc cca ggg tcc aat tcc cag gct gtg gkg	103	
Leu Phe Leu Leu Thr Cys Cys Pro Gly Ser Asn Ser Gln Ala Val Xaa		
	-10	-5
act cag gag ccc ctc act gac tgt gtc ccc cgg ann aca gtc act ctc	151	
Thr Gln Glu Pro Leu Thr Asp Cys Val Pro Arg Xaa Thr Val Thr Leu		
5	10	15
acc tgt ggc tcc agt att gga gct gtc acc aat ggt cat ttt ccc tac	199	
Thr Cys Gly Ser Ser Ile Gly Ala Val Thr Asn Gly His Phe Pro Tyr		
	25	30
tgg ttc caa cag aag cct ggc caa gcc ccc agg aca ctg att tct gat	247	
Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr Leu Ile Ser Asp		
	40	45
acg ttc aac aga cag tcc tcg aca cct gcc cgc ttc tct ggc tcc ctc	295	
Thr Phe Asn Arg Gln Ser Ser Thr Pro Ala Arg Phe Ser Gly Ser Leu		
	55	60
ctg ggg ggc aaa gct gtc ctg act ctt tcg gat gcg caa cct gac gat	343	
Leu Gly Gly Lys Ala Val Leu Thr Leu Ser Asp Ala Gln Pro Asp Asp		
	70	75
gag gct gaa tat tat tgt gtc ctc tcc tat agt ggt ggt cgg ccg gtg	391	

Glu	Ala	Glu	Tyr	Tyr	Cys	Val	Leu	Ser	Tyr	Ser	Gly	Gly	Arg	Pro	Val	
85					90					95					100	
ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	agt	cag					427
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln					
				105					110							

<210> 40
 <211> 97
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..96

<221> sig_peptide
 <222> 22..84
 <223> Von Heijne matrix
 score 11.8999996185303
 seq LALCLLLGPLAGA/KP

<400> 40																
agatcaggaa	gcaccgggaa	g	atg	cag	gcc	tgc	atg	gtg	ccg	ggg	ctg	gcc				51
			Met	Gln	Ala	Cys	Met	Val	Pro	Gly	Leu	Ala				
			-20						-15							
ctc	tgc	ctc	cta	ctg	ggg	cct	ctt	gca	ggg	gcc	aag	cct	gtg	cag	g	97
Leu	Cys	Leu	Leu	Leu	Gly	Pro	Leu	Ala	Gly	Ala	Lys	Pro	Val	Gln		
-10					-5						1					

<210> 41
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..249

<221> sig_peptide
 <222> 13..81
 <223> Von Heijne matrix
 score 11.8000001907349
 seq CLFVCLFLSQSFA/FV

<400> 41																
aaaagtattg	gg	atg	cct	agt	tac	aar	gtg	tgt	ggg	ggt	ttt	tgt	ttg	ttt		51
		Met	Pro	Ser	Tyr	Lys	Val	Cys	Gly	Val	Phe	Cys	Leu	Phe		
			-20						-15							
ggt	tgt	ttg	ttt	ttg	agc	cag	agt	ttt	gct	ttt	gtc	ctc	cag	gct	gga	99
Val	Cys	Leu	Phe	Leu	Ser	Gln	Ser	Phe	Ala	Phe	Val	Leu	Gln	Ala	Gly	
-10				-5				1				5				
gtg	cag	tg	g	cgc	gat	ctc	tgc	tca	ctg	caa	cct	cag	ctt	ccc	agg	ttc
Val	Gln	Trp	Arg	Asp	Leu	Cys	Ser	Leu	Gln	Pro	Gln	Leu	Pro	Arg	Phe	147
				10				15					20			

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ggg cca tcc tcc tgc ctc agc ctc cca agt ggc tgg gac tgc agg cgc      195
Gly Pro Ser Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg
      25                      30                      35

cca cca cca cgc ctg gct aat tct tgt gtt ttc ggt gga gac ggg gtt      243
Pro Pro Pro Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val
      40                      45                      50

tca ccg gg      251
Ser Pro
55

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<210> 42
<211> 319
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 143..319

<221> sig_peptide
<222> 143..205
<223> Von Heijne matrix
      score 11.6000003814697
      seq LLLCLALSGAAET/KP

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<221> misc_feature
<222> 139
<223> n=a, g, c or t
      Oligonucleotide

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<400> 42
agcagaggga acaggaaga aacctaaagg ctgcaggctg ccagggtgtgc ttggagagcc      60
cccttcttcc gccgggctc gcaagcagcg taggactgtg gagaagggcg gtgggcaagg      120
agggaactcg agagcarcny cc atg ggc aca cag gag ggc tgg wgc ctg ctg      172
                      Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu
                      -20                      -15

ctc tgc ctg gct cta tct gga gca gca gaa acc aag ccc cac cca gca      220
Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys Pro His Pro Ala
      -10                      -5                      1                      5

gag ggg cag tgg cgg gca gtg gdc gtg gtc cta gac ygt ttc ctg gtg      268
Glu Gly Gln Trp Arg Ala Val Xaa Val Val Leu Asp Xaa Phe Leu Val
      10                      15                      20

aag gac svt gcg cac cgt gga gct ctc gcc agc agt gag gac agg gca      316
Lys Asp Xaa Ala His Arg Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala
      25                      30                      35

agg      319
Arg

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<210> 43
<211> 412
<212> DNA
<213> Homo sapiens

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<220>

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<221> CDS
 <222> 35..412

<221> sig_peptide
 <222> 35..82
 <223> Von Heijne matrix
 score 11.1999998092651
 seq LVVFLLLWGVTVG/PV

<221> misc_feature
 <222> 148
 <223> n=a, g, c or t
 Oligonucleotide

<400> 43
 agacactcac tgcaccggag tgagcgcgac catc atg tcc atg ctc gtg gtc ttt 55
 Met Ser Met Leu Val Val Phe
 -15 -10
 ctc ttg ctg tgg ggt gtc acc tgg ggc cca gtg aca gaa gca gcc ata 103
 Leu Leu Leu Trp Gly Val Thr Trp Gly Pro Val Thr Glu Ala Ala Ile
 -5 1 5
 ttt tat gag acg cag scc agc ctg tgg gca gag tcc gaa cac tgn ctg 151
 Phe Tyr Glu Thr Gln Xaa Ser Leu Trp Ala Glu Ser Glu His Xaa Leu
 10 15 20
 aaa acc ctt ggc caa tgt gac gct gac gtg cca ggc ccg cct gga gac 199
 Lys Thr Leu Gly Gln Cys Asp Ala Asp Val Pro Gly Pro Pro Gly Asp
 25 30 35
 tcc aga ctt cca gct gtt caa gaa tgg ggg gcc cag gag cct gtg cac 247
 Ser Arg Leu Pro Ala Val Gln Glu Trp Gly Ala Gln Glu Pro Val His
 40 45 50 55
 ctt gac tca cct gcc atc aag cac cag ttc ctg ctg acg ggt gac acc 295
 Leu Asp Ser Pro Ala Ile Lys His Gln Phe Leu Leu Thr Gly Asp Thr
 60 65 70
 cag ggc cgc tac cgc tgc cgc tcg ggc ttg tcc aca gga tgg mcc cag 343
 Gln Gly Arg Tyr Arg Cys Arg Ser Gly Leu Ser Thr Gly Trp Xaa Gln
 75 80 85
 ctg agc aag ctc ctg gag ctg aca ggg cca aaa gtc ctt gcc tgc tcc 391
 Leu Ser Lys Leu Leu Glu Leu Thr Gly Pro Lys Val Leu Ala Cys Ser
 90 95 100
 ctg gct ctc gat ggc gcc agt 412
 Leu Ala Leu Asp Gly Ala Ser
 105 110

<210> 44
 <211> 331
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..331
 <221> sig_peptide
 <222> 32..88

<223> Von Heijne matrix
 score 11.1999998092651
 seq IGFLLLWVPASRG/EI

<400> 44

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atgagcaaaa ctgacaagtc aaggcaggaa g atg ttg cca tca caa ctc att      52
                                Met Leu Pro Ser Gln Leu Ile
                                -15
ggg ttt ctg ctg ctc tgg gtt cca gcc tcc agg ggt gaa att gtg ctg      100
Gly Phe Leu Leu Leu Trp Val Pro Ala Ser Arg Gly Glu Ile Val Leu
-10                                -5                                1
act cag tct cca gac ttt ctg tct gtg act cca aag gag aaa gtc acc      148
Thr Gln Ser Pro Asp Phe Leu Ser Val Thr Pro Lys Glu Lys Val Thr
5                                10                                15                                20
atc acc tgc cgg gcc agt sag agc att ggt agt agt tta tac tgg tac      196
Ile Thr Cys Arg Ala Ser Xaa Ser Ile Gly Ser Ser Leu Tyr Trp Tyr
25                                30                                35
cag cag aaa cca cat cag tct cca aag ctc gtc atc aag tat gct tcc      244
Gln Gln Lys Pro His Gln Ser Pro Lys Leu Val Ile Lys Tyr Ala Ser
40                                45                                50
cag tcc ttc tca ggg gtc tcc tcg agg ttc agt ggc agt gga tct ggg      292
Gln Ser Phe Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
55                                60                                65
aca gat ttc acc ctc aca atc aat agc ctg gaa cct ggg      331
Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro Gly
70                                75                                80

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<210> 45

<211> 520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 176..520

<221> sig_peptide

<222> 176..235

<223> Von Heijne matrix
 score 11.1999998092651
 seq AFLLLVALSYTLA/RD

<400> 45

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gaagataatc acttggggaa aggaagggtc gtttctgagt tagcaacaag taaatgcagc      60
actagtgggt gggattgagg tatgccttgg tgcataaata gagactcagc tgtgctggca      120
cactcagaag cttggaccgc atcctagccg ccgactcaca caaggcagag ttgcc atg      178
                                Met
                                -20
gag aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac      226
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Val Ala Leu Ser Tyr
-15                                -10                                -5
act ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca      274
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
1                                5                                10

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aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt	322
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly	
15 20 25	
gac caa ctc atc tgg act cag aca tat gaa gaa gct cta tat aaa tcc	370
Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys Ser	
30 35 40 45	
aag aca agc aac aaa ccc ttg atg att att cat cac ttg gat gag tgc	418
Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu Cys	
50 55 60	
cca cac agt caa gct tta aag aaa gtg ttt gct gaa aat aaa gaa atc	466
Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu Ile	
65 70 75	
cag aaa ttg gca gag cag ttt gtc ctc ctc aat ctg gtt tat gaa aca	514
Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu Thr	
80 85 90	
act gac	520
Thr Asp	
95	

<210> 46
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..381
 <221> sig_peptide
 <222> 25..84
 <223> Von Heijne matrix
 score 11.1000003814697
 seq LLALLFFLGQAAG/DL

<400> 46	
agcggctcca gctaagagga caag atg agg ccc ggc ctc tca ttt ctc cta	51
Met Arg Pro Gly Leu Ser Phe Leu Leu	
-20 -15	
gcc ctt ctg ttc ttc ctt ggc caa gct gca ggg gat ttg ggg gat gtg	99
Ala Leu Leu Phe Phe Leu Gly Gln Ala Ala Gly Asp Leu Gly Asp Val	
-10 -5 1 5	
gga cct cca att ccc agc ccc ggc ttc agc tct ttc cca ggt gtt gac	147
Gly Pro Pro Ile Pro Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp	
10 15 20	
tcc agc tcc agc ttc agc tcc agc tcc agg tcg ggc tcc agc tcc agc	195
Ser Ser Ser Ser Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser	
25 30 35	
cgc agc tta ggc agc gga ggt tct gtg tcc cag ttg ttt tcc aat ttc	243
Arg Ser Leu Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe	
40 45 50	
acc ggc tcc gtg gat gac cgt ggg acc tgc cag tgc tct gtt tcc ctg	291
Thr Gly Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu	
55 60 65	
cca gac acc acc ttt ccc gtg gac aga gtg gaa cgc ttg gaa ttc aca	339

atg gtc atc atc tct tca gcc tc
Met Val Ile Ile Ser Ser Ala
115 120

459

<210> 48
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..436

<221> sig_peptide
<222> 20..76
<223> Von Heijne matrix
score 11
seq TLLLLTVPSWVLS/QV

<400> 48
gtgaatcctg ctctccacc atg gac ata ctt tgt tcc acg ctc ctg ctm ctg 52
Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu
-15 -10
ack gtc ccg tcc tgg gtc tta tcc car gtc acc ttg arg gaa tct ggt 100
Thr Val Pro Ser Trp Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly
-5 1 5
cct gcg ctg gtg aaa gcc aca cag acc ctc aga ctg acc tgc acc ttc 148
Pro Ala Leu Val Lys Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe
10 15 20
tct ggg ttc tca ctc agc act aat aga atg cgt gtg agt tgg atc cgt 196
Ser Gly Phe Ser Leu Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg
25 30 35 40
cag ccc cca ggg aag gcc ctg gag tgg ctt gca cgg att gat tgg gat 244
Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp
45 50 55
gat tat aag agg tac agc aca tct ctg aag acc agg gtc acc atc tcc 292
Asp Tyr Lys Arg Tyr Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser
60 65 70
aag gac acg tcc aaa aac cag gtg atc ctg aca atg acc aac gtg gac 340
Lys Asp Thr Ser Lys Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp
75 80 85
cct gcg gac aca gcc acc tat tac tgt gca cgc ctt tca acg gca gct 388
Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Leu Ser Thr Ala Ala
90 95 100
acc cca cag ttt ttt gac ttc tgg ggc cag gga gtc ctg gtc tcc gtc t 437
Thr Pro Gln Phe Phe Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
105 110 115 120

<210> 49
<211> 456
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
 <222> 40..456

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 49
 aaatactttc tgagagtcct ggacctcctg tgcaagaac atg adw cat ctg tgg 54
 Met Xaa His Leu Trp
 -15
 ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg 102
 Phe Phe Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg kwg acc ctg 150
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Xaa Thr Leu
 5 10 15
 tcc ctc acc tgc act gtc tct ggt gac tcc atc agt agt tac tac tgg 198
 Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr Tyr Trp
 20 25 30
 agc tgg atc cgg cag ccc cca ggg aag gga ctg gag tgg att ggc tat 246
 Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr
 35 40 45 50
 atc tat tac agt ggg agc acc aac tac aac ccc tcc ctc aag agt cga 294
 Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc acc ata tca gtg gac acg tcc aag aac caa ttc tcc ctg aag ctg 342
 Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
 70 75 80
 agc tct gtg acc gca gcg gac acg gcc gtg tat tac tgt gcg aga sgg 390
 Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
 85 90 95
 ctg cma tac tat gat agg agt ggt tat ttc aga tat ttt gac tac tgg 438
 Leu Xaa Tyr Tyr Asp Arg Ser Gly Tyr Phe Arg Tyr Phe Asp Tyr Trp
 100 105 110
 ggc cag gga acc tgg tca 456
 Gly Gln Gly Thr Trp Ser
 115 120

<210> 50
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..445
 <221> sig_peptide
 <222> 38..94
 <223> Von Heijne matrix
 score 10.8999996185303

seq FLLLVAAPRWVLS/QV

<221> misc_feature

<222> 16

<223> n=a, g, c or t
Oligonucleotide

<400> 50

atactttctg agagtncctgg acctcctgtg caagaac atg aaa cat ctg tgg ttc	55
Met Lys His Leu Trp Phe	
-15	
ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag	103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln	
-10	
ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag acc ctg tcc	151
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser	
5	
10	
15	
ctc acc tgc aca gtc tct ggt ggc tcc atc gac agt ggt aat tac tac	199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asp Ser Gly Asn Tyr Tyr	
20	
25	
30	
35	
tgg agc tgg atc cgg cag ccc gcc ggg aag gga ctg gag tgg att ggg	247
Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly	
40	
45	
50	
cgc atc tat agt act ggg agc acc aat tac aac ccc tcc ctc agc agt	295
Arg Ile Tyr Ser Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Ser Ser	
55	
60	
65	
cga gtc cag ata tcg tta gac acg tcc aag aac ctg ctc tcc ttg aac	343
Arg Val Gln Ile Ser Leu Asp Thr Ser Lys Asn Leu Leu Ser Leu Asn	
70	
75	
80	
ctg acc tct gtg acc gcc gca gac acg gcc gtc tat ttt tgt gcg cga	391
Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg	
85	
90	
95	
acc ttc ccc ttc tac tgg tac ctc gat ctc tgg ggc cgt ggc atc ctg	439
Thr Phe Pro Phe Tyr Trp Tyr Leu Asp Leu Trp Gly Arg Gly Ile Leu	
100	
105	
110	
115	
gtc act gt	447
Val Thr	

<210> 51

<211> 466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 38..466

<221> sig_peptide

<222> 38..94

<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAPRWVLS/QV

<221> misc_feature

<222> 423

<223> n=a, g, c or t
Oligonucleotide

<400> 51

atactttctg agagtctctg acctcctgtg caagaac atg aaa cac ctg tgg ttc 55
Met Lys His Leu Trp Phe

-15

ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln

-10

-5

1

ctg cag gag tgc ggc cca aga ctg gtg aag cct tca cag acc ctg tcc 151
Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gln Thr Leu Ser

5

10

15

ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt ggt tac ttc 199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly Gly Tyr Phe

20

25

30

35

tgg agt tgg atc cgc cag cac cca ggg cgg ggc ctg gag tgg att ggc 247
Trp Ser Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu Trp Ile Gly

40

45

50

tac atc tat tac aat tgg agc acc tac tac aat ccg tcc ctc agg agt 295
Tyr Ile Tyr Tyr Asn Trp Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser

55

60

65

cga gtt acc atg tca atg gac acg tct aag aac cag ttc tcc ctg aac 343
Arg Val Thr Met Ser Met Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn

70

75

80

ctg aac tct gta act gcc gcg gac acg gsc atg tat tac tgt gcs aga 391
Leu Asn Ser Val Thr Ala Ala Asp Thr Xaa Met Tyr Tyr Cys Ala Arg

85

90

95

ggt cgc gga cgc ctt ggc tgg ttc ash mct tng ggg mca ggg rac cca 439
Gly Arg Gly Arg Leu Gly Trp Phe Xaa Xaa Gly Xaa Gly Xaa Pro

100

105

110

115

ggt cac cgt ctc atc agc cgt cca ggg 466
Gly His Arg Leu Ile Ser Arg Pro Gly

120

<210> 52

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..391

<221> sig_peptide

<222> 59..115

<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAAPRWVLS/QV

<221> misc_feature

<222> 342

<223> n=a, g, c or t

Oligonucleotide

<400> 52

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agggtcctgc tcacatggga aatacttttct gagagtcctg gacctcctgt gcaagaac      58
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      106
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
          -15          -10          -5
gtc ctg tcc cag gtg cag ctg cag gag tgc ggc cca gga ctg gtg aag      154
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
          1          5          10
cct tca gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc      202
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
          15          20          25
agg act ggt tct tac tac tgg act tgg gtt cgc cag ccc ccc ggg aag      250
Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys
          30          35          40          45
ggc ctg gag tgg att ggc tac att tat tat act ggg gac acc tac tac      298
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr
          50          55          60
aac ccg tcc ctc aag agt cga att acc atg tcr cta gac acg tny wag      346
Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa
          65          70          75
aac cag ttc kcc ctg agc ctg acc tct gtg act gtc gca gac acg g      392
Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr
          80          85          90

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<210> 53

<211> 172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 14..172

<221> sig_peptide

<222> 14..58

<223> Von Heijne matrix

score 10.8999996185303

seq LSVCLLLVTLALC/CY

<400> 53

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aaaacaagcc acc atg aag ctg tgc gtg tgt ctc ctg ctg gtc acg ctg      49
          Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu
          -15          -10          -5
gcc ctc tgc tgc tac cag gcc aat gcc gag ttc tgc cca gct ctt gtt      97
Ala Leu Cys Cys Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val
          1          5          10
tct gag ctg tta gac ttc ttc ttc att agt gaa cct ctg ttc aag tta      145
Ser Glu Leu Leu Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu
          15          20          25
agt ctt gcc aaa ttt gat gcc cct cga      172
Ser Leu Ala Lys Phe Asp Ala Pro Arg
          30          35

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<210> 54
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 190..258

<221> sig_peptide
 <222> 190..237
 <223> Von Heijne matrix
 score 10.8999996185303
 seq VLLVLSLSQCLLS/DP

<400> 54
 tacctggaaa gaacagaaat ttgttaattt acaggtctga aggtgagaaa tctgaaatta 60
 gtcttacaaa actaaaatga agttgttga agccttggct ccttctggag gttccagggg 120
 aaaaaagtat gtttccttga ctttccagcc kstacaggcc cacagcattc ctgcttgcag 180
 ccctatgtc atg tca cct gtc ctc ttg gtg ctg tca ttg tca caa tgc ctt 231
 Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu
 -15 -10 -5
 ctt tct gac cct gtc att cct ggc ctc c 259
 Leu Ser Asp Pro Val Ile Pro Gly Leu
 1 5

<210> 55
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..318

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWVLS/QV

<400> 55
 aaacacsyyt tgagagtcct ggacctcctg tgcaggacc atg aaa cat ctg tgg 54
 Met Lys His Leu Trp
 -15
 ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg 102
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 cgg ctg cag gag tgg ggc cca cgg ctg gtg aag cct tgg gag amc ctg 150
 Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Glu Xaa Leu
 5 10 15
 tcc ctc acc tgt agt gtc tct ggt gtc tcc gtc act aat ttc ttc tgg 198
 Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val Thr Asn Phe Phe Trp

20	25	30	
aac tgg atc cgg aag ccc cca ggc aag ggc ctg gag tgg ctt ggc tac			246
Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr			
35	40	45	50
atg tct tat ggc gtg agc aca aac tat cac ccc gcc tac cag agt cgg			294
Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro Ala Tyr Gln Ser Arg			
	55	60	65
gtc agt ata tcg att gac acg tgg gg			320
Val Ser Ile Ser Ile Asp Thr Trp			
70			

<210> 56
 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..455

<221> sig_peptide
 <222> 39..95
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 56	
aatacttttct gagagtctctg gacctcctgt gcaagaac atg aaa cat ctg tgg ttc	56
	Met Lys His Leu Trp Phe
	-15
ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag	104
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln	
	-10
	-5
	1
ctg cag gag gcg ggc cca cga ctg gtg aag cct tcg gag gcc ctg tcc	152
Leu Gln Glu Ala Gly Pro Arg Leu Val Lys Pro Ser Glu Ala Leu Ser	
	5
	10
	15
ctc acc tgc act gtc tct ggt gtc tcc agc agc aat tac gac tgg agt	200
Leu Thr Cys Thr Val Ser Gly Val Ser Ser Ser Asn Tyr Asp Trp Ser	
	20
	25
	30
	35
tgg att cgg cag gcc cca ggg aag gga ctg gaa tgg att ggg tat ata	248
Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile	
	40
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	50
gac gat agt aag aat aga ggg agt acg acc tac aac ccc tcc ctc aag	296
Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Lys	
	55
	60
	65
agt cga gtc acc ata tcg stg gac acg tcc aag ast cag ttg tcc ctg	344
Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser Lys Xaa Gln Leu Ser Leu	
	70
	75
	80
agg ctg acc tct gtg acc kcs gca gac acg gcc gtc tat tat tgt gcg	392
Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr Ala Val Tyr Tyr Cys Ala	
	85
	90
	95
aga aag tca tct atg cat agt agt ggc tgg cat aac cgg agt ctc tac	440
Arg Lys Ser Ser Met His Ser Ser Gly Trp His Asn Arg Ser Leu Tyr	
	100
	105
	110
	115

tgg tac ttc gat cct gg
 Trp Tyr Phe Asp Pro
 120

457

<210> 57
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..418

<221> sig_peptide
 <222> 17..94
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 57
 atactttctg agactc atg gac ctc ctg cac aag aac atg aaa gac ctg tgg 52
 Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp
 -25 -20 -15
 ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tct cag gtg 100
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
 -10 -5 1
 ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg acc ctg tcc 148
 Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser
 5 10 15
 ctc acc tgc gct gtc tct ggt ggc tcc atc ata agt agt aat tgg tgg 196
 Leu Thr Cys Ala Val Ser Gly Ser Ile Ile Ser Ser Asn Trp Trp
 20 25 30
 agt tgg gtc cgc cag acc cca ggg aag ggg ctg gag tgg att ggg gaa 244
 Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
 35 40 45 50
 atc tat gaa gat ggg atc acc aac tac aac ccg tcc ctc aag agt cga 292
 Ile Tyr Glu Asp Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc atc att tca gtg gac aag gcc aag aac cag ttc tcc ctg aag atg 340
 Val Ile Ile Ser Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met
 70 75 80
 agg tct gtg acc gcc tcg gac acg gcc gtc tat tac tgt gcg aga ggt 388
 Arg Ser Val Thr Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
 85 90 95
 agc agc tcg gtt cgg aca gac tac tgg ggc ca 420
 Ser Ser Ser Val Arg Thr Asp Tyr Trp Gly
 100 105

<210> 58
 <211> 469
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 38..469

<221> sig_peptide
 <222> 38..94
 <223> Von Heijne matrix
 score 10.8999996185303
 seq FLLLVAAPRWLS/QV

<400> 58
 atactttctg agagtcctgg acctcctgtg caagaac atg aaa cac ctg tgg ttc 55
 Met Lys His Leu Trp Phe
 -15
 ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
 Phe Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
 -10 -5 1
 ctg cag gag tcc ggt tca gga ccg gtg gat sct tsa cag acc ctg tsc 151
 Leu Gln Glu Ser Gly Ser Gly Pro Val Asp Xaa Xaa Gln Thr Leu Xaa
 5 10 15
 ctc acc tgc act gks tct ggt gtc tcc atc agc agt agt gat aat tgt 199
 Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile Ser Ser Ser Asp Asn Cys
 20 25 30 35
 tgg agc tgg atc cgg cag cca cca ggg aag ggc ctg gag tgg att gga 247
 Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
 40 45 50
 tac atc tat cay agt ggg ggg acc tac tac aac ccg acc ctc aag agc 295
 Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr Asn Pro Thr Leu Lys Ser
 55 60 65
 cga gtc acc atc tcg gba gac agg atc agg aac caa ttc tcc ctg aag 343
 Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg Asn Gln Phe Ser Leu Lys
 70 75 80
 ctg agc tct gtg acg gcc gyg gac acg gcc gtg tat kac tgt ggc aga 391
 Leu Ser Ser Val Thr Ala Xaa Asp Thr Ala Val Tyr Xaa Cys Gly Arg
 85 90 95
 gca cag ggt aga atg ggg atc ggg acg acg att ttt gat ctc tgg ggc 439
 Ala Gln Gly Arg Met Gly Ile Gly Thr Thr Ile Phe Asp Leu Trp Gly
 100 105 110 115
 ggg gga caa tgg tca ccg tct ctg cag cct 469
 Gly Gly Gln Trp Ser Pro Ser Leu Gln Pro
 120 125

<210> 59
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..471

<221> sig_peptide
 <222> 52..108
 <223> Von Heijne matrix
 score 10.8000001907349

seq ILFLVAAATGAHS/QV

<221> misc_feature

<222> 210

<223> n=a, g, c or t
Oligonucleotide

<400> 59

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acccaacaac cacatccctc ctcagmagcc cccagagcac aackcctyac c atg gac      57
                                     Met Asp
tgg acc tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gcc cac      105
Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala His
      -15                      -10                      -5
tcc cag gtc cag ctt gtg cag tct ggg gct gag gtg aag aag cct ggg      153
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
      1           5           10           15
gcc tca gtg aag gtt tcc tgc aag gct tct gga tac ayc ttc act ary      201
Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe Thr Xaa
      20                      25                      30
tmt gct atn cat tgg gtg cgc cag gcc ccc gga car agr ctt gag tgg      249
Xaa Ala Xaa His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
      35                      40                      45
atg ggr tgg atc aac gct gcc amt ggt wam aca awa tat tca cag aas      297
Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser Gln Xaa
      50                      55                      60
ttc cag grc aga gtc acc wtt acc agg gac aca tcc gcg agc aca gtc      345
Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser Thr Val
      65                      70                      75
tcc atg gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat ttc      393
Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
      80           85           90           95
tgt gcg aga gat tgg gaa att gca gta gta cca act gct ata aac tct      441
Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile Asn Ser
      100          105          110
tac ggg ttc gac cct ggg gcc agg gaa cct      471
Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro
      115          120
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<210> 60

<211> 348

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 193..348

<221> sig_peptide

<222> 193..270

<223> Von Heijne matrix
score 10.8000001907349
seq VLFLCVFLGMSWA/GA

<400> 60

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agagcaaaga ggcaatctga agagaaaagc ataggaaagg aaacagtggg aataggaatt      60
ggggtaaaat gaggatcctt cccacaaac attgctatta ttcagctcat ttcaaaggat      120
tccgstgcwg ccatttgtga gagccgctgg aggctgagtg aaagtcattt tgaaagactg      180
atccaaagaa ga atg gag gcc aga gtg gag cgt gct gtg cag aaa agg caa      231
          Met Glu Ala Arg Val Glu Arg Ala Val Gln Lys Arg Gln
          -25          -20          -15

gtc tta ttt ctt tgt gta ttt ctg gga atg tct tgg gct ggc gcc gaa      279
Val Leu Phe Leu Cys Val Phe Leu Gly Met Ser Trp Ala Gly Ala Glu
          -10          -5          1

ccg ctt cgg tat ttt gtg gcg gag gaa acc gag aga ggc acc tdk ctt      327
Pro Leu Arg Tyr Phe Val Ala Glu Glu Thr Glu Arg Gly Thr Xaa Leu
          5          10          15

acc aac ttg gca aaa gac cta      348
Thr Asn Leu Ala Lys Asp Leu
20          25

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<210> 61
<211> 457
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..456

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<221> sig_peptide
<222> 55..111
<223> Von Heijne matrix
      score 10.8000001907349
      seq ILFLVAAATGAHS/QV

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<400> 61
acccaaaaaac cacacccctc cttgggagaa tcccctagat cacagctcct cacc atg      57
          Met
gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gcg aca ggt gcc      105
Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala
          -15          -10          -5

cac tcc cag gtt cag ctg gtg cag tct gga ggt gag gtg aag aag cct      153
His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys Pro
          1          5          10

ggg gcc tcc gtc aag gtc tcc tgc aag gct tct ggt tac acc ttt acc      201
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
15          20          25          30

aga tat gat atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag      249
Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
          35          40          45

tgg atg gga tgg atc agc gct dcc aat ggt aac aca aat tat gca cag      297
Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala Gln
50          55          60

daa gtc cag ggc aga gtc acc atg acc aca gac aca tcc acg aga aca      345
Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg Thr
65          70          75

gcc tac atg gaa ctg agg agc ctg cga tct gac gac acg gcc att tat      393
Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr

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80	85	90	
tac tgt gcg cga gag atm bta gtg gba sta tgt gat gga cag ttg ggg			441
Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu Gly			
95	100	105	110
cca ggg aac ctg gtc a			457
Pro Gly Asn Leu Val			
115			

<210> 62
 <211> 439
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..437
 <221> sig_peptide
 <222> 18..95
 <223> Von Heijne matrix
 score 10.8000001907349
 seq FLLLVAAPRWVLS/QE

<400> 62	
agtgcttyct gasagtc atg gac gtc ctg cac aaa cac atg aaa cac ctg	50
Met Asp Val Leu His Lys His Met Lys His Leu	
-25	-20
tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag	98
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln	
-15	-10
gag cag tta cgg cag tgg ggc gca sga ctg ttg aag cct tcg gag acc	146
Glu Gln Leu Arg Gln Trp Gly Ala Leu Leu Lys Pro Ser Glu Thr	
5	10
ctg tcc ctc acc tgt agt gtc tat ggt ggg tcc ttc aat ggt tac tac	194
Leu Ser Leu Thr Cys Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr	
20	25
tgg agc tgg atc cgc cag tcc cca ggg aag ggg ctg gag tgg att ggg	242
Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly	
35	40
gga atc aat cac agc gga agc acc ctc tcc aac ccg tcc ctc aag agt	290
Gly Ile Asn His Ser Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser	
50	55
cgc gtc gac ctc tca gtt gat gcg tcc aag gac cag gtg tcc ctg agg	338
Arg Val Asp Leu Ser Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg	
70	75
ctg aaa ctt gtg acc gcc gcg gac acg gct gtg tac ttc tgc gcg aga	386
Leu Lys Leu Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg	
85	90
ccc cat tac gat atg tcg act gat tct tcg ttt gac ggt ttt gat ctc	434
Pro His Tyr Asp Met Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu	
100	105
tgg gg	439
Trp	

<210> 63
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..213

<221> sig_peptide
 <222> 82..126
 <223> Von Heijne matrix
 score 10.6999998092651
 seq LLALFFLLRIALA/SQ

<400> 63
 accattggtg tgtctgtttt tatgccagta ctgtgatgtt ttggttatat agctttgtaa 60
 tatattttga agccagatag t atg atg ctt cta gct ttg ttc ttt ttg ctt 111
 Met Met Leu Leu Ala Leu Phe Phe Leu Leu
 -15 -10
 agg att gct ttg gct agt caa ggt ctt ttg tgg ttc cat aca aat ttt 159
 Arg Ile Ala Leu Ala Ser Gln Gly Leu Leu Trp Phe His Thr Asn Phe
 -5 1 5 10
 aag gtt ttt gtt gtt tcy att tgt gtg aag act atc att ggg att tcg 207
 Lys Val Phe Val Val Ser Ile Cys Val Lys Thr Ile Ile Gly Ile Ser
 15 20 25
 ggg ggc a 214
 Gly Gly

<210> 64
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..296

<221> sig_peptide
 <222> 63..119
 <223> Von Heijne matrix
 score 10.6999998092651
 seq ILFLVAAATGALS/QV

<400> 64
 gtgcatcacc cagcaaccac atctgtcctc tagagaatcc cctgagadht ccgttcctca 60
 cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gcr gcc aca 107
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
 -15 -10 -5
 gga gcc ctc tcc cag gtg cag ctg gtr cag tct gga ggt gar gtg aag 155
 Gly Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys
 1 5 10
 aag cct ggg gcc tca gtg agg gtc tcc tgc aag gcc tct gga tac agc 203
 Lys Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser

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15	20	25	
ttc atc ggc tat tat gta cac tgg ata cga cag act cct ggg cga sgc			251
Phe Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa			
30	35	40	
ctt gag tgg atg ggg tgg gtc aac cct crs act ggc gac aac ggg g			297
Leu Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly			
45	50	55	

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<400> 65	
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gaccttggtgt ctttagtttg acctgtcctt cagtgagtgt atataaaatt ctaagctaaa	120
acatatatttc tgaaattgtg aaggtattgc atgtctatct tcttgccctac tctaaatata	180
tcaatcgttt tcttgggaag ttagtctttc tttcacactt gtctgtagat ctttac atg	239
	Met
ttc ttt cag ttt tgg aag tcc tct gca tat tta ata ttt gtt agt att	287
Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser Ile	
-35 -30 -25	
tgt aaa ggt ttt ctt cct gtc tac ctc ctt ctt gtt ctc tct ctc tct	335
Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Leu Val Leu Ser Leu Ser	
-20 -15 -10 -5	
ctc tct ctc tgt tgc tct ctc ttg ctc tct ctc ca	370
Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu	
1 5	

<210> 66
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 <212> DNA
 <213> Homo sapiens

<220>
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<221> sig_peptide
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 score 10.6000003814697
 seq ILFLVAAATGVHS/QV

<221> misc_feature
 <222> 342..343
 <223> n=a, g, c or t
 Oligonucleotide

<400> 66
 aaccacmycc ctcctcagaa gccccagag cacaacgcct cacc atg gac tgg acc 56
 Met Asp Trp Thr
 tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gtc cac tcc cag 104
 Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Val His Ser Gln
 -15 -10 -5 1
 gtc cac ctt gtt cag tct ggg gct gar gtg aag aag cct ggg act ccg 152
 Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Thr Pro
 5 10 15
 gtg aac att tcc tgt aag gct ttt ggc tac acc ttc cct gcc ttt gct 200
 Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe Pro Ala Phe Ala
 20 25 30
 ata cat tgg gtt cgc cag gcc ccc gga caa agt ctt gag tgg atg gga 248
 Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu Glu Trp Met Gly
 35 40 45
 tgg gtc aac att ggc cat ggc aac aca aag tat tca cag aag ttt cag 296
 Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
 50 55 60 65
 ggc aga ctc gcc atc tcc aga gac acg tcc gcg aac ata gtc tac nng 344
 Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn Ile Val Tyr Xaa
 70 75 80
 gaa ctg agc ggc ctg aga tct gaa gac acg gct gtc tat tac tgt gcg 392
 Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 agg gat aat ctt ttc ttt ggc agt atg ggc ttt gac 428
 Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp
 100 105

<210> 67
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 Met Ala Trp Thr Val Leu
 -15
 ctc ctc ggc ctc ctc tct cac tgc aca ggc tct gtg acc tcc tat gtg 103
 Leu Leu Gly Leu Leu Ser His Cys Thr Gly Ser Val Thr Ser Tyr Val

-10	-5	1	5	
ctg act cag cct ccc tcg gtg tca gtg gcc cca gga aag acg gcc agc				151
Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Ser				
10	15	20		
att acc tgt ggg gga gac aac att gaa agt caa gtt gta cac tgg cac				199
Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser Gln Val Val His Trp His				
25	30	35		
cag cag aag cca ggg cag gcc cct ata ttg gtc atc tat gat gat acc				247
Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Ile Tyr Asp Asp Thr				
40	45	50		
gac cgg ccc tca ggg atc cct gac cga ttc tct ggc tcc aac tct ggg				295
Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Asn Ser Gly				
55	60	65	70	
cac acg gcc acc ctg acc atc agc agg gtc gaa gcc ggg gat gag gcc				343
His Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala				
75	80	85		
gac tat tat tgt cag gtg tgg gat aga agt agt ggt cag gga ata ttc				391
Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Gly Gln Gly Ile Phe				
90	95	100		
ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc aag gct gcc ccc				439
Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala Pro				
105	110	115		
tcg gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc aac aag				487
Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys				
120	125	130		
gcc aca				493
Ala Thr				
135				

<210> 68
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<221> sig_peptide
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Met Arg Leu Leu Phe Leu	
-15	-10
ttg ttg ttt gtt tgt ttt tcg aga cag ggt ctc gct ttg tct ctc agg	101
Leu Leu Phe Val Cys Phe Ser Arg Gln Gly Leu Ala Leu Ser Leu Arg	
-5	1
ctg gaa tgc agt ggt atg atc atg gct tac tgc agc atc agc ctc cca	149
Leu Glu Cys Ser Gly Met Ile Met Ala Tyr Cys Ser Ile Ser Leu Pro	
10	15
	20

ggc tca agc agt cct ctc acc tca gcc tcc a
 Gly Ser Ser Ser Pro Leu Thr Ser Ala Ser
 25 30

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<210> 69
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 score 10.6000003814697
 seq FLLLV SAPRWLS/QV

<400> 69
 atacttyctg agagtctgg acctcctgca caagaac atg aaa cac ctg tgg ttc 55
 Met Lys His Leu Trp Phe
 -15
 ttc ctc ctc ctg gtg tca gct ccc aga tgg gtc ctg tct cag gtg cag 103
 Phe Leu Leu Leu Val Ser Ala Pro Arg Trp Val Leu Ser Gln Val Gln
 -10 -5 1
 cta cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg agg ctg tcc 151
 Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Arg Leu Ser
 5 10 15
 ctc gcc tgc gat gtg gtg gaa ttg agt ccg ccg gcc ccc agg ggc ggg 199
 Leu Ala Cys Asp Val Val Glu Leu Ser Pro Pro Ala Pro Arg Gly Gly
 20 25 30 35
 tct gca gtg cat ctc aga aat ctt tca tca tgg gag ccc cac cta caa 247
 Ser Ala Val His Leu Arg Asn Leu Ser Ser Trp Glu Pro His Leu Gln
 40 45 50
 ccc gtc tcg ggg 259
 Pro Val Ser Gly
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<210> 70
 <211> 178
 <212> DNA
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<221> sig_peptide
 <222> 7..102
 <223> Von Heijne matrix
 score 10.6000003814697
 seq VVFLLLL VSTLSS/VV

<400> 70
 cgtata atg act tac ttt cct ctg ggt aga tac cca gta atg gga ttg 48
 Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu
 -30 -25 -20
 ctg gat caa atg gta gtt gtg ttt tta ctt ctt tta gtc tcc aca ctt 96
 Leu Asp Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu
 -15 -10 -5
 tct tcc gta gtg gtt tta cta gtt tgc att ccc acc agc agt gta aaa 144
 Ser Ser Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys
 1 5 10
 ttg ttc cct ttt cac cat atc cac acc aac tgg g 178
 Leu Phe Pro Phe His His Ile His Thr Asn Trp
 15 20 25

<210> 71
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 <221> sig_peptide
 <222> 40..96
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 score 10.5
 seq WVLLVAMLRGLQC/QV

<400> 71
 agctctggga gacgagccca gctctgcagt ggactcacc atg gag ttt ggg ctg 54
 Met Glu Phe Gly Leu
 -15
 agc tgg gtt ctc ctc gtt gct atg tta aga ggt ctc cag tgt caa gtg 102
 Ser Trp Val Leu Leu Val Ala Met Leu Arg Gly Leu Gln Cys Gln Val
 -10 -5 1
 cag ctg gtg gag tct ggg gga acc gcg gg 131
 Gln Leu Val Glu Ser Gly Gly Thr Ala
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<210> 72
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 <212> DNA
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 <222> 47..217

 <221> sig_peptide
 <222> 47..91
 <223> Von Heijne matrix
 score 10.5
 seq LSLILLLENVSG/FP

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<400> 72
ttgcttacaa ttttaatgtg tctcattgct actggtcctc cttcta atg tat ctg      55
                                   Met Tyr Leu
                                   -15
agc ttg tta att cta ctt ttg gaa aat gtc agt ggc ttt ccc ttt cct      103
Ser Leu Leu Ile Leu Leu Leu Glu Asn Val Ser Gly Phe Pro Phe Pro
      -10                    -5                    1
cta att ttc cag ctt cat gca tcc cct ggc cat aag ata ctt cca gac      151
Leu Ile Phe Gln Leu His Ala Ser Pro Gly His Lys Ile Leu Pro Asp
5          10          15          20
tgt atg ata tat tct atc act gtc agc ctt atg ttc cct gtg gtt gac      199
Cys Met Ile Tyr Ser Ile Thr Val Ser Leu Met Phe Pro Val Val Asp
          25          30          35
tat ata agc acg caa ggg      217
Tyr Ile Ser Thr Gln Gly
      40
  
```

```

<210> 73
<211> 192
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..192

<221> sig_peptide
<222> 100..183
<223> Von Heijne matrix
      score 10.5
      seq SLWFXCLLFLLFA/WP
  
```

```

<400> 73
agttaaaatc atgtactgtg atcagtcacc tggtttttga tttttatgaa gggttttttt      60
gttttagatag ttgttaaatt tgggtgttcct gtggggagg atg atg aga gcc ttc      114
                                   Met Met Arg Ala Phe
                                   -25
tat ttg gct atc ttg ttc tgc ctc tct ctc tcc tta tgg ttc tdk tgt      162
Tyr Leu Ala Ile Leu Phe Cys Leu Ser Leu Ser Leu Trp Phe Xaa Cys
      -20          -15          -10
tta ctt ttt ttg ctt ttt gct tgg cct ggg      192
Leu Leu Phe Leu Leu Phe Ala Trp Pro Gly
      -5          1
  
```

```

<210> 74
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..328
  
```

<221> sig_peptide

<222> 23..82

<223> Von Heijne matrix

score 10.3999996185303

seq FLTLLHCTGSLA/QL

<400> 74

```
agagctctgga ggagctctgca cc atg gct tgg acc cca ctc ctc ttc ctc acc      52
                        Met Ala Trp Thr Pro Leu Leu Phe Leu Thr
                        -20                               -15
ctc ctc ctc cac tgc aca ggg tct ctc gcc cag ctt gtg ctg act caa      100
Leu Leu Leu His Cys Thr Gly Ser Leu Ala Gln Leu Val Leu Thr Gln
-10                               -5                               5
tcg ccc tct gcc tct gcc tcc ctg gga gcc tcg gtc aag ctc acc tgc      148
Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala Ser Val Lys Leu Thr Cys
                        10                               15                               20
act ctg agc agt ggg cac agc aac tac ggc atc gct tgg tat cag cag      196
Thr Leu Ser Ser Gly His Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln
                        25                               30                               35
cag cca gag aag ggc cct cga ttc ttg atg aaa gtt aac agt gat ggc      244
Gln Pro Glu Lys Gly Pro Arg Phe Leu Met Lys Val Asn Ser Asp Gly
                        40                               45                               50
agc cac atg aag gcg gac ggg atc cct gat cgc ttc tca ggc tcc agc      292
Ser His Met Lys Ala Asp Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
55                               60                               65                               70
tct ggg gct gag cgc tac ctc tcc atc tcc agc ctc a      329
Ser Gly Ala Glu Arg Tyr Leu Ser Ile Ser Ser Leu
                        75                               80
```

<210> 75

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 259..312

<221> sig_peptide

<222> 259..300

<223> Von Heijne matrix

score 10.3999996185303

seq PLALFFLLSVALA/IQ

<400> 75

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taggggtgaga gatgggggato tagtttttatt cttctgcata tggatatcca gttttccag      60
taacatttat tgaagagact ggcctttccc caatgagtgt tcttggcacc tttgtcaaaa      120
gtcagttggc cgtagatatg tggattaatt tctgtgttcc ctgttttgtt ccattggcct      180
atgtgtctgt ttttatgaca gtaccaggtt gttttggtta ctacagcttt gtagtttact      240
ttgaggtctg ttagtgtg atg cct cta gct ttg ttc ttt ttg ctc agt gtt      291
                        Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val
                        -10                               -5
gct ttg gct att cag ggt cag gg      314
Ala Leu Ala Ile Gln Gly Gln
```

1

<210> 76
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..445

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
score 10.3999996185303
seq XFCLLAVAPGAHS/QV

<400> 76
atcatccaac aaccacatcc cttctctaca gaagcctctg agaggaaagt tcttcacc 58
atg gac tgg acc tgg agg rwc ttc tgc ttg ctg gct gta gct cca ggt 106
Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 154
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 202
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
acc agc cac tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt 250
Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga ata atc tac cct gat agt gat acc act aag tac cba 298
Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa
50 55 60
cag aac ttc cag ggc aga gtc acc atg act agg gac acg tcc acg agc 346
Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
65 70 75
aca gtc tac atg gag ctg agc agc ctg aca tct gac gac acg gcc gtg 394
Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
80 85 90
tat tat tgt gct aga gag gcg tat agt ggg agc tac cgc ttt gac tac 442
Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr
95 100 105
tgg gg 447
Trp
110

<210> 77
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 16..387

<221> sig_peptide

<222> 16..93

<223> Von Heijne matrix

score 10.3000001907349

seq LLLLVAAPRWLS/QL

<400> 77

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agctttctga gagtc atg gat ctc atg tgc aag aaa atg aga cac ctg tgg      51
                Met Asp Leu Met Cys Lys Lys Met Arg His Leu Trp
                -25                -20                -15
ttc ctc ctc ctg ctg gtg gcg gct ccc aga tgg gtc ctg tcc cag ctg      99
Phe Leu Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu
                -10                -5                1
cag ctt cag gag tcg ggc cca gga ctg gtg aag gct tcg gag acc ctg      147
Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Ala Ser Glu Thr Leu
                5                10                15
tcc ctc gcc tgc agt gtc tct ggt gac tcc atc agc agt ggt aat tat      195
Ser Leu Ala Cys Ser Val Ser Gly Asp Ser Ile Ser Ser Gly Asn Tyr
                20                25                30
tac tgg ggc tgg atc cgg cag ccc cca ggg aag gga ctg cag tgg ctt      243
Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Leu
                35                40                45                50
ggg agt ctt tgg aat cgt ggc ggt ccg caa tac aay hcc tcc ctc aag      291
Gly Ser Leu Trp Asn Arg Gly Gly Pro Gln Tyr Asn Xaa Ser Leu Lys
                55                60                65
aat cga gtc acc gtg tcc gta gac acg tcc acg aat cat ttc ttt ctg      339
Asn Arg Val Thr Val Ser Val Asp Thr Ser Thr Asn His Phe Phe Leu
                70                75                80
aga ctg aat tcc gtg aay vgh gga cac ggc aat tta tta ctg tgc gcg a      388
Arg Leu Asn Ser Val Asn Xaa Gly His Gly Asn Leu Leu Leu Cys Ala
                85                90                95
```

<210> 78

<211> 121

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..120

<221> sig_peptide

<222> 25..72

<223> Von Heijne matrix

score 10.1999998092651

seq XLXLSVLLGXXXX/KX

<400> 78

```
ctgaccttcc ctcccggcag cagc atg cgg grg tkg ctg kys ttg agt gtc      51
                Met Arg Xaa Xaa Leu Xaa Leu Ser Val
                -15                -10
ctg ttr ggg sck rts tbt kgc aag gmg gac ttt gtg ggg cat cag gtg      99
```


Leu Leu Gly Xaa Xaa Xaa Xaa Lys Xaa Asp Phe Val Gly His Gln Val
 -5 1 5
 ctc cga atc tct gta gcc gat g 121
 Leu Arg Ile Ser Val Ala Asp
 10 15

<210> 79
 <211> 149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..149

<221> sig_peptide
 <222> 36..143
 <223> Von Heijne matrix
 score 10.1999998092651
 seq FLLFFCFVFCLRG/QG

<400> 79
 tccgagcagc cagctctgtg taagcacatc cagga atg gca gaa tcc agg gag 53
 Met Ala Glu Ser Arg Glu
 -35
 gaa ggt gaa agc tgt gtt gag agc cac tgt gtg ctc ttt ttc acc ctg 101
 Glu Gly Glu Ser Cys Val Glu Ser His Cys Val Leu Phe Phe Thr Leu
 -30 -25 -20 -15
 ttt ttt ttg ttg ttt ttt tgt ttt gtt ttt tgt ttg agg gga cag ggg 149
 Phe Phe Leu Leu Phe Phe Cys Phe Val Phe Cys Leu Arg Gly Gln Gly
 -10 -5 1

<210> 80
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..409

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 10.1000003814697
 seq WLFLVAFLKGVQC/EV

<400> 80
 agctctgaga gaggagccca gccctgggat tttcaggtgt tttcatgttg tgatcaggac 60
 tgaacagaga gaactcacc atg gag ctt ggg ctg agc tgg ctt ttt ctt gtg 112
 Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val
 -15 -10
 gct ttt tta aaa ggt gtc cag tgt gag gtg cag ttg ttg gag tct ggg 160
 Ala Phe Leu Lys Gly Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly

	-5		1		5		
gga ggc ttg gtc cag cct ggg ggg tcc ctg aga ctc tca tgt gca gcc						208	
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala							
10		15		20			
tcc gga ttc acc ttt agc tcc tat gcc atg ctc tgg gtc cgc cag gct					256		
Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Leu Trp Val Arg Gln Ala							
25		30		35	40		
cca ggt aag ggg ctg gag tgg gtc tca ggt att agt gct ggt gct gat					304		
Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Ala Gly Ala Asp							
	45		50		55		
gat aca tat gat gca gac tcc gtg aag ggc cgg ttc acc att tcc aga					352		
Asp Thr Tyr Asp Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg							
	60		65		70		
gac gat tcc aag aaa atc cta tat cta caa atg aac agc ctg aga gcc					400		
Asp Asp Ser Lys Lys Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala							
	75		80		85		
gag gac agg c					410		
Glu Asp Arg							
90							

<210> 81
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..217

<221> sig_peptide
 <222> 38..106
 <223> Von Heijne matrix
 score 10.1000003814697
 seq VLGLLVLF LTCYA/DD

<400> 81	
gaacaatttta tctgcaogaa taccctgtgc taccaga atg gct gtc tca gta ctt	55
	Met Ala Val Ser Val Leu
	-20

cgc ctg aca gtt gtc ctg gga ctg ctt gtc tta ttc ctg acc tgc tat	103
Arg Leu Thr Val Val Leu Gly Leu Leu Val Leu Phe Leu Thr Cys Tyr	
	-15
	-10
	-5

gca gac gac aaa cca gac aag cca gac gac aag cca gac gac tgc ggc	151
Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp Lys Pro Asp Asp Ser Gly	
	1
	5
	10
	15

aaa gac cca aag cca gac ttc ccc aaa ttc cta agc ctc ctg ggc aca	199
Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe Leu Ser Leu Leu Gly Thr	
	20
	25
	30

gag atc att gag aat gcg gg	219
Glu Ile Ile Glu Asn Ala	
	35

<210> 82
 <211> 399

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..398

<221> sig_peptide
<222> 81..152
<223> Von Heijne matrix
score 10
seq LLLLQALPSPLSA/RA

<400> 82
gaagaagagg gtagaggagg agagggagga ggaggaggga ggtggcggcg ccgtggcgga 60
ggagcaggag caggaggggg atg gag agg aga agg ctc ctg ggt ggc atg gcg 113
Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala
-20 -15
ctc ctg ctc ctc cag gcg ctg ccc agc ccc ttg tca gcc agg gct gaa 161
Leu Leu Leu Leu Gln Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu
-10 -5 1
ccc ccg cag gat aag gaa gcc tgt gtg ggt acc aac aat caa agc tac 209
Pro Pro Gln Asp Lys Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr
5 10 15
atc tgt gac aca gga cac tgc tgt gga cag tct cag tgc tgy aac tac 257
Ile Cys Asp Thr Gly His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr
20 25 30 35
tac tat gaa ctc tgg tgg ttc tgg ctg gtg tgg acc atc atc atc atc 305
Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile
40 45 50
ctg agc tgc tgc tgt gtt tgc cac cac cgc cga gcc aag cac cgc ctt 353
Leu Ser Cys Cys Cys Val Cys His His Arg Arg Ala Lys His Arg Leu
55 60 65
cag gcc cag cag cgg caa cat gaa atc aac ctg atc gct tac cga g 399
Gln Ala Gln Gln Arg Gln His Glu Ile Asn Leu Ile Ala Tyr Arg
70 75 80

<210> 83
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 288..398

<221> sig_peptide
<222> 288..368
<223> Von Heijne matrix
score 9.89999961853027
seq LCLLLFSLSLFLC/HE

<400> 83
cactctacct ctgacagcat gtatattgca ccagtagcta acaaaaaactg gtctagtcaa 60

```

accaaatggg cacaaaagaa ccaggataacc aaaagttaag ctcatacagc tgcaaaccat 120
atcacttctt ggtaacaatg caagacctca taaacctaaa gaagagaaag aaaagaaaac 180
ttttgttact ttvctttttt gcttgtcact tatatacagg ctatgtgaga atataatttg 240
taggtataac acattaagaa aaagttatct tcattggata gaattga atg gtg gtc 296
                               Met Val Val
                               -25
gct gat agg aat agg gcg tcc tct agc tct tat ctc tgt ctc tta ctc 344
Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys Leu Leu Leu
                               -20                -15                -10
ttt tct ctt tct ctt ttt ctc tgt cat gag act gtg tgt gac agg gcc 392
Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys Asp Arg Ala
                               -5                1                5
acc tgt 398
Thr Cys
10

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<210> 84
<211> 488
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 62..487

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<221> sig_peptide
<222> 62..118
<223> Von Heijne matrix
      score 9.89999961853027
      seq FLFVVAATGVQS/QV

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<221> misc_feature
<222> 210,293
<223> n=a, g, c or t
      Oligonucleotide

```

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<400> 84
agcatcacat aacaaccaca ttctctctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                               -15                -10                -5
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
                               1                5                10
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc 205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
15                20                25
agc anc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 253
Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                35                40                45
gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca nac tac gca 301
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala
50                55                60
cag aag ttc cag ggc aga gtc acs att acc gcg gac gra tcc acg asc 349

```

Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Xaa	Ser	Thr	Xaa	
			65					70					75			
aca	rcc	tac	atg	gag	ctg	agc	agc	ctg	aga	tct	gag	gac	acg	gcc	stg	397
Thr	Xaa	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Xaa	
		80					85					90				
tat	tac	tgt	gcg	aga	ggc	caa	gcc	ccc	ggc	agg	gta	gta	gta	cca	ctt	445
Tyr	Tyr	Cys	Ala	Arg	Gly	Gln	Ala	Pro	Gly	Arg	Val	Val	Val	Pro	Leu	
		95				100					105					
ttc	ctc	tgg	ggc	cag	gga	acc	tgg	tca	ccg	tct	cct	cag	cct	c		488
Phe	Leu	Trp	Gly	Gln	Gly	Thr	Trp	Ser	Pro	Ser	Pro	Gln	Pro			
110					115					120						

<210> 85
 <211> 290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..290
 <221> sig_peptide
 <222> 30..164
 <223> Von Heijne matrix
 score 9.89999961853027
 seq LLSLLSFLDETS/LS

<400> 85																
cttctttttt	ttcgtaactt	catggcaac	atg	acc	tac	agt	tac	tca	ttt	ttc						53
			Met	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe						
			-45					-40								
agg	cct	gag	ttg	atc	gtt	aat	cat	ctt	aat	tat	gtt	cat	tct	gaa	gcc	101
Arg	Pro	Glu	Leu	Ile	Val	Asn	His	Leu	Asn	Tyr	Val	His	Ser	Glu	Ala	
		-35				-30					-25					
aac	agg	aga	acc	aag	acc	aaa	act	tta	ttg	tct	ctg	ctt	tca	ttt	ctt	149
Asn	Arg	Arg	Thr	Lys	Thr	Lys	Thr	Leu	Leu	Ser	Leu	Leu	Ser	Phe	Leu	
		-20				-15					-10					
gat	gaa	acc	tct	gga	cta	agc	aca	cat	ctt	cct	tgt	tta	tct	ctc	tca	197
Asp	Glu	Thr	Ser	Gly	Leu	Ser	Thr	His	Leu	Pro	Cys	Leu	Ser	Leu	Ser	
		-5			1			5					10			
aag	gag	tgt	gga	gtg	ctt	cat	ctg	gac	atc	cac	ggg	aag	aag	gaa	gac	245
Lys	Glu	Cys	Gly	Val	Leu	His	Leu	Asp	Ile	His	Gly	Lys	Lys	Glu	Asp	
		15					20				25					
atg	aga	gat	gag	gtc	ttg	ctg	gcc	ttg	aac	tyc	tgc	acc	cac	agg		290
Met	Arg	Asp	Glu	Val	Leu	Leu	Ala	Leu	Asn	Xaa	Cys	Thr	His	Arg		
		30					35				40					

<210> 86
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 100..336

<221> sig_peptide

<222> 100..156

<223> Von Heijne matrix

score 9.89999961853027

seq ILFLVFLLAGLRS/KA

<400> 86

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ccagatctgt tctgcaacat tcaccgttct ctgcatccag ctctgcttat ctgctgttac    60
cttggacacc agagcagcta taggtatctg ccagragcw atg aaa tca ttc agc    114
                                   Met Lys Ser Phe Ser
                                   -15
cgg atc ctc ttc ctc gtc ttc ctc ctc gcc ggc ctg agg tcc aag gcc    162
Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly Leu Arg Ser Lys Ala
      -10                    -5                    1
gct ccc tca gcc cct ctg cct ttg ggc tgt ggc ttt ccg gac atg gcc    210
Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly Phe Pro Asp Met Ala
      5                    10                    15
cac ccc tct gag act tcc cct ctg aag ggt gct tct gaa aat tcc aaa    258
His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala Ser Glu Asn Ser Lys
      20                    25                    30
cga gat cgc ctt aac cca gaa ttt cct ggg act cct tac cct gag cct    306
Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr Pro Tyr Pro Glu Pro
      35                    40                    45                    50
tcc aag cta cct cat acg gtt tcc ctg gaa    336
Ser Lys Leu Pro His Thr Val Ser Leu Glu
      55                    60
```

<210> 87

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 108..260

<221> sig_peptide

<222> 108..230

<223> Von Heijne matrix

score 9.89999961853027

seq SLCHLGWSAVVQS/QP

<400> 87

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taggagtgga gtgactgggt gatatgataa ctctatgttt aacttttttaa ggaactgcta    60
gacttttctg aagtgactat gccatttttac attaacacca ggagtgt atg agg gtg    116
                                   Met Arg Val
                                   -40
ccg att ttt cca cat cct cac caa ctc tcg tta tta ttc atc cat tta    164
Pro Ile Phe Pro His Pro His Gln Leu Ser Leu Leu Phe Ile His Leu
      -35                    -30                    -25
ttt att tat tta ttt aga gaa agg gtc tct ctc tgt cac cta ggc tgg    212
Phe Ile Tyr Leu Phe Arg Glu Arg Val Ser Leu Cys His Leu Gly Trp
```

```

      -20              -15              -10
agt gca gtg gta caa tca cag cca act aca acc ttg acc tcc cgc gct      260
Ser Ala Val Val Gln Ser Gln Pro Thr Thr Thr Leu Thr Ser Arg Ala
      -5              1              5              10
am

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<210> 88
<211> 149
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 18..149

```

```

<221> sig_peptide
<222> 18..128
<223> Von Heijne matrix
      score 9.89999961853027
      seq FLFVLFCFGGSRA/LL

```

```

<400> 88
ttcggagctt gaccagc atg tgg aag gag agc tct cat ggc tgc aat aac      50
              Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn
              -35              -30

tta ggg agt tcc tac ctg gat gac act ggg gta gga agt ttt ctg ttt      98
Leu Gly Ser Ser Tyr Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe
      -25              -20              -15

gtt ttg ttc tgt ttc gga ggg tcc cgt gca ctt ctc ttg cct gga tct      146
Val Leu Phe Cys Phe Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser
      -10              -5              1              5

ggg
Gly

```

```

<210> 89
<211> 315
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 236..313

```

```

<221> sig_peptide
<222> 236..283
<223> Von Heijne matrix
      score 9.69999980926514
      seq FLCLLFYLVSCG/AV

```

```

<400> 89
gtaaaagaca aataacttgt atggtttgca aaatgatctg aatatgtgct tttataacat      60
tcagaataca cccaaaagta aacttttaggt ttaatgtaca gtatgttttc tatgtaattg      120
ttttgaataa gtaatamcat ybtacatggc ttaaaaactga aaaacgtatt cctgttactt      180
cttgatgctt ttgagaaatg aataatgttt totccotttt aaatggtagt acagc atg      238

```

```

                                     Met
cac act ttt ctg tgc ttg ctt ttt tat ctc ata gta tct tgt gga gct      286
His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly Ala
-15                               -10                -5                1
gtt ttc tta aca gtc cct tct ccc caa gg                                315
Val Phe Leu Thr Val Pro Ser Pro Gln
                    5                      10

```

```

<210> 90
<211> 179
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 24..179

```

```

<221> sig_peptide
<222> 24..140
<223> Von Heijne matrix
      score 9.69999980926514
      seq SIILXLXFPGILG/QA

```

```

<221> misc_feature
<222> 57
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 90
agmrctctgg ggcagtctgc acc atg gcc tgg cac ccc act cct cct cct ctt      53
                               Met Ala Trp His Pro Thr Pro Pro Pro Leu
                               -35                -30
csb ncw cct cct cca ctg mac agg gwc tcy ctc cca gcc tgt gct gac      101
Xaa Xaa Pro Pro Pro Leu Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp
                    -25                -20                -15
tca atc atc ctc tgm ctc tgm ttc cct ggg atc ctc ggw caa gct cac      149
Ser Ile Ile Leu Xaa Leu Xaa Phe Pro Gly Ile Leu Gly Gln Ala His
                    -10                -5                1
ctg mac tct gag cag tgg aca cag tac cta                                179
Leu Xaa Ser Glu Gln Trp Thr Gln Tyr Leu
    5                      10

```

```

<210> 91
<211> 423
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 311..421

```

```

<221> sig_peptide
<222> 311..373
<223> Von Heijne matrix

```


score 9.69999980926514
seq LHLILLSGTCFT/WI

```
<400> 91
gactctatag srcaaatggt taagaacata tacttgggag tcagttgatc tgggttcaaa      60
ttctagctgt gctactttct acctatgctg tattggacaa atgatactgt gtatctgttt      120
cttcaaccgt aagttgggta tattaatatc cttacctcaa aaggatcatga tgattaagtg      180
agtbaatgca tgtaaaatgc cttctgtgcc gggcagtcag aaaccactca ataaatattg      240
attattctca ccaaagatgt gcttcctgac ctcaaaagcc tgtcagccta atataaagac      300
agtgtgacaa atg cca atc ctg cct cag gac atc ttg cac ttg ctg atc      349
      Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile
      -20          -15          -10
ctt ctg tct gga aca tgc ttc act tgg att ctt ttg tgg ctt cca ctc      397
Leu Leu Ser Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu
      -5          1          5
tcc cct ctg ttg ggc ctg aaa tgc ta      423
Ser Pro Leu Leu Gly Leu Lys Cys
      10          15
```

```
<210> 92
<211> 316
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 62..316

<221> sig_peptide
<222> 62..121
<223> Von Heijne matrix
      score 9.60000038146973
      seq LLALLLCGRPGRG/QT
```

```
<221> misc_feature
<222> 264,266
<223> n=a, g, c or t
      Oligonucleotide
```

```
<400> 92
accgcagctc cagagccctg cgaggaggact cagagtcagg gacacagcag cgtccggcga      60
g atg aag gcg ctc ggg gct gtc ctg ctt gcb ctc ttg ctg tgc ggg cgg      109
      Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
      -20          -15          -10          -5
cca ggg aga ggg cag aca cag cag gag gaa gag gaa gag gac gag gac      157
Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Glu Asp Glu Asp
      1          5          10
cac ggg cca gat gac tac gac gag gaa gat gag gat gag gtt gaa gag      205
His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
      15          20          25
gag gag acc aac agg ctc cct ggt ggc agg agc aga gtg ctg ctg cgg      253
Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
      30          35          40
tgc tac acc tnk nag tcc ctg ccc agg gac gag cgc tgc aac ctg acg      301
```


<221> sig_peptide
 <222> 36..92
 <223> Von Heijne matrix
 score 9.60000038146973
 seq FLLLVAAPRWAMS/QV

<400> 94
 actttctgag aggcctggac ctctgcaca agaac atg aaa cac ctg tgg ttc 53
 Met Lys His Leu Trp Phe
 -15
 ttc ctg ctg ctg gtg gca gct ccc aga tgg gcc atg tct cag gtg caa 101
 Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Met Ser Gln Val Gln
 -10 -5 1
 ctg cag gaa tcg ggc ccg aga ctg gtg aaa cct tcg ggg acc ctg tcc 149
 Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gly Thr Leu Ser
 5 10 15
 ctg acc tgc agt gtc tct ggt ggc tcc atg gcc act agt gac tgg tgg 197
 Leu Thr Cys Ser Val Ser Gly Gly Ser Met Ala Thr Ser Asp Trp Trp
 20 25 30 35
 agt tgg ttt cga cag acm ccg gag aag ggt ctg gag tgg att ggg gaa 245
 Ser Trp Phe Arg Gln Thr Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu
 40 45 50
 atc ttt cag act ggg ccc acc aat tac aac ccg tcc ctg aag agc cgc 293
 Ile Phe Gln Thr Gly Pro Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
 55 60 65
 gtc tcc atg tca gtg gac atg tcc aag a 321
 Val Ser Met Ser Val Asp Met Ser Lys
 70 75

<210> 95
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..401

<221> sig_peptide
 <222> 15..92
 <223> Von Heijne matrix
 score 9.5
 seq FLLLVAAPRWALS/QL

<400> 95
 gctttctgag agtc atg gat ctg acg tgc aag aaa atg aag cac ctg tgg 50
 Met Asp Leu Thr Cys Lys Lys Met Lys His Leu Trp
 -25 -20 -15
 ttc ttc ctg ctg ctg gtg gcg gct ccc aga tgg gcc ctg tcc caa ctg 98
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Leu Ser Gln Leu
 -10 -5 1
 cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag acc ctg 146
 Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
 5 10 15

tcc ctc acg tgc act gtc tct ggt gaa tcc atc acc act aat tca ttc	194
Ser Leu Thr Cys Thr Val Ser Gly Glu Ser Ile Thr Thr Asn Ser Phe	
20 25 30	
tgc tgg gcc tgg atc cgc cag ccc ccg ggg aag ggg ctg gaa tgg ctt	242
Cys Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu	
35 40 45 50	
ggg act gta tgt tat ggt ggg acc acc tac krc aac kcg tcc ctg aag	290
Gly Thr Val Cys Tyr Gly Gly Thr Thr Tyr Xaa Asn Xaa Ser Leu Lys	
55 60 65	
agt cga gtc aag tta tcg ttg gac acg tcc acg aat cag ttc tcc ctg	338
Ser Arg Val Lys Leu Ser Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu	
70 75 80	
aag gtc acc tct atg acc gcc gga gac gcg gct gtc cat tac tgt gcg	386
Lys Val Thr Ser Met Thr Ala Gly Asp Ala Ala Val His Tyr Cys Ala	
85 90 95	
ggg ctg cgt gtt agt g	402
Gly Leu Arg Val Ser	
100	

<210> 96
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 118..315
 <221> sig_peptide
 <222> 118..306
 <223> Von Heijne matrix
 score 9.5
 seq VLLFLILLYMSWS/AS

<400> 96	
agagacacac ttggacgrtt cctgcagraa tcagtgaggc agtctcctcc caggggcttg	60
gsgcctggct cgaggcgagg ctgccggccc ggacgctgac tgcccagtgc cacagac	117
atg gcc aac ggg acc aac gcc tct gcc cca tac tac agc tat gaa tac	165
Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr	
-60 -55 -50	
tac ctg gac tat ctg gac ctc att ccc gtg gac gag aag aag ctg aaa	213
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys	
-45 -40 -35	
gcc cac aaa cat tcc atc gtg atc gca ttc tgg gtg agc ctg gct gcc	261
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala	
-30 -25 -20	
ttc gtg gtg ctg ctc ttc ctc atc ttg ctc tac atg tcc tgg tcc gcs	309
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala	
-15 -10 -5 1	
tcc ccg	315
Ser Pro	

<210> 97
 <211> 460

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..460

<221> sig_peptide
 <222> 62..118
 <223> Von Heijne matrix
 score 9.39999961853027
 seq FLFVVAATGVQS/QX

<400> 97
 agcatcacat aacaaccasa ttctctctct aaagaagccc ctgggagcac agctcatcac 60
 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcm cag gks cas ctg gwg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg tcc tcg gtg aaa gtc tcc tgc arg gcy tct gga ggc atc ytc 205
 Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
 15 20 25
 agc asc tat agc ttc aac tgg gtg cgm cag gcc cct gga cag ggg ttt 253
 Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
 30 35 40 45
 gag tgg ttg gga agg atc atc ccc atc ctc ggt ata aca aac tac gca 301
 Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
 50 55 60
 gag aag ttt cgg ggc aga ctc acg atc acc gtg gac aaa tcc acg cgt 349
 Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg
 65 70 75
 gtt gtt tac atg gag cag agc agt ctg aca tct gcg gac acg gcc gta 397
 Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val
 80 85 90
 tat tat tgt gcg aaa ccg act atg act tcg gaa cta cgg gtc tac tat 445
 Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr
 95 100 105
 cag wct aca cta tgg 460
 Gln Xaa Thr Leu Trp
 110

<210> 98
 <211> 230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 140..229

<221> sig_peptide
 <222> 140..205

<223> Von Heijne matrix
 score 9.39999961853027
 seq LLLLSAFTSQTVS/GQ

<400> 98
 aacagaacaa tatcaaataag ctaacttcac ccccaaccac agtccttgct gttggcattt 60
 actcaactag tctttaattc ctgttttgac aaactttata aggtgctaca agacagatga 120
 tttttcacca tctaccata atg tgg aac aga tat ttt gtc ttc tat ctc ctg 172
 Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu
 -20 -15
 ctt ttg tca gcg ttt acg agt caa aca gta tcc gga caa aga aag aaa 220
 Leu Leu Ser Ala Phe Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys
 -10 -5 1 5
 gga ccc cgg g 230
 Gly Pro Arg

<210> 99
 <211> 467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..465

<221> sig_peptide
 <222> 40..96
 <223> Von Heijne matrix
 score 9.39999961853027
 seq FLLLVAAPRWVLS/QL

<400> 99
 aaatactttc tgagagccct ggacctctg tgcaagaac atg aaa cac ctg ggg 54
 Met Lys His Leu Gly
 -15
 ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag ctg 102
 Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu
 -10 -5 1
 cag ctc cag gag tcc ggc tca gga ctg gag aag cct tca cag acc ctg 150
 Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys Pro Ser Gln Thr Leu
 5 10 15
 tcc ctc acc tgc tct gtc tct ggt ggc tcc atc agt agt gat gat ttg 198
 Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ser Ser Asp Asp Leu
 20 25 30
 tcg tgg agc tgg atc cga cag ccg cca ggg aag ggc ctg gag tgg att 246
 Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45 50
 ggc tac att tat caa aat gag agg acc ctc tac aac ccg tcc ctc aag 294
 Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr Asn Pro Ser Leu Lys
 55 60 65
 agt cga gcc gcc att tca gtg gac agg tcc aag aac cag ttc tcc ctg 342
 Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys Asn Gln Phe Ser Leu
 70 75 80
 aaa ctg acc tct gtg acc gcc gcg gac atg gcc gta tat tac tgt gcc 390

```

Lys Leu Thr Ser Val Thr Ala Ala Asp Met Ala Val Tyr Tyr Cys Ala
      85                      90                      95
acc agt gtc atg awt tcc ttt ggg ggc gtt ctc gtc cct aat ctg ttt      438
Thr Ser Val Met Xaa Ser Phe Gly Gly Val Leu Val Pro Asn Leu Phe
      100                      105                      110
ttg act act ggg gcc agg gaa tct cgt ca      467
Leu Thr Thr Gly Ala Arg Glu Ser Arg
115                      120

<210> 100
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..503

<221> sig_peptide
<222> 39..95
<223> Von Heijne matrix
      score 9.30000019073486
      seq FLLLVAGPRWVLS/QV

<400> 100
aatacttttct gagagtcctg gacctcctgt gcaagaac atg aaa cac ctg tgg ttc      56
                                Met Lys His Leu Trp Phe
                                -15
ttc ctc ctg ctg gtg gca ggt ccc aga tgg gtc ctg tcc cag gtg cag      104
Phe Leu Leu Leu Val Ala Gly Pro Arg Trp Val Leu Ser Gln Val Gln
      -10                      -5                      1
ctg sdk gag tcg ggc cca aga ctg gtg aag cct tca cag acc ctg tcc      152
Leu Xaa Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gln Thr Leu Ser
      5                      10                      15
ctc acc tgc act gta tct ggg gcc tcc gtc agc agt cgt ggg tac tat      200
Leu Thr Cys Thr Val Ser Gly Ala Ser Val Ser Ser Arg Gly Tyr Tyr
      20                      25                      30                      35
tgg acc tgg atc cgc cag ctc cca ggg aag ggc ctg gag tgg att ggc      248
Trp Thr Trp Ile Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Ile Gly
      40                      45                      50
tac atc tgc tac act ggg agc acc ttc tac aac ccg tcc ctc aag agt      296
Tyr Ile Xaa Tyr Thr Gly Ser Thr Phe Tyr Asn Pro Ser Leu Lys Ser
      55                      60                      65
cga tta acc ata tca ata gac acg tct aag aat cag ttc tcc ctg aac      344
Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
      70                      75                      80
ctg agg tct gtg act acc gcg gac acg gcc gtc tat tac tgt gcg aga      392
Leu Arg Ser Val Thr Thr Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
      85                      90                      95
gac cat ttc gat ctt cta ttc gac ccc tgg ggc cag gga acc ctg gtc      440
Asp His Phe Asp Leu Leu Phe Asp Pro Trp Gly Gln Gly Thr Leu Val
      100                      105                      110                      115
acc gtc tcc tct gcm tcc acc aag ggc cca tcg gtc ttc ccc ctg gca      488
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala

```

120 125 130 504
 scc tcc tcc aag agc a
 Xaa Ser Ser Lys Ser
 135

<210> 101
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 148..336

<221> sig_peptide
 <222> 148..270
 <223> Von Heijne matrix
 score 9.30000019073486
 seq VLXLFCFVFEAES/RS

<400> 101
 agagctcgcg gtggactccg acccggcgca acatggccgc agcctcgct ctgcgcgact 60
 gccaggcctg gaaggatgcg aggtctccgc tctccaccac aagcaacgaa gcctgcaagc 120
 tggtcgatgc cacgctgacc cagggtat atg gcc tgc cga gag agg ccg cgg ccc 174
 Met Ala Cys Arg Glu Arg Pro Arg Pro
 -40 -35
 ctt ctg tgg agg tct agg gga agg ttt ttt aat tgg gga aag ctg ttt 222
 Leu Leu Trp Arg Ser Arg Gly Arg Phe Phe Asn Trp Gly Lys Leu Phe
 -30 -25 -20
 ttt tgt ttt gtt ttg mtt ttg ttt tgt ttt gtt ttt gag gcg gag tct 270
 Phe Cys Phe Val Leu Xaa Leu Phe Cys Phe Val Phe Glu Ala Glu Ser
 -15 -10 -5
 cgc tct gtc gcc cag gct gga gtg cag tgg cgc tat ttc ggc tca cta 318
 Arg Ser Val Ala Gln Ala Gly Val Gln Trp Arg Tyr Phe Gly Ser Leu
 1 5 10 15
 caa gct ttg cct ccc tgg 336
 Gln Ala Leu Pro Pro Trp
 20

<210> 102
 <211> 289
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 214..288

<221> sig_peptide
 <222> 214..276
 <223> Von Heijne matrix
 score 9.19999980926514
 seq FILFHWSLCLCLC/QY


```

<400> 102
cccttatggtt ttcttttagt aatttcatag tttcaagttt tatatataag tctttaatcc      60
atatttgagtt gatttgtgta tatggtggag acaggggtcta gtcttgggtct tctgcatgtg    120
actttccaat tttcccagca ccattttattg gagaaactgt ctttttccca gtgcatgttc      180
ttggcacctt tgttgaaaaa cagttggcca tag atg cat gaa ttt att tct ggg          234
                               Met His Glu Phe Ile Ser Gly
                               -20                               -15

ttc ttt att ctc ttt cat tgg tct ctg tgt ttg tgt tta tgc caa tac          282
Phe Phe Ile Leu Phe His Trp Ser Leu Cys Leu Cys Leu Cys Gln Tyr
                               -10                               -5                               1

cat gcc g                                                                289
His Ala

```

```

<210> 103
<211> 383
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 252..383

<221> sig_peptide
<222> 252..377
<223> Von Heijne matrix
      score 9.19999980926514
      seq LLVCLFAVTSILC/SS

```

```

<400> 103
atctctccagc taataagtgt ccaagctggg actcaaactt gggcctttta actgtgctgc      60
tattctacct ctcccttgct ctttccagac caggcttggg acataacact aacacccttt      120
tcttttcatt tcatctcttg tcttccagtc attcctaaac attgacaybc attgagttcc      180
ttggctctgg ccatagtcct ttctcccttt cccctctggg gcatcaaata gtgattacag      240
tatccacagg g atg gca tat gcc att tca cca ttt cac agt tcc tgg aat          290
      Met Ala Tyr Ala Ile Ser Pro Phe His Ser Ser Trp Asn
      -40                               -35                               -30

cca ctt ttc act tct cat aaa gct tca gca agc cat tct cat ctt ggg          338
Pro Leu Phe Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly
      -25                               -20                               -15

ttg ctt gtt tgc cta ttt gct gtt aca tcc att ctc tgc tcc tca          383
Leu Leu Val Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser
      -10                               -5                               1

```

```

<210> 104
<211> 211
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 30..209

<221> sig_peptide
<222> 30..74

```

<223> Von Heijne matrix
 score 9.19999980926514
 seq PVLLLALLGFILP/LP

<221> misc_feature

<222> 83

<223> n=a, g, c or t
 Oligonucleotide

<400> 104

agaaagagat taccagccac agacgggtc atg agc ccg gta tta ctg ctg gcc	53
Met Ser Pro Val Leu Leu Leu Ala	
-15 -10	
ctc ctg ggg ttc atc ctc cca ctg cca ggn agt gca rgc gct gss tck	101
Leu Leu Gly Phe Ile Leu Pro Leu Pro Gly Ser Ala Xaa Ala Xaa Ser	
-5 1 5	
gcc agt ttg gga cag ttc agc atg tgt gga agg tgt ccg acm tgc ccc	149
Ala Ser Leu Gly Gln Phe Ser Met Cys Gly Arg Cys Pro Thr Cys Pro	
10 15 20 25	
ggc aat gga ccc cta aga aca cca gct gcg aca sgg vtt rgg gtg cca	197
Gly Asn Gly Pro Leu Arg Thr Pro Ala Ala Thr Xaa Xaa Xaa Val Pro	
30 35 40	
gga cac gtt gat gc	211
Gly His Val Asp	
45	

<210> 105

<211> 492

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 29..490

<221> sig_peptide

<222> 29..97

<223> Von Heijne matrix
 score 9.10000038146973
 seq SLLLFSLMCETSA/FY

<400> 105

agtcattacg gcgacacgtg gatccaag atg gcg acg gcg atg gat tgg ttg	52
Met Ala Thr Ala Met Asp Trp Leu	
-20	
ccg tgg tct tta ctg ctt ttc tcc ctg atg tgt gaa aca agc gcc ttc	100
Pro Trp Ser Leu Leu Phe Ser Leu Met Cys Glu Thr Ser Ala Phe	
-15 -10 -5 1	
tat gtg cct ggg gtc gcg cct atc aac ttc cac cag aac gat ccc gta	148
Tyr Val Pro Gly Val Ala Pro Ile Asn Phe His Gln Asn Asp Pro Val	
5 10 15	
gaa atc aag gct gtg aag ctc acc agc tct cga acc cag cta cct tat	196
Glu Ile Lys Ala Val Lys Leu Thr Ser Ser Arg Thr Gln Leu Pro Tyr	
20 25 30	

gaa tac tat tca ctg ccc ttc tgc cag ccc agc aag ata acc tac aag	244
Glu Tyr Tyr Ser Leu Pro Phe Cys Gln Pro Ser Lys Ile Thr Tyr Lys	
35 40 45	
gca gag aat ctg gga gag gtg ctg aga ggg gac cgg att gtc aac acc	292
Ala Glu Asn Leu Gly Glu Val Leu Arg Gly Asp Arg Ile Val Asn Thr	
50 55 60 65	
cct ttc cag gtt ctc atg aac agc gag aag aag tgt gaa gtt ctg tgc	340
Pro Phe Gln Val Leu Met Asn Ser Glu Lys Lys Cys Glu Val Leu Cys	
70 75 80	
agc cag tcc aac aag cca gtg acc ctg aca gtg gag cag agc cga ctc	388
Ser Gln Ser Asn Lys Pro Val Thr Leu Thr Val Glu Gln Ser Arg Leu	
85 90 95	
gtg gcc gag cgg atc aca gaa gac tac tac gtc cac ctc att gct gac	436
Val Ala Glu Arg Ile Thr Glu Asp Tyr Tyr Val His Leu Ile Ala Asp	
100 105 110	
aac ctg cct gtg gcc acc ggc tgg agc tct act cca acc gag aca gcg	484
Asn Leu Pro Val Ala Thr Gly Trp Ser Ser Thr Pro Thr Glu Thr Ala	
115 120 125	
atg aca ag	492
Met Thr	
130	

<210> 106
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 <212> DNA
 <213> Homo sapiens

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 <222> 41..94
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 score 9.10000038146973
 seq LISLLQCAHVSLG/LQ

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Met Pro Ser Pro Cys	
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ctg atc tct ctt ctt caa tgt gct cat gtg tcc ctt ggc tta cag tat	103
Leu Ile Ser Leu Leu Gln Cys Ala His Val Ser Leu Gly Leu Gln Tyr	
-10 -5 1	
cca tgc stt ctc ctt ctc cct cc	126
Pro Cys Xaa Leu Leu Leu Pro	
5 10	

<210> 107
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 <212> DNA
 <213> Homo sapiens

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 <222> 82..132
 <223> Von Heijne matrix
 score 9.10000038146973
 seq LVLAAFCLGIASA/VP

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 accagaccgc ggacgtctgt aatctcagag gcttgtttgc tgaggggtgcc tgcgcastgc 60
 gacggctgct ggttttgaaa c atg aat ctt tgc ctc gtc ctg gct gcc ttt 111
 Met Asn Leu Ser Leu Val Leu Ala Ala Phe
 -15 -10
 tgc ttg gga ata gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat 159
 Cys Leu Gly Ile Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp
 -5 1 5
 aca aag tgg tac cag tgg aag gca aca cac aga aga tta tat ggc gcg 207
 Thr Lys Trp Tyr Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala
 10 15 20 25
 aat gaa gaa gga tgg agg aga gca gcg tgg gag gg 242
 Asn Glu Glu Gly Trp Arg Arg Ala Ala Trp Glu
 30 35

<210> 108
 <211> 336
 <212> DNA
 <213> Homo sapiens

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 <222> 81..335

<221> sig_peptide
 <222> 81..137
 <223> Von Heijne matrix
 score 9
 seq WVFLVAIFTGVHC/EV

<400> 108
 agctctggga gaggagcccc agccgtgaga ttcccagaag tttccacttg gtgatcagca 60
 ctgaacacag accaccaacc atg gag ttt ggc ctt aat tgg gtt ttc ctt gtt 113
 Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val
 -15 -10
 gct att ttt aca ggt gtc cac tgt gag gtg cag ttg gtg gag tct ggg 161
 Ala Ile Phe Thr Gly Val His Cys Glu Val Gln Leu Val Glu Ser Gly
 -5 1 5
 gga gac ctg gta cag cca ggg cgg tcc ctg aga ctc tcc tgt aca gct 209
 Gly Asp Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala
 10 15 20
 tct gga ttc acc ttt ggt gat tat gcc atg acc tgg ttc cgc cag gct 257
 Ser Gly Phe Thr Phe Gly Asp Tyr Ala Met Thr Trp Phe Arg Gln Ala
 25 30 35 40
 tca ggg aag cga ctg gag tgg cta ggt ttc att aga aat aga ggt tcs 305

Ser Gly Lys Arg Leu Glu Trp Leu Gly Phe Ile Arg Asn Arg Gly Ser
45 50 55
ggt ggg tca gca gag tac ggc gcg tct gtg a 336
Gly Gly Ser Ala Glu Tyr Gly Ala Ser Val
60 65

<210> 109
<211> 160
<212> DNA
<213> Homo sapiens

<220>
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<222> 6..158

<221> sig_peptide
<222> 6..56
<223> Von Heijne matrix
score 9
seq LLILLMLLLFAIH/IN

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cagct atg aaa aac tgc cta ctc ata ctc ctc atg ctt ctc tta ttt gca 50
Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala
-15 -10 -5
ata cac ata aac cgt atg aat gta agg aat gtg gga aat act tta gtc 98
Ile His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val
1 5 10
gta gtg caa atc tta ttc agc atc aga gta ttc ata ctg gag aga aac 146
Val Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn
15 20 25 30
cct ttg aat gtg gg 160
Pro Leu Asn Val

<210> 110
<211> 527
<212> DNA
<213> Homo sapiens

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<222> 81..527

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
score 9
seq WIFLLAILKGVQC/EV

<221> misc_feature
<222> 307..308,466..467
<223> n=a, g, c or t
Oligonucleotide

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<400> 110
agctctggga gaggagcccc agccctgaga ttcccagggtg tttccattca gtgatcagca      60
ctgaacacag aggactcacc atg gag ttg gga ctg agc tgg att ttc ctt ttg      113
                Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu
                        -15                                -10

gct att tta aaa ggt gtc cag tgt gaa gtg cag ctg gtg gag tct ggg      161
Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly
                -5                                1                                5

gga ggc ttg gta cag cct ggc agg tcc ctg aga ctc tcc tgt gca gcc      209
Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala
                10                                15                                20

tct gga ttc acc ttt gat gat tac gcc atg cac tgg gtc cgg caa gct      257
Ser Gly Phe Thr Phe Asp Tyr Ala Met His Trp Val Arg Gln Ala
                25                                30                                35                                40

cca ggg aag ggc ctg gag tgg gtc tca gga att act tgg aat agt ggt      305
Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly
                45                                50                                55

ann ata ggc tac gcg gac tct gtg aag ggc cga ttc acc atc tcc aga      353
Xaa Ile Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
                60                                65                                70

gac aac gcc aag aac tcc ctg tat ttg caa atg aac agt ctg aga act      401
Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr
                75                                80                                85

gag gac acg gcc ttc tat ttc tgt gca aaa gct cgc ggg ctc ttt agc      449
Glu Asp Thr Ala Phe Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser
                90                                95                                100

gat acc tgg ccc tac vnn cac tac gct atg gac gtc tgg ggc caa ggg      497
Asp Thr Trp Pro Tyr Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly
                105                                110                                115                                120

acc acg gtc acc gtc tcc tca gcc tcc acc      527
Thr Thr Val Thr Val Ser Ser Ala Ser Thr
                125                                130

<210> 111
<211> 154
<212> DNA
<213> Homo sapiens

<220>
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<222> 80..154

<221> sig_peptide
<222> 80..121
<223> Von Heijne matrix
        score 8.89999961853027
        seq LLVFFVLWTCSLA/LL

<400> 111
ctggaaaggg aggagccaaa aggggaacgc tttcttgatt gtcccagcct cattaggagc      60
taccacaggg ctctcctgc atg ctc ctt gtt ttc ttt gtg ctc tgg act tgc      112
                Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys
                        -10                                -5

tca ctt gca ctg ctt gct tct tcc cca atc gcm gcc yac cca      154
  
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Ser Leu Ala Leu Leu Ala Ser Ser Pro Ile Ala Ala Xaa Pro
1 5 10

<210> 112
<211> 441
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 59..439

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
score 8.899999961853027
seq ILLLVAAATDASS/QM

<400> 112
atcacccatc aaccacatcc ctccctctaga gagtcccctg aaagcacagc tcctcacc 58
atg gac tgg acc tgg aga atc ctc ctc ttg gtg gca gca gcc aca gat 106
Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
-15 -10 -5
gcc tcc tcc cag atg cag ctg ttg cag tct ggg cct gaa gtg aag aag 154
Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
1 5 10
act ggg tcc tca gtg aaa ctt tcc tgc acg gcc tcc ggc gac acc ctc 202
Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
15 20 25
gcc tac cac tac ctg cac tgg gtg cga cag gcc ccc gga caa gcg ctt 250
Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
30 35 40 45
gag tgg atg gga tgg atc aca cct ttc agt gga gac acc aac ttc gca 298
Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
50 55 60
cag cga ttc cag gac aga ctc acc ttc acc agg gac agg tct atg agc 346
Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
65 70 75
aca gtc tac atg acc ctg acc agc ctg ata tct gaa gac aca gcc atg 394
Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
80 85 90
tat tac tgt gcc act gat gga cgt cgc acc aac cgt ctt ttt gaa ca 441
Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
95 100 105

<210> 113
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 164..367

<221> sig_peptide
 <222> 164..217
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LGCLLWLLTHIKA/QD

<221> misc_feature
 <222> 290..292
 <223> n=a, g, c or t
 Oligonucleotide

<400> 113
 cagtttcagt ttctctccct tcctagtaga gacaaaaagg agacacattt tatccgtgca 60
 tccaaagact ccgatgttgg tcatggactt gggaagacag tcttcccttg gcgtttgatc 120
 actgcggaga tgccttcctt gatcattcac ccacattccc ttg atg gca ggt caa 175
 Met Ala Gly Gln
 -15
 ttg ctg gga tgc ctg ctt tgg ctg ctc acc cac att aaa gcc cag gac 223
 Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile Lys Ala Gln Asp
 -10 -5 1
 tca gtc agg gat gcc tac tgg aag act ggt agc tgc cca cct cca ttt 271
 Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys Pro Pro Pro Phe
 5 10 15
 ctc cat gtg tct acc ttc nnn kkt aaa ctt acc ttc tcc act aag ggc 319
 Leu His Val Ser Thr Phe Xaa Xaa Lys Leu Thr Phe Ser Thr Lys Gly
 20 25 30
 aac ctt ctg cat tcc att cct ctc tct tcc ccc tta gcc tgt gtt ctt 367
 Asn Leu Leu His Ser Ile Pro Leu Ser Ser Pro Leu Ala Cys Val Leu
 35 40 45 50
 ag 369

<210> 114
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..334

<221> sig_peptide
 <222> 20..292
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LFLMLLGELGVFA/SY

<221> misc_feature
 <222> 295
 <223> n=a, g, c or t
 Oligonucleotide

<400> 114
 agctctgaat tgggaaggg atg aag gag gct gtg cct ccg ggt tgc acg aag 52
 Met Lys Glu Ala Val Pro Pro Gly Cys Thr Lys

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 100

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                                -90                                -85
agt ccg agt cat ttc tca gaa ggt ttt gat agg tgg gcc tta gag gag      100
Ser Pro Ser His Phe Ser Glu Gly Phe Asp Arg Trp Ala Leu Glu Glu
-80                                -75                                -65
acg ccg ccg gaa aac ctg att ggc gcc ctc ttg gcg atc ttc ggg cac      148
Thr Pro Pro Glu Asn Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His
                                -60                                -55                                -50
ctc gtg gtc agc att gca ctt aac ctc cag aag tac tgc cac atc cgc      196
Leu Val Val Ser Ile Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg
                                -45                                -40                                -35
ctg gca ggc tcc aag gat ccc cgg gcc tat ttc aag acc aag aca tgg      244
Leu Ala Gly Ser Lys Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp
                                -30                                -25                                -20
tgg ctg ggc ctg ttc ctg atg ctt ctg ggc gag ctg ggt gtg ttc gcm      292
Trp Leu Gly Leu Phe Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala
                                -15                                -10                                -5
tcn tac gcc ttc gcg ccg ctg tca ctc atc gtg ccc ctc agc      334
Ser Tyr Ala Phe Ala Pro Leu Ser Leu Ile Val Pro Leu Ser
1                                5                                10

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<210> 115
 <211> 153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..152
 <221> sig_peptide
 <222> 21..74
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LLSCWALLGTTFG/CG

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<400> 115
acaccctgc cagcggcacc atg gct ttc ctc tgg ctc ctc tcc tgc tgg gcc      53
                                Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala
                                -15                                -10
ctc ctg ggt acc acc ttc ggc tgc ggg gtc ccc gcc atc cac cct ggc      101
Leu Leu Gly Thr Thr Phe Gly Cys Gly Val Pro Ala Ile His Pro Gly
                                -5                                1                                5
tgc caa ctg agc ccg cgg ctc cct ccg acc ctg ctc ccc aca gag cgc      149
Cys Gln Leu Ser Pro Arg Leu Pro Pro Thr Leu Leu Pro Thr Glu Arg
10                                15                                20                                25
ggg g
Gly

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<210> 116
 <211> 292
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 47..292

<221> sig_peptide
 <222> 47..106
 <223> Von Heijne matrix
 score 8.80000019073486
 seq LWLFFVLNLGSFA/FS

<400> 116
 taccagtaac ttctttcatg gttcaataaa atcatagctt tagttt atg gca cct 55
 Met Ala Pro
 -20
 ttt caa aac ttc ctt tgg ctt ttc ttt gtg ctt aat tta ggw agt ttt 103
 Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu Gly Ser Phe
 -15 -10 -5
 gct ttt agc tca mtt ccd aat tct ctt ttt tac aca att cat ttt ggt 151
 Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile His Phe Gly
 1 5 10 15
 cct aat ttc ttt act tta cta tat aaa caa ggt gct gaa atg tgt gtg 199
 Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu Met Cys Val
 20 25 30
 tat gta ttt aac ttc ctc tac cca ttt gct ctt ggt tat ttc ttc agt 247
 Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr Phe Phe Ser
 35 40 45
 tat gat att ctg gat ttg cca gtc akt gtc cgt cct cct agc ggg 292
 Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro Ser Gly
 50 55 60

<210> 117
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 141..302

<221> sig_peptide
 <222> 141..245
 <223> Von Heijne matrix
 score 8.69999980926514
 seq LLLSVAFNQLVFA/LY

<400> 117
 tttctcatca atttcttgct tctctggcaa cctcaacctc tgattcctga ggccaataaa 60
 actgaaactt tctgcttgag ctcttggttt gccaggctga tggggctgag gtgcaccctc 120
 tgaggaaaag ctgtaaatac atg gat ttt acc caa tgc cat tcc ctt ctt tta 173
 Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu
 -35 -30 -25
 agg gtt gaa tat tct cca gtg tct gtc tgc ttt tta tta ctt tcc gtt 221
 Arg Val Glu Tyr Ser Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val
 -20 -15 -10
 gcc ttc aat cag ttg gtt ttt gct ttg tat cca ata caa gct acw btc 269


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cta tca aga cga gct ggt acc att cct act gaa aca att cca aaa aaa      270
Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu Thr Ile Pro Lys Lys
      1              5              10
ttg agg agg aga gac ggg      288
Leu Arg Arg Arg Asp Gly
15              20

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<210> 120
<211> 386
<212> DNA
<213> Homo sapiens

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<220>
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<222> 71..385

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<221> sig_peptide
<222> 71..142
<223> Von Heijne matrix
      score 8.5
      seq XALLMGFLMVCLG/AF

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<400> 120
aattctcttg gagcaagcag ggaagcagag gagcagcagg gtcagggtgc tgggttccta      60
aggtgcaagg atg cag aac aga act ggc ctc att ctc tgt gct ytt gcc      109
      Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala
              -20              -15
ctc ctg atg ggt ttc ctg atg gtc tgc ctg ggg gcc ttc ttc att tcc      157
Leu Leu Met Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser
      -10              -5              1              5
tgg ggc tcc ata ttc gac tgt cag ggg agc ctg att gcg gcc tat ttg      205
Trp Gly Ser Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu
              10              15              20
ctt ctg cct ctg ggg ttt gtg atc ctt ctg agt gga att ttc tgg agc      253
Leu Leu Pro Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser
              25              30              35
aac tat cgc cag gtg act gaa agc aaa gga gtg ttg agg cac atg ctc      301
Asn Tyr Arg Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu
              40              45              50
cga caa cac ctt gct cat ggg gcc ctg ccc gtg gcc aca gta gac agt      349
Arg Gln His Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser
              55              60              65
gct gct ctt ctg aaa atc atg tgt aag car ttg ctt t      386
Ala Ala Leu Leu Lys Ile Met Cys Lys Gln Leu Leu
70              75              80

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<210> 121
<211> 190
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 34..189

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<221> sig_peptide
 <222> 34..165
 <223> Von Heijne matrix
 score 8.5
 seq LTCTSSLLSFALG/RS

<400> 121
 atcttgaaaa cggaaaataa aaacagcaga cct atg aag gtc gaa ggg gaa gaa 54
 Met Lys Val Glu Gly Glu Glu
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 aag ctg tat cga ttg ttg aga tct ggc gac ttg ttt aaa ttt cat cag 102
 Lys Leu Tyr Arg Leu Leu Arg Ser Gly Asp Leu Phe Lys Phe His Gln
 -35 -30 -25
 cct cac ttc tat gaa ctc tca ggc ctc acg tgt acc agc tct ctg ctc 150
 Pro His Phe Tyr Glu Leu Ser Gly Leu Thr Cys Thr Ser Ser Leu Leu
 -20 -15 -10
 tcc ttt gcc ttg gga cgt tcc atc cct gga agt ttc cca g 190
 Ser Phe Ala Leu Gly Arg Ser Ile Pro Gly Ser Phe Pro
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<210> 122
 <211> 211
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 32..211
 <221> sig_peptide
 <222> 32..88
 <223> Von Heijne matrix
 score 8.5
 seq LLLFSGAVALIQT/WA

<400> 122
 agattctccc cagacgccaa ggttgcggggt c atg gag tcc cga acc ctc ctc 52
 Met Glu Ser Arg Thr Leu Leu
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 ctg ctg ttc tcg gga gcc gtg gcc ctg atc cag acc tgg gca ggt gag 100
 Leu Leu Phe Ser Gly Ala Val Ala Leu Ile Gln Thr Trp Ala Gly Glu
 -10 -5 1
 tgc ggg gtc ggg agg gaa aag gcc tct gcg gga agg agc gag ggg ccc 148
 Cys Gly Val Gly Arg Glu Lys Ala Ser Ala Gly Arg Ser Glu Gly Pro
 5 10 15 20
 gcc cgg agg agt aaa tct gca cat ata kbt aat tac aga tta caa tta 196
 Ala Arg Arg Ser Lys Ser Ala His Ile Xaa Asn Tyr Arg Leu Gln Leu
 25 30 35
 caa tca agg cag ggg 211
 Gln Ser Arg Gln Gly
 40

<210> 123

<211> 353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 249..353

<221> sig_peptide
 <222> 249..296
 <223> Von Heijne matrix
 score 8.39999961853027
 seq SVPLLCFWSLCYC/FA

<221> misc_feature
 <222> 187
 <223> n=a, g, c or t
 Oligonucleotide

<400> 123
 agcgagtcct tgccctcccg cggtccagga cgagggcaga tctcgttctg gggcaagccg 60
 ttgacactcg ctccctgccg ccgcccgggc tccgtgccgc caagttttca ttttccacct 120
 tctctgcctc cagtccccc gcccctggcc gagagaaggg tcttaccggc cgggattgct 180
 ggaaacncaa gaggtggttt ttgtttttta aaacttctgt ttcttgggag ggggtgtggc 240
 ggggcagg atg agc aac tcc gtt cct ctg ctc tgt ttc tgg agc ctc tgc 290
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys
 -15 -10 -5
 tat tgc ttt gct gcg ggg agc ccc gta cct ttt ggt cca gag gga cgg 338
 Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg
 1 5 10
 ctg gaa gat aag ctc 353
 Leu Glu Asp Lys Leu
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<210> 124
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 93..248

<221> sig_peptide
 <222> 93..134
 <223> Von Heijne matrix
 score 8.39999961853027
 seq PWTILLFAAGSLA/IP

<400> 124
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 cagccggatt tcccagccaa acgcagagag ag atg ccc tgg acc atc ttg ctc 113
 Met Pro Trp Thr Ile Leu Leu
 -10

ttt gca gct ggc tcc ttg gcg atc cca gca cca tcc atc cgg gtg gtg	161
Phe Ala Ala Gly Ser Leu Ala Ile Pro Ala Pro Ser Ile Arg Val Val	
-5 1 5	
ccc ccg tac cca agc agc caa gag gac ccc atc cac atc gca tgc atg	209
Pro Pro Tyr Pro Ser Ser Gln Glu Asp Pro Ile His Ile Ala Cys Met	
10 15 20 25	
gcc gct ggg aac ttc ccg ggg gcg aat ttc aca ctg tat c	249
Ala Ala Gly Asn Phe Pro Gly Ala Asn Phe Thr Leu Tyr	
30 35	

<210> 125
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 175..375

<221> sig_peptide
 <222> 175..366
 <223> Von Heijne matrix
 score 8.39999961853027
 seq GFLFFGFLFPVFS/FP

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ccctctgtcc ccgcggctgg gtctcgtctg ctccggttcc tgggctccta attcttggtc	120
cagcttcttc caggtcagtg tgcgggcctt ccacgctgcc agcgggaacac tgga atg	177
	Met
gcg gaa ggg gaa cgg gtc tgc gcg tct gtk gtt ccc agc gct ctg cga	225
Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu Arg	
-60 -55 -50	
acg ctg aaa agg agg agc aac ctg tcc aga atc ccc gca gga cag gaa	273
Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln Glu	
-45 -40 -35	
aag gag ggg aaa tct cga cat gtt gct ccc cct ttt cgc ttt ttc cct	321
Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe Pro	
-30 -25 -20	
ttt tcc ggt ttt ttg ttt ttt ggt ttt ctt ttt ccc gtc ttt tct ttc	369
Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser Phe	
-15 -10 -5 1	
ccc tcc	375
Pro Ser	

<210> 126
 <211> 437
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..435

<221> sig_peptide
 <222> 223..261
 <223> Von Heijne matrix
 score 8.39999961853027
 seq MFCLAAILASASA/QR

<221> misc_feature
 <222> 404
 <223> n=a, g, c or t
 Oligonucleotide

<400> 126
 tcaataacca tgtgaacagt ttctgtggagg gttttaagta ttttccactg gctggctttg 60
 ggtataagta cctttccttc ttctgtcggt aaccacgccg aggggagaaa actatgcccc 120
 cgtgaaagtc cccactctgt ttctggtggg gaatactgga gcttaacctc ttggaggggg 180
 ttgttccata ccaaggggtcc ttccgtaggt atttctaatt gg atg ttc tgc ctg 234
 Met Phe Cys Leu
 -10
 gca gca att tta gcc tca gca tct gcc caa cgg ttt cct tct gcc ttt 282
 Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe Pro Ser Ala Phe
 -5 1 5
 tct cct tca cct tty yga tgg ctt yrg car tgt aas act gcc acc tcc 330
 Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa Thr Ala Thr Ser
 10 15 20
 ttg ggt ttt trc act gtg tgy art aac tcc ata att tcc ttg tgg tat 378
 Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile Ser Leu Trp Tyr
 25 30 35
 tta ayg ggr gtt ccc cca gag gtt ang gaa ctc cct ttc ttt cca tat 426
 Leu Xaa Gly Val Pro Glu Val Xaa Glu Leu Pro Phe Phe Pro Tyr
 40 45 50 55
 tgc agc atg gg 437
 Cys Ser Met

<210> 127
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..302

<221> sig_peptide
 <222> 24..74
 <223> Von Heijne matrix
 score 8.39999961853027
 seq TLLLLLSEALALT/QT

<400> 127
 ctcaggactc agaggctggg atc atg gta gat gga acc ctc ctt tta ctc ctc 53
 Met Val Asp Gly Thr Leu Leu Leu Leu Leu
 -15 -10
 tcg gaa gcc ctg gcc ctt acc car acc tgg gcg ggc tcc cac tcc tkr 101
 Ser Glu Ala Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Xaa

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

	-5		1		5												
aag	tat	ttc	cac	act	tcc	gtg	tcc	cgg	mcc	ggc	cgc	ggg	gag	ccc	cgc		149
Lys	Tyr	Phe	His	Thr	Ser	Val	Ser	Arg	Xaa	Gly	Arg	Gly	Glu	Pro	Arg		
10					15				20					25			
ttc	atc	tct	gtg	ggc	tac	gtg	gac	gac	acc	cgg	tca	gag	tat	tgg	gac		197
Phe	Ile	Ser	Val	Gly	Tyr	Val	Asp	Asp	Thr	Arg	Ser	Glu	Tyr	Trp	Asp		
			30				35				40						
cgg	gag	aca	cgg	agc	gcc	agg	gac	acc	gca	cag	att	ttc	cga	gtg	aac		245
Arg	Glu	Thr	Arg	Ser	Ala	Arg	Asp	Thr	Ala	Gln	Ile	Phe	Arg	Val	Asn		
		45				50			55								
ctg	cgg	acg	ctg	cgc	ggc	tac	tac	aat	cag	agc	gag	gcc	ggg	tct	cam		293
Leu	Arg	Thr	Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser	Glu	Ala	Gly	Ser	Xaa		
	60				65				70								
acc	ctg	cag	tg														304
Thr	Leu	Gln															
	75																

<210> 128
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 19..243

 <221> sig_peptide
 <222> 19..99
 <223> Von Heijne matrix
 score 8.39999961853027
 seq LVLSLISLSIAWS/MV

<221> misc_feature
 <222> 112
 <223> n=a, g, c or t
 Oligonucleotide

<400>	128																
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				Met	Asn	Phe	Arg	Gly	Pro	Gln	Thr	Phe	Ser	Leu			
					-25					-20							
tca	cac	agc	ctt	gtg	tta	tcc	cta	atc	agt	ctc	tcc	att	gca	tgg	tct		99
Ser	His	Ser	Leu	Val	Leu	Ser	Leu	Ile	Ser	Leu	Ser	Ile	Ala	Trp	Ser		
	-15				-10					-5							
atg	gtc	gaa	atg	nbc	act	tct	gca	agc	tac	aar	caa	aag	ttt	gcc	ctt		147
Met	Val	Glu	Met	Xaa	Thr	Ser	Ala	Ser	Tyr	Lys	Gln	Lys	Phe	Ala	Leu		
1		5						10					15				
aga	atc	cta	gtt	gtg	cag	ttg	ccc	aca	tgg	gtg	gaa	tgt	cca	gta	aac		195
Arg	Ile	Leu	Val	Gln	Leu	Pro	Thr	Trp	Val	Glu	Cys	Pro	Val	Asn			
	20				25				30								
cac	agg	tgt	gca	cta	ggg	aga	aag	aat	tgt	tct	att	agg	acc	cag	cca	c	244
His	Arg	Cys	Ala	Leu	Gly	Arg	Lys	Asn	Cys	Ser	Ile	Arg	Thr	Gln	Pro		
	35				40				45								

<210> 129
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..230

<221> sig_peptide
 <222> 156..215
 <223> Von Heijne matrix
 score 8.39999961853027
 seq SCICLFLPSLIHS/FP

<400> 129
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 ccttgggtgtc atttgtggca gcctatagca ttagagcctt tgagaacaga tctttccaga 120
 ttctgcttaa gtccagggat tctgtgaccg cagaa atg act ggc atc tcc atc 173
 Met Thr Gly Ile Ser Ile
 -20 -15
 tgc tcg tgc atc tgt ttg ttt ctt cct tca ttg att cac tca ttc ccc 221
 Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser Leu Ile His Ser Phe Pro
 -10 -5 1
 ccg ccc tgc gg 232
 Pro Pro Cys
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<210> 130
 <211> 312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..310

<221> sig_peptide
 <222> 17..94
 <223> Von Heijne matrix
 score 8.30000019073486
 seq FLLLVAAPRWQL/QE

<400> 130
 atgctttctg agagtc atg gac ctc ctg tgc aag aac atg aag cac ctg tgg 52
 Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp
 -25 -20 -15
 ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg gtc cag ctg cag gag 100
 Phe Phe Leu Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu
 -10 -5 1
 tcg ggc cca cgc ctg gtg agg cct ccg gag acc ctg aag cct tcg gag 148
 Ser Gly Pro Arg Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu
 5 10 15
 acc ctg tcc ctc acc tgc act att tct ggt gac tcc atg agc agt gct 196

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Ile	Ser	Gly	Asp	Ser	Met	Ser	Ser	Ala	
20					25					30						
tct	tac	tat	tgg	gcc	tgg	atc	cgc	cag	ccc	cca	ggc	aag	ggc	ctg	gaa	244
Ser	Tyr	Tyr	Trp	Ala	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	
35				40					45					50		
ttc	att	ggg	cgt	gcc	tta	tat	agt	ggg	acc	acc	gac	tac	aat	ccg	tcc	292
Phe	Ile	Gly	Arg	Ala	Leu	Tyr	Ser	Gly	Thr	Thr	Asp	Tyr	Asn	Pro	Ser	
			55					60					65			
ctc	agc	agt	cga	atc	acc	ct										312
Leu	Ser	Ser	Arg	Ile	Thr											
			70													

<210> 131
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..274

<221> sig_peptide
 <222> 119..253
 <223> Von Heijne matrix
 score 8.19999980926514
 seq PLSLSLCLSLCHT/HT

<400> 131																
gccttcatct	ctccatctct	gcgctgctgc	cggtgcgcgc	atccagcacc	cagactccag											60
caccggccga	ggacccccac	tccggctgca	gggacctgt	cccagcgaga	ccgcaggc											118
atg tca tcc	gaa aag tca	gga ctc cca	gac tca gtc	cct cac act	tct											166
Met Ser Ser	Glu Lys Ser	Gly Leu Pro	Asp Ser Val	Pro His Thr	Ser											
-45		-40		-35												
ccg ccg ccc	tac aat gcc	cct cag cct	cca gcc gaa	ccc cca gcc	ccg											214
Pro Pro Pro	Tyr Asn Ala	Pro Gln Pro	Pro Ala Glu	Pro Pro Ala	Pro											
	-25		-20		-15											
cct ctc tct	ctc tct ctc	tgt ctc tct	ctc tgt cac	aca cac aca	cac											262
Pro Leu Ser	Leu Ser Leu	Cys Leu Ser	Leu Cys His	Thr His Thr	His											
	-10		-5		1											
aca cac aca	cac ac															276
Thr His Thr	His															
5																

<210> 132
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..172

<221> sig_peptide
 <222> 35..118

<223> Von Heijne matrix
 score 8.19999980926514
 seq LVSLLMQPEGALG/EE

<400> 132
 actctgctga gctcctctgc acctgcccag gacc atg acg cct gct ctg cgc tgc 55
 Met Thr Pro Ala Leu Arg Cys
 -25
 gca ttc gct ctg gcc ata gcg ggc ctc gtg tcg ctg ctg atg cag ccc 103
 Ala Phe Ala Leu Ala Ile Ala Gly Leu Val Ser Leu Leu Met Gln Pro
 -20 -15 -10
 gag ggc gcc ctc ggc gag gag gct gca agt gcc gca gcc cag ggc cgc 151
 Glu Gly Ala Leu Gly Glu Glu Ala Ala Ser Ala Ala Ala Gln Gly Arg
 -5 1 5 10
 cag ttg gct gaa ctt agg ctc ca 174
 Gln Leu Ala Glu Leu Arg Leu
 15

<210> 133
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..342

<221> sig_peptide
 <222> 133..246
 <223> Von Heijne matrix
 score 8.19999980926514
 seq LLLIFLSFPYTLC/IL

<400> 133
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 cttttaactt caactgttct tttttcctgt aaatcttaaat tttctttttt tttctcccaa 120
 tttttctcct ac atg tct gga ctc ttc cca gtt cct gtc aga gta aat gtt 171
 Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val
 -35 -30
 gat att gcc cag aac ata act tgc tct tcc ttt tct ctc ctt ctc att 219
 Asp Ile Ala Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile
 -25 -20 -15 -10
 ttt ctt tct ttc ccc tac acc ctc tgt ata ctc tat aga gta aaa tca 267
 Phe Leu Ser Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser
 -5 1 5
 tat aca ccc acg gag tca ata act gcc ttt aat cta aca att ggg wga 315
 Tyr Thr Pro Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa
 10 15 20
 ttc cca tat ctt taw wtt tcw acc ccg gg 344
 Phe Pro Tyr Leu Xaa Xaa Ser Thr Pro
 25 30

<210> 134
 <211> 244

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 128..244

<221> sig_peptide
<222> 128..226
<223> Von Heijne matrix
score 8.19999980926514
seq HALSLCLCTCAFA/FL

<400> 134
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ctcttccctg gggcagggct ggcttccata ggggtgcttg ttgggccctt tggaaggggg 120
tgtgcgg atg tgc agg gct gct tgt atc att aga atg gct gtt aga att 169
Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile
-30 -25 -20
tca ttc ttt ctt tct tac cat gct ctg tct ctc tgc ctt tgt aca tgt 217
Ser Phe Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys
-15 -10 -5
gcg ttt gca ttt ctc tcc ctc ctc ggg 244
Ala Phe Ala Phe Leu Ser Leu Leu Gly
1 5

<210> 135
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..216

<221> sig_peptide
<222> 40..90
<223> Von Heijne matrix
score 8.19999980926514
seq LLXALGFLXQVNP/XP

<400> 135
attaaaccac caccagstcc ccaagccacc ccttcagcc atg aag ttc ctg ctc 54
Met Lys Phe Leu Leu
-15
ctg gma gcc ctc gga ttc ctg amc cag gtg aat ccc arc cca att sma 102
Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn Pro Xaa Pro Ile Xaa
-10 -5 1
ggd ggg tca aaa atg tgt gag twa cac ccc agg ata ctg cag gac atg 150
Gly Gly Ser Lys Met Cys Glu Xaa His Pro Arg Ile Leu Gln Asp Met
5 10 15 20
ttg cca ctg ggg gga gac agc att gtt cat gtg caa cgc tks cag aaa 198
Leu Pro Leu Gly Gly Asp Ser Ile Val His Val Gln Arg Xaa Gln Lys
25 30 35

atg ctg cat cag yta ctc c
Met Leu His Gln Leu Leu
40

217

<210> 136
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 114..428

<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
score 8.10000038146973
seq LFCFLLLCLSAAS/LL

<400> 136
aggcgtctgt gtgcgccgcc aagtcggtgg ggcggggaag cgaggtgtgg atgggggggtc 60
gccttgacct ctgcctcagc cagtagcgca gtctcggcct cgccgttacg gag atg 116
Met
gtg ccc tgg gtg cgg acg atg ggg cag aag ctg aag cag cgg ctg cga 164
Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu Arg
-40 -35 -30
ctg gac gtg gga cgc gag atc tgc cgc cag tac ccg ctg ttc tgc ttc 212
Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys Phe
-25 -20 -15 -10
ctg ctg ctc tgt ctc agc gcc gcc tcc ctg ctt ctt aac agg tat att 260
Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr Ile
-5 1 5
cat att tta atg atc ttc tgg tca ttt gtt gct gga gtt gtc aca ttt 308
His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr Phe
10 15 20
tac tgc tca cta gga cct gat tct ctc tta cca aat ata ttc ttc aca 356
Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe Thr
25 30 35
ata aaa tac aaa ccc aag cag tta gga ctt cag gaa tta ttt cct caa 404
Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro Gln
40 45 50 55
ggg cat agc tgt gct gtt tgt ggt 428
Gly His Ser Cys Ala Val Cys Gly
60

<210> 137
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 305..433

<221> sig_peptide
 <222> 305..406
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLCLFXLFFFSFL/KR

<400> 137
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 cagctgctcc acattttag cgaacacttt gactccaaag agaaggagga agacaaagac 120
 aagaaggaaa agaaagacaa ggacaagaag gaagcccctg ctgacatggg agcacatcag 180
 ggagtggctg ttctggggat tgcccttatt gctatggggg aggagattgg tgcagagatg 240
 gcattacgaa cctttggcca cttggtgagt atagcatgaa gaaaattgga atatactggt 300
 ttg atg gcc tgg ggt tcc cca ggg aag att ttt ctg atg ggt ttt ctt 349
 Met Ala Trp Gly Ser Pro Gly Lys Ile Phe Leu Met Gly Phe Leu
 -30 -25 -20
 ggt gga gag ctg gtc ttt ttg ctg tgc ctt ttc ttw ctt ttt ttc ttt 397
 Gly Gly Glu Leu Val Phe Leu Leu Cys Leu Phe Xaa Leu Phe Phe Phe
 -15 -10 -5
 tct ttt ttg aag cgg agt ttt gct cta gag tgc aat g 434
 Ser Phe Leu Lys Arg Ser Phe Ala Leu Glu Cys Asn
 1 5

<210> 138
 <211> 395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 310..393
 <221> sig_peptide
 <222> 310..357
 <223> Von Heijne matrix
 score 8.10000038146973
 seq SILLLLAPPLPSA/VS

<221> misc_feature
 <222> 189
 <223> n=a, g, c or t
 Oligonucleotide

<400> 138
 aaaagctctg taaacatata ataaatggaa ttccattgac attcaagcct tacgtatttc 60
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 cattcttctc ataatagttc tccctcsatt cttcagtgat tyccttgtgt ttataggata 180
 aagtccacnt gttatttttg cagtcagttc aagatccaca aatcagtcct tacccttaca 240
 tccttatttc tcactgctgt tctaatatag tctttataacc agtcaggctg gtctgttcac 300
 tattcctga atg ttt ttc tcc att ctt ttg tta ttg gca ccc ccg cta ccc 351
 Met Phe Phe Ser Ile Leu Leu Leu Ala Pro Pro Leu Pro
 -15 -10 -5
 tct gca gtg tct ttg cta cct ttc ttt ttc tac tgt gtg cag gg 395
 Ser Ala Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln
 1 5 10

<210> 139
 <211> 268
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..266

<221> sig_peptide
 <222> 141..206
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLVCSWLSISLHA/HT

<400> 139
 caactctgct gttttgtagg aagccacatg gaggtcattt acggttacta gttatcttag 60
 tcagcttggg cagccattaa aaaataatac tgtagacgga gtggcccaaa cgagagaaat 120
 ttatttctta tagttttggc atg gta gat ttc atc ctg agg tct ctt ctc ttg 173
 Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu
 -20 -15
 gtt tgt agt tgg ctg tca atc tcc ctg cat gct cac acg acc gct ttt 221
 Val Cys Ser Trp Leu Ser Ile Ser Leu His Ala His Thr Thr Ala Phe
 -10 -5 1 5
 tgt aca tac agt aag aaa ata cac act gtc atg tca ttt ttt tgt aa 268
 Cys Thr Tyr Ser Lys Lys Ile His Thr Val Met Ser Phe Phe Cys
 10 15 20

<210> 140
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 93..170

<221> sig_peptide
 <222> 93..140
 <223> Von Heijne matrix
 score 8.10000038146973
 seq LLYFLCVSSYVTS/FF

<400> 140
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 actctattgc cttctatctt gcatagtttc tg atg aga agt ctg ttg tat ttc 113
 Met Arg Ser Leu Leu Tyr Phe
 -15 -10
 tta tgt gtt tct tca tat gta aca tct ttt ttc ttt ttt ttt ttt ttt 161
 Leu Cys Val Ser Ser Tyr Val Thr Ser Phe Phe Phe Phe Phe Phe Phe
 -5 1 5
 ttt ttt ttt 170
 Phe Phe Phe

10

<210> 141
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..395

<221> sig_peptide
<222> 192..236
<223> Von Heijne matrix
score 8
seq FISFLCLIALAGT/SS

<400> 141
gattctcagc ttagttgctg ttggtgtata ggagagctac tgatttgtgt acattaattt 60
tgtatccgga aactttgttg aattatttta tcagttctag gagctttttg gaggagtctt 120
tagggttctc taggtataca atcatatcat cagcaaacag tgacaattcg aottcctctt 180
tatggatttg t atg ccc ttt att tct ttc ctt tgt ctg att gct ctg gct 230
Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala
-15 -10 -5
ggg act tcc agt act atg ttg aga agt gct ctg gct ggg act tcc agt 278
Gly Thr Ser Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser
1 5 10
act atg tkg arg aga agt ggt gam agt ggg wat cct kgh ctk gty cma 326
Thr Met Xaa Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa
15 20 25 30
gtc ctm aga ggg aat gct ttc agc ttt ttc cca ttc agt ctg atg twg 374
Val Leu Arg Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa
35 40 45
gct atg ggt tgt cat aga tgg c 396
Ala Met Gly Cys His Arg Trp
50

<210> 142
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 292..357

<221> sig_peptide
<222> 292..339
<223> Von Heijne matrix
score 8
seq FLLGAIFIALSSS/RI

<400> 142
cgtgcctgcg caatgggtgt cgggtccgct ttttcccaat ccggacgtaa tcgtgggttt 60

tgttctgcaa taggcgggctt agagggaggg gctttttcgc ctatacctac tgtagcttct	120
ccacgtatgg accctaaagg ctactgctgc tactacgggg ctagacagtt actgtctcag	180
ctctaggatg tgcgttcttc cactagaagc tcttctgagg gaggtaatta aaaaacagtg	240
gaatggaaaa acagtgctgt agtcatcctg taatatgctc cttgtcaaca a atg tat	297

Met Tyr
-15

aca ttc ctg cta ggt gcc ata ttc att gct tta agc tca agt cgc atc	345
Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser Arg Ile	
-10 -5 1	

tta cta gtg aag	357
Leu Leu Val Lys	
5	

<210> 143
<211> 159
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..157

<221> sig_peptide
<222> 26..151
<223> Von Heijne matrix
score 7.90000009536743
seq LVCVCVCVCVCXC/XR

<400> 143	
tgtgtgtgtg tgtgtctgcg tgtgt atg tgt ttg tgt ccc tgc tgg gat gtg	52
Met Cys Leu Cys Pro Cys Trp Asp Val	
-40 -35	

ttt act gtg ttt gtg tgt gtc tct gtg tgt gtg tct gtg tct gtc cct	100
Phe Thr Val Phe Val Cys Val Ser Val Cys Val Ser Val Ser Val Pro	
-30 -25 -20	

gtc ggg atg tat tta gtg tgt gtg tgt gtg tgt gtg tgt stc	148
Val Gly Met Tyr Leu Val Cys Val Cys Val Cys Val Cys Val Cys Xaa	
-15 -10 -5	

tgc gyg cgt gg	159
Cys Xaa Arg	
1	

<210> 144
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 282..431

<221> sig_peptide
<222> 282..383
<223> Von Heijne matrix

score 7.90000009536743
seq LFSLLMLTQSP/LA/GQ

<221> misc_feature
<222> 132,149
<223> n=a, g, c or t
Oligonucleotide

<400> 144
aaaataagggt atctggcaaa agaataatg aaagagtatg aagaactctc cttgaaagct 60
gtggcccca ttggccatgg ctgcagagcc gatgtcccgg ccaatccagg cgggatcccc 120
ttgaagcmgg knsmwhbtcy kragscwknc cmabtctccg ggggcaastc tttcccttc 180
cctgtgaccc kcttcggaca gttgaccatc tcaacaccta gtggttaaaa agaagagcat 240
ggacggcctg gggcctgcac tggctgtgct gggagtttgt c atg ttg ata gct aag 296
Met Leu Ile Ala Lys
-30
cag gcc cag ccc caa ggc ctc act gcc atc tgc ttc cct ctc aca cct 344
Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys Phe Pro Leu Thr Pro
-25 -20 -15
ctc ttc tcc ctc ctc atg ctc act cag agc ccc ctt gca ggt cag gaa 392
Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro Leu Ala Gly Gln Glu
-10 -5 1
gga aga gaa gga ggg aaa gaa cgg tac ttg ttg gtg att ca 433
Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu Val Ile
5 10 15

<210> 145
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..200

<221> sig_peptide
<222> 15..92
<223> Von Heijne matrix
score 7.90000009536743
seq RVCLLSLSLFLWA/NR

<400> 145
aatacgccag gaac atg cta agg acc tgg agc tct cta ccc tgg acc cgt 50
Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg
-25 -20 -15
ttt cgg gtt tgc ttg ctc tct ctc tct ctc ttt ctc tgg gct aat cgt 98
Phe Arg Val Cys Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg
-10 -5 1
tta gag gac agt cgc tcc tgc caa cct aat ccc atg agc ctg act acc 146
Leu Glu Asp Ser Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr
5 10 15
ttg ccg ggc cac agg ctc aaa gaa gca gtg tgg ctg cca gca ccc tca 194
Leu Pro Gly His Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser
20 25 30

ctt ggg 200
 Leu Gly
 35

<210> 146
 <211> 297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..295

<221> sig_peptide
 <222> 80..166
 <223> Von Heijne matrix
 score 7.90000009536743
 seq LVVXWLLPXQCSC/ER

<400> 146
 aacacccag cccaagttca tccccggtcc cttggcagca gtgcgcatcc acaaagccag 60
 cggcacaatt taattactg atg gcc cct ttc cta cga cag gtg gat rtg tgg 112
 Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp
 -25 -20
 gga gca cag gcc ggt ctg gtg gtb gsm tgg tta cta cca tgs caa tgc 160
 Gly Ala Gln Ala Gly Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys
 -15 -10 -5
 agc tgt gaa cga tca gag caa tat ctg agc acc tgt ctc cca cag cac 208
 Ser Cys Glu Arg Ser Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His
 1 5 10
 tca agc atc aag cag tcg tgc atc aag cat cca gca ggc ccg atc ccc 256
 Ser Ser Ile Lys Gln Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro
 15 20 25 30
 gca ggc cac cta cag gga aag gcc aca gct gcg ccc ctg gg 297
 Ala Gly His Leu Gln Gly Lys Ala Thr Ala Ala Pro Leu
 35 40

<210> 147
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..298

<221> sig_peptide
 <222> 80..136
 <223> Von Heijne matrix
 score 7.90000009536743
 seq WLFLVAILKGVRC/EV

<400> 147
 agctctgaga gaggagccca gccctgggat cttcaggtgt tttcactcgg tgatcaggac 60

tgcacagaga gaactcacc atg gag ttt ggg ctg aag tgg ctt ttt ctt gtg	112
Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val	
-15 -10	
gca att tta aaa ggt gtc cgg tgt gaa gtg aag ctg gtg gag tct ggg	160
Ala Ile Leu Lys Gly Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly	
-5 1 5	
gga ggc ctg gtg cag ccg ggg ggg tcc ctg aga ctc tcc tgt gta gga	208
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly	
10 15 20	
tct gga ttc gtc ttc gat aaa tat ggc ata agt tgg gtg cgc cag gca	256
Ser Gly Phe Val Phe Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala	
25 30 35 40	
cca gga aag ggc cta cag tgg gtc gcg ggg atc ggt ggc ggg gg	300
Pro Gly Lys Gly Leu Gln Trp Val Ala Gly Ile Gly Gly Gly	
45 50	

<210> 148
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..404
 <221> sig_peptide
 <222> 21..68
 <223> Von Heijne matrix
 score 7.90000009536743
 seq AMLVLVSPWSAA/RG

<400> 148	
gcggtcttcc agcagggaaa atg gcg ctg gcc atg ctg gtc ttg gtg gtt tcg	53
Met Ala Leu Ala Met Leu Val Leu Val Val Ser	
-15 -10	
ccg tgg tct gcg gcc ccg gga gtg ctt cga aac tac tgg gag cga ctg	101
Pro Trp Ser Ala Ala Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu	
-5 1 5 10	
cta ccg aag ctt ccg cag agc ccg ccg ggc ttt ccc agt cct ccg tgg	149
Leu Arg Lys Leu Pro Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp	
15 20 25	
gga cca gca tta gca gta cag ggc cca gcc atg ttt aca gag cca gca	197
Gly Pro Ala Leu Ala Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala	
30 35 40	
aat gat acc agt gga agt aaa gag aat tcc agc ctt ttg gac agt atc	245
Asn Asp Thr Ser Gly Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile	
45 50 55	
ttt tgg atg gca gct ccc aaa aat aga cgc acc att gaa gtt aac ccg	293
Phe Trp Met Ala Ala Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg	
60 65 70 75	
tgt agg aga aga aat ccg cag aag ctt att aaa gtt aag aac aac ata	341
Cys Arg Arg Arg Asn Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile	
80 85 90	
gac gtt tgt cct gaa tgt ggt cac ctg aaa cag aaa srt gtc ctt tgt	389

Asp Val Cys Pro Glu Cys Gly His Leu Lys Gln Lys Xaa Val Leu Cys
 95 100 105
 gct act gct atg aaa a 405
 Ala Thr Ala Met Lys
 110

<210> 149
 <211> 146
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..145

<221> sig_peptide
 <222> 56..115
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LLLFPLSLLFTLG/FL

<400> 149
 aaaccttctg actactaacc ttagatccc ttagttcct tagcagtatt cacia atg 58
 Met
 -20
 ttt ttc tac tca cac ttt tta ctt ctt ttt ccc ctc tcg tta ctt ttc 106
 Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu Phe
 -15 -10 -5
 aca ctt gga ttt ttg ttt gtc ttt ttt ttt ttt ttt t 146
 Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe
 1 5 10

<210> 150
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..407

<221> sig_peptide
 <222> 105..242
 <223> Von Heijne matrix
 score 7.80000019073486
 seq LVLLGTRVPLSGG/GP

<400> 150
 aaacagggcc attggcaaag ctggggtacc agtcacccag ccacgctcta ggggtgtagc 60
 caagaagacg gaccccgagt gggaggcaga gagacaagag gtgg atg aag cag agc 116
 Met Lys Gln Ser
 -45
 aag cgt gas atg gtg aag aga aga cgg agc ccc gcg ctg gga gag gaa 164
 Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala Leu Gly Glu Glu

<221> sig_peptide

<222> 99..236

<223> Von Heijne matrix

score 7.80000019073486

seq LLYLSFAALGVVA/LR

<400> 152

ttttacacac acacatacat acacacacac agctaattga gttttaaagt aatattcttg 60

ctaattcccta ctgaattgta gcttggtgtt gtttctga atg gtt ttt gga tat tgg 116

Met Val Phe Gly Tyr Trp

-45

aag cag ccg ctg att acc ctt gca aag aaa tct gta aaa tgt gca cgt 164

Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys Ser Val Lys Cys Ala Arg

-40 -35 -30 -25

gaa tgt ctg aga tgc tct ctc agg cct cta gtc ctt ctg tat ctt tcc 212

Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu Val Leu Leu Tyr Leu Ser

-20

-15

-10

ttt gca gcc ctg ggt gta gta gca ctc agg agt gtt gaa tca ccc ctg 260

Phe Ala Ala Leu Gly Val Val Ala Leu Arg Ser Val Glu Ser Pro Leu

-5

1

5

gcc gag acc cac tcc tgc tgg ctc agc ctg ggc atg tgt gtg ctc cag 308

Ala Glu Thr His Ser Cys Trp Leu Ser Leu Gly Met Cys Val Leu Gln

10

15

20

tgt gaa cag cag tgg gtt cca acc cca gtc tcc ttt ctc tgt ggc ctc 356

Cys Glu Gln Gln Trp Val Pro Thr Pro Val Ser Phe Leu Cys Gly Leu

25 30 35 40

tct ggc tcc agc acc atc atc gtt ag 382

Ser Gly Ser Ser Thr Ile Ile Val

45

<210> 153

<211> 208

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 10..207

<221> sig_peptide

<222> 10..81

<223> Von Heijne matrix

score 7.80000019073486

seq CVYVVCLVSCVLC/VV

<400> 153

tgcaatgtc atg tgt gtt gtg tgc agt gtg cat ggt gtg tgt tgt gta tat 51

Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr

-20

-15

gtg gtg tgc ctg gtg tgc tgt gtt ttg tgt gtc gtg tgt cct gtg tgt 99

Val Val Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys

-10 -5 1 5

tgg gtt atg tgt tgt gtg tgg tgc atc tgt gtg tgt gtg tgg tgt gtc 147

Trp	Val	Met	Cys	Cys	Val	Trp	Cys	Ile	Cys	Val	Cys	Val	Trp	Cys	Val		
			10					15					20				
tgt	tgt	atg	tgt	tgt	gtg	ttg	tca	tgt	gtt	gtg	tca	cat	ggg	ttg	tgt		195
Cys	Cys	Met	Cys	Cys	Val	Leu	Ser	Cys	Val	Val	Ser	His	Gly	Leu	Cys		
		25					30					35					
ggt	gtg	tca	tgg	g													208
Gly	Val	Ser	Trp														
			40														

<210> 154
 <211> 251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..249

<221> sig_peptide
 <222> 73..129
 <223> Von Heijne matrix
 score 7.80000019073486
 seq WVFLVAVLEVVC/EI

<400> 154																	
agagaggagc	ctcagcccta	gactccaagg	cctttccact	tggtgatcag	cactgagcac												60
agaggactca	cc atg gaa	ctg ggg	ctg tcc	tgg gtc	ttc ctt	gtt gct	gtt										111
	Met Glu	Leu Gly	Leu Ser	Trp Val	Phe Leu	Val Ala	Val										
			-15				-10										
tta gaa	gtt gtc	cag tgt	gaa att	caa ctg	att gac	gcc ggg	gga ggc										159
Leu Glu	Val Val	Gln Cys	Glu Ile	Gln Leu	Ile Asp	Ala Gly	Gly Gly										
	-5		1		5		10										
cac gtc	cag ggc	ggg ggg	tca ctg	aga ctc	tcc tgt	gtt gcc	tct gac										207
His Val	Gln Ala	Gly Gly	Ser Leu	Arg Leu	Ser Cys	Val Ala	Ser Asp										
		15		20		25											
ttc ctg	ttt aga	agc tat	tgg atg	acc tgg	gtc cgc	cat ccg	gg										251
Phe Leu	Phe Arg	Ser Tyr	Trp Met	Thr Trp	Val Arg	His Pro											
		30		35		40											

<210> 155
 <211> 147
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..146

<221> sig_peptide
 <222> 24..140
 <223> Von Heijne matrix
 score 7.80000019073486
 seq ILLFLFLILFIWH/IR

<400> 155
ggattttgtc aaatgctttt tct atg tgc att ttg ctg agg gtt tta ggc ata 53
Met Ser Ile Leu Leu Arg Val Leu Gly Ile
-35 -30
aag gga tgc tgg att ttg tca aat cct ttt tct gca tgt att gag atg 101
Lys Gly Cys Trp Ile Leu Ser Asn Pro Phe Ser Ala Cys Ile Glu Met
-25 -20 -15
atc ttg tta ttt ttg ttt tta att ctg ttt ata tgg cac att cgg g 147
Ile Leu Leu Phe Leu Phe Leu Ile Leu Phe Ile Trp His Ile Arg
-10 -5 1

<210> 156
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..141

<221> sig_peptide
<222> 61..135
<223> Von Heijne matrix
score 7.69999980926514
seq LVPIILLIGWIVG/CT

<400> 156
gctggataac aaaagaaaga ggtaagcgtg gcctgacctt gccacccacc aacaggaata 60
atg gct gaa aaa gcg ggg tct aca ttt tca cac ctt ctg gtt cct att 108
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25 -20 -15 -10
ctt ctc ctg att ggc tgg att gtg ggc tgc acc 141
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
-5 1

<210> 157
<211> 115
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..113

<221> sig_peptide
<222> 12..68
<223> Von Heijne matrix
score 7.69999980926514
seq RLYLWMCLAAALA/SF

<400> 157
ctcaagaagc c atg gcg gaa tcc agg ggc cgt ctg tac ctt tgg atg tgc 50
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys
-15 -10

ttg gct gct gcg ctg gca tct ttc ctg atg gga ttt atg gtg ggc tgg	98
Leu Ala Ala Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp	
-5 1 5 10	
ttt att aag cct ctg gg	115
Phe Ile Lys Pro Leu	
15	

<210> 158
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..173

<221> sig_peptide
 <222> 54..131
 <223> Von Heijne matrix
 score 7.69999980926514
 seq FLTTYFFXIAVT/HP

<400> 158	
caattcaaca tgagatttag tggtagacaaa tatccaaact ctatcaacct cta atg	56
	Met
ctg acc tca ctg cct ttc ctc ctg ccc acc atc agc ttt ctc ctc ctc	104
Leu Thr Ser Leu Pro Phe Leu Leu Pro Thr Ile Ser Phe Leu Leu Leu	
-25 -20 -15 -10	
ttg tat ttt ttt cma att gct gtc acc cat ccg tca gtt ctc atc aac	152
Leu Tyr Phe Phe Xaa Ile Ala Val Thr His Pro Ser Val Leu Ile Asn	
-5 1 5	
ttc tct ttc tcc ttc ccc aga tc	175
Phe Ser Phe Ser Phe Pro Arg	
10	

<210> 159
 <211> 230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 121..228

<221> sig_peptide
 <222> 121..180
 <223> Von Heijne matrix
 score 7.59999990463257
 seq LLFFTCGLPALHG/DS

<221> misc_feature
 <222> 18
 <223> n=a, g, c or t
 Oligonucleotide

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<400> 159
aggaggggcc gtcagggngg gatacagcct ggaaggtgcg tgtggggctg ggtctcgag      60
tgggagacgt ggagtgcagg taatgcatgt ccatggtaca caaatcacaca aggtttgtaa      120
atg aga aaa gac gtg agg ttc ctt ttg ttc ttt acc tgt ggc ctc cct      168
Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro
-20          -15          -10          -5
gcc cta cac ggg gac tct agg gtg gaa tgt agc aaa gcc cat cca cca      216
Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro
          1          5          10
gcc atg tac tac cc      230
Ala Met Tyr Tyr
          15

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<210> 160
<211> 346
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 202..345

<221> sig_peptide
<222> 202..282
<223> Von Heijne matrix
      score 7.59999990463257
      seq WTLLSISLSVFWS/EP

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<400> 160
ttctttctaca tacagctacc caactagccc acaccattta ttgaatacag agtagtcttt      60
tccctgtttgg ttattttttct taacttttgtt aaagatcaga tatctgtagg tgtgcagctt      120
tattttctggg tttttctgttc cgttccattg gtctatgtgt ctgtttttgt accagtacca      180
tgctgtttctg gcaccagtac c atg cta ttt tgg tta cca tct cca tct gag      231
                        Met Leu Phe Trp Leu Pro Ser Pro Ser Glu
                        -25          -20

acc act tca gcc tgg act tta ttg tcc ata tca cta tca gta ttt tgg      279
Thr Thr Ser Ala Trp Thr Leu Leu Ser Ile Ser Leu Ser Val Phe Trp
      -15          -10          -5
tca gag cca ttc aat aag tct cta gga agt tcc aaa cta cca tgt cat      327
Ser Glu Pro Phe Asn Lys Ser Leu Gly Ser Ser Lys Leu Pro Cys His
      1          5          10          15
ttt ttt tct ata aaa cgg g      346
Phe Phe Ser Ile Lys Arg
          20

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<210> 161
<211> 388
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 194..388

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<221> sig_peptide
 <222> 194..334
 <223> Von Heijne matrix
 score 7.59999990463257
 seq LXLGEGLTFLCLC/QV

<221> misc_feature
 <222> 352
 <223> n=a, g, c or t
 Oligonucleotide

<400> 161
 agtgagagct tagtcttggt actatttggt tttgtttctt actgtttgtc tgtttatggt 60
 tggttgcaag aaaattgtgt tgtaaattat cccttgcttt ctctattagt taatagcctt 120
 ccccttctgt agtaaagtaa msagsctttt kcctgttcaa atattttagg cttgtttttt 180
 gttttgattg tac atg cct gtg tgt ttt tat tcc tta att tgt ttc ttt 229
 Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe
 -45 -40
 att tat ttc tgt ttg tta tct cca aga gaa aca ata gaa gag gtg gcc 277
 Ile Tyr Phe Cys Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala
 -35 -30 -25 -20
 ctc ttc cag ttt tct ctg cth mtc ttg gga gag ggt ctc acc ttt ctt 325
 Leu Phe Gln Phe Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu
 -15 -10 -5
 tgc ctc tgc cag gta atg acg aat aan atg caa ctg ctg ttc ttg agt 373
 Cys Leu Cys Gln Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser
 1 5 10
 ggg gta gtc tgt ggg 388
 Gly Val Val Cys Gly
 15

<210> 162
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 172..234

<221> sig_peptide
 <222> 172..210
 <223> Von Heijne matrix
 score 7.5
 seq MAPLLLSLSCSFS/CH

<400> 162
 cccctccaaa tctcatgttg agatttgatc cctaattgtg gagatggggc ctggtgggag 60
 atattcggat catgagggca gatccctcac taatggcctg gtgccctccc tgtggaaatg 120
 agtaagtctt cactcttttg gttcacctga gagctgtttg tttaaaagag c atg gca 177
 Met Ala
 ccc ctc ctt ctc tct ctg tct tgc tcc ttt tct tgc cat gtg aca ctc 225
 Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val Thr Leu

Leu	Ile	Ser	Glu	Leu	Leu	Leu	Leu	Arg	Ser	Val	Thr	Ser	His	Asn	Thr	
			-10					-5					1			
atg	atg	aga	gct	tta	tca	agc	cag	atg	ctt	agt	cag	agc	ttt	cca	aga	148
Met	Met	Arg	Ala	Leu	Ser	Ser	Gln	Met	Leu	Ser	Gln	Ser	Phe	Pro	Arg	
	5					10				15						
ccc	agc	ttt	ggt	ttt	atc	agc	aaa	atc	cat	cct	tcc	cac	ccc	ccc	aa	195
Pro	Ser	Phe	Gly	Phe	Ile	Ser	Lys	Ile	His	Pro	Ser	His	Pro	Pro		
20					25				30							

<210> 165
 <211> 256
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..255
 <221> sig_peptide
 <222> 34..186
 <223> Von Heijne matrix
 score 7.5
 seq VVSLTFLLGMTWG/FA

<221> misc_feature
 <222> 18
 <223> n=a, g, c or t
 Oligonucleotide

<400> 165																		
tat	ttt	atg	tgt	ac	ct	gt	gn	gg	gt	at	ttt	ttt	ct	g	aac	att	gcc	54
										Met	Phe	Phe	Leu	Asn	Ile	Ala		
										-50					-45			
atg	ttc	att	gtg	gta	atg	gtg	cag	atc	tgt	ggg	agg	aac	gga	aga			102	
Met	Phe	Ile	Val	Val	Met	Val	Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg			
			-40					-35					-30					
agc	aac	cgg	acc	ctg	aga	gaa	gaa	gtg	tta	agg	aac	ctg	cgc	agt	gtg		150	
Ser	Asn	Arg	Thr	Leu	Arg	Glu	Glu	Val	Leu	Arg	Asn	Leu	Arg	Ser	Val			
			-25					-20					-15					
gtt	agc	ttg	acc	ttt	ctg	ttg	ggc	atg	aca	tgg	ggt	ttt	gca	ttc	ttt		198	
Val	Ser	Leu	Thr	Phe	Leu	Leu	Gly	Met	Thr	Trp	Gly	Phe	Ala	Phe	Phe			
			-10				-5				1							
gcc	tgg	gga	ccc	tta	aat	atc	ccc	ttc	atg	tac	ctc	ttc	tcc	atc	ttc		246	
Ala	Trp	Gly	Pro	Leu	Asn	Ile	Pro	Phe	Met	Tyr	Leu	Phe	Ser	Ile	Phe			
5				10					15					20				
aat	tca	tta	c														256	
Asn	Ser	Leu																

<210> 166
 <211> 209
 <212> DNA
 <213> Homo sapiens

<220>

<210> 168
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 97..216

<221> sig_peptide
 <222> 97..177
 <223> Von Heijne matrix
 score 7.40000009536743
 seq ILLLTICAAGIXG/TR

<400> 168
 ccttccctcc ggcacaggc tgccggtca ccgcttgcta atggcagccg ggggtctccct 60
 gggacagcaa gacctccgct caggcccctc ttctga atg ckc cam gcm ctc ctg 114
 Met Xaa Xaa Ala Leu Leu
 -25
 cga tct aga atg att cag ggc agg atc ctg ctc ctg acc atc tgc gct 162
 Arg Ser Arg Met Ile Gln Gly Arg Ile Leu Leu Leu Thr Ile Cys Ala
 -20 -15 -10
 gcc ggc att rgt ggg act cgt cag ttt ggc tat aac ctc tct atc atc 210
 Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly Tyr Asn Leu Ser Ile Ile
 -5 1 5 10
 aat gac cc 218
 Asn Asp

<210> 169
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 317..478

<221> sig_peptide
 <222> 317..457
 <223> Von Heijne matrix
 score 7.40000009536743
 seq SCLFSXAWLXCXC/HG

<400> 169
 gtctcgtggg ctggtcccca gcggctccct ccccgaacag ctgctgctcc agggaggaag 60
 cggcggyrrgt gmtgtccagc ttcccgggtgc tgaaaaccgg agggctcgtc atccaccact 120
 accatgtaag ggccatgaga aggggtcctc ctggcgcasg cggacatgga ggaggactta 180
 ttccagctaa ggcagctgcc ggttgtgaaa ttccgtcgca caggcgagag tgcaagggtca 240
 gaggacgaca cggcttcagg agagcatgaa gtccagattg aaggggtcca cgtgggccta 300
 gaggctgtgg agctgg atg atg ggg cak ctg tgc cca agg agt ttg cca atc 352
 Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile
 -45 -40

cca ccg atg ata ctt tca tgg tgg aag atg cag tgg aag cca ttg gct	400
Pro Pro Met Ile Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala	
-35 -30 -25 -20	
ttg gaa aat ttc agt gga agc tgt ctg ttc tca mtg gct tgg ctt kga	448
Leu Glu Asn Phe Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa	
-15 -10 -5	
tgc tsa tgc cat gga gat gat gat ctc agc at	480
Cys Xaa Cys His Gly Asp Asp Asp Leu Ser	
1 5	

<210> 170
 <211> 280
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..278
 <221> sig_peptide
 <222> 135..179
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LLQLLAFSFLGNS/VE

<221> misc_feature
 <222> 104
 <223> n=a, g, c or t
 Oligonucleotide

<400> 170	
ttcttttgggc tcgggggctc ccggagcagg gcgagagctc gcgtcgccgg aaaggaagac	60
gggaagaaag ggcaggcggc tcggcgggcg tcttctccac tccntgccgc gcccgtggc	120
tgcagggagc cggc atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta	170
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu	
-15 -10 -5	
ggt aat tcc gtg gaa acg gtg cgg gga ggc gga cgg act tgg gca tgg	218
Gly Asn Ser Val Glu Thr Val Arg Gly Gly Gly Arg Thr Trp Ala Trp	
1 5 10	
gga agg aaa acc caa aag ctg ctt gct cac ctt cgt ggg atc ctg ggg	266
Gly Arg Lys Thr Gln Lys Leu Leu Ala His Leu Arg Gly Ile Leu Gly	
15 20 25	
gct tgg gas agg ga	280
Ala Trp Xaa Arg	
30	

<210> 171
 <211> 103
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..102

<221> sig_peptide
 <222> 28..69
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LVLVHSSLSKTLS/QK

<400> 171
 actgggatgc agaggctgca gtgagcc atg ttg gtg ctg gtg cac tcc agc ctg 54
 Met Leu Val Leu Val His Ser Ser Leu
 -10
 agc aag acc ttg tct cag aaa aaa aaa aag ttc aca aas ccc acc agg g 103
 Ser Lys Thr Leu Ser Gln Lys Lys Lys Lys Phe Thr Xaa Pro Thr Arg
 -5 1 5 10

<210> 172
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..216

<221> sig_peptide
 <222> 73..129
 <223> Von Heijne matrix
 score 7.40000009536743
 seq LILVISCLLLAFE/CV

<400> 172
 caattttgtt gatcttttca aaaaaccagc tcctggattc attaatTTTT tgaagggttt 60
 tttgatgtct ct atg tcc ttc agt tct gct ctg att tta gtt att tct tgc 111
 Met Ser Phe Ser Ser Ala Leu Ile Leu Val Ile Ser Cys
 -15 -10
 ctt ctg cta gct ttt gaa tgt gtt tgc tct tgc ttt tct ggt tct ttt 159
 Leu Leu Leu Ala Phe Glu Cys Val Cys Ser Cys Phe Ser Gly Ser Phe
 -5 1 5 10
 aat tgt gat gtt agg gtg tca att tcg gat ctt tcc tgc ttt ctc ttg 207
 Asn Cys Asp Val Arg Val Ser Ile Ser Asp Leu Ser Cys Phe Leu Leu
 15 20 25
 tgg ggc aag gg 218
 Trp Gly Lys

<210> 173
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 295..378

<221> sig_peptide

<222> 295..360
 <223> Von Heijne matrix
 score 7.40000009536743
 seq CLXVFLLTDRTLS/CR

<400> 173
 tattggttat tctagttata cattagtcta aatttttttc aaagttttca acttctttgc 60
 ctttggtttg aatttccctcc tgtagcttgg agtagtttga tcatctgaag ctttcttctc 120
 tcaactcatc aaagtcattc tccatccagc tttgttccat tgctggtgag gaactgtgtt 180
 ccttcggagg aggagaggtg ctctgctttt ttgagtttcc agtttttctg ctctgttttt 240
 tccccatctt tgtggtttta tctacttttg gtctttgatg ctggtgatgt acag atg 297
 Met
 ggt ttt tgg tgt gga tgt cct ttc tgt ttg twa gtt ttc ctt cta aca 345
 Gly Phe Trp Cys Gly Cys Pro Phe Cys Leu Xaa Val Phe Leu Leu Thr
 -20 -15 -10
 gac agg acc ctc agc tgc agg tct gtt gga gtt gc 380
 Asp Arg Thr Leu Ser Cys Arg Ser Val Gly Val
 -5 1 5

<210> 174
 <211> 139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..139
 <221> sig_peptide
 <222> 59..103
 <223> Von Heijne matrix
 score 7.30000019073486
 seq LLSLSLWGISTLS/ST

<400> 174
 ataacagaat gatttacatt cctttgggta tataaccagt gatgggatat atgtgtca 58
 atg gta tta ctg tct tta agt ctt tgg ggc atc tcc aca ctg tct tcc 106
 Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser
 -15 -10 -5 1
 aca aca att gaa cta att tac acc ccc atc ggg 139
 Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly
 5 10

<210> 175
 <211> 122
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..121
 <221> sig_peptide
 <222> 38..112

<223> Von Heijne matrix
 score 7.30000019073486
 seq LLHVHSFLPPVFS/TQ

<400> 175
 ctacctgtcc ttgcgcacca cccttgtctg ggccttc atg gcc tct ctc ctg agt 55
 Met Ala Ser Leu Leu Ser
 -25 -20
 ggc ttt act agc ttc tgt ctt ttg cac gtt cac tct ttc ctc cct oca 103
 Gly Phe Thr Ser Phe Cys Leu Leu His Val His Ser Phe Leu Pro Pro
 -15 -10 -5
 gtg ttt tcc acc cag aat g 122
 Val Phe Ser Thr Gln Asn
 1

<210> 176
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 175..300

<221> sig_peptide
 <222> 175..264
 <223> Von Heijne matrix
 score 7.30000019073486
 seq AILLXXWEAGSEA/VR

<221> misc_feature
 <222> 51..52,63,239
 <223> n=a, g, c or t
 Oligonucleotide

<400> 176
 aaaaactcta aaagaaggac gcatttttagg taagatctag tggctagatc nncaggggtgg 60
 gcnkcggttct tgtggaaatc agtcaagaaa gatcggattc gcggttatct atgcaaatca 120
 tctgggtgga ttgtgtacgg agttaaaactg cgccttctg accgggtctg aaca atg 177
 Met
 -30
 gag act gcg cta saa tka acg cca cag aaa agg caa gtt atg ttt ctt 225
 Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe Leu
 -25 -20 -15
 gct ata ttg ttg cnt twg tgg gag gct ggc tct gag gca gth agg tat 273
 Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg Tyr
 -10 -5 1
 tcc ata cca gaa gaa aca gaa agt ggc 300
 Ser Ile Pro Glu Glu Thr Glu Ser Gly
 5 10

<210> 177
 <211> 466
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 268..465

<221> sig_peptide

<222> 268..372

<223> Von Heijne matrix

score 7.30000019073486

seq LDLLGSSSPPTSA/SQ

<400> 177

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cttaaacttt attatgttgk kttcacaaag agcagccttt gttgactttg aaatcattgc      60
ttcagtattc tagaaaatct tgtttttggt aaacatgggc agtaacttac tatttttgta    120
tagttgttgt wcatckttacc cccaccctgt tttaaaaata aaaagtagtt gtcagattac    180
tttggcttta gaagtaacctt ttcacttgcc ttagaatctt cattactttg agcctacact    240
ccacctotta ttggaacttc atgaaga atg atg ttg gat ttc gct ctg tcg ccc      294
                               Met Met Leu Asp Phe Ala Leu Ser Pro
                               -35                               -30
agg cta gag cgc agt ggt ctg atc atg gct tgc tgt acc ctt gac ctc      342
Arg Leu Glu Arg Ser Gly Leu Ile Met Ala Cys Cys Thr Leu Asp Leu
-25                               -20                               -15
ctg ggt tca agc agt cct ccc acc tca gcc tcc cag gtg gct ggg act      390
Leu Gly Ser Ser Ser Pro Pro Thr Ser Ala Ser Gln Val Ala Gly Thr
-10                               -5                               1                               5
ggg cat gtg cca cca cac cca gct agt ttt ttt tac ttt ktt gta wga      438
Gly His Val Pro Pro His Pro Ala Ser Phe Phe Tyr Phe Xaa Val Xaa
10                               15                               20
cag gtc tac tat gtt tcg cag ctg atc t      466
Gln Val Tyr Tyr Val Ser Gln Leu Ile
25                               30
```

<210> 178

<211> 222

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..221

<221> sig_peptide

<222> 30..95

<223> Von Heijne matrix

score 7.19999980926514

seq QVFFLVFPDGVVRP/QP

<400> 178

```
acgtcggacc cggaggccct gaatgcccc atg cgc acc cca cag ctc gcg ctc      53
                               Met Arg Thr Pro Gln Leu Ala Leu
                               -20                               -15
ctg caa gtg ttc ttt ctg gtg ttc ccc gat ggc gtc cgg cct cag ccc      101
Leu Gln Val Phe Phe Leu Val Phe Pro Asp Gly Val Arg Pro Gln Pro
```

	-10		-5		1	
tct tcc tcc cca tca ggg gca gtg ccc acg tct ttg gag ctg cag cga						149
Ser Ser Ser Pro Ser Gly Ala Val Pro Thr Ser Leu Glu Leu Gln Arg						
5		10		15		
ggg acg gat ggc gga acc ctc cag tcc cct tca gag gcg act gca act						197
Gly Thr Asp Gly Gly Thr Leu Gln Ser Pro Ser Glu Ala Thr Ala Thr						
20		25		30		
cgc ccg gcc gtg ccc gga ctc cgg g						222
Arg Pro Ala Val Pro Gly Leu Arg						
35		40				

<210> 179
 <211> 171
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..170

<221> sig_peptide
 <222> 33..95
 <223> Von Heijne matrix
 score 7.19999980926514
 seq SWPLLA AVSGLRG/LE

<400> 179	
ccttttgctt tcaaccttcg agccgccacg ta atg cca cgt ccc cgc gca tgc	53
	Met Pro Arg Pro Arg Ala Cys
	-20 -15
gca tct tgg ccg ctg ctg gcg gct gtt tcc ggg ctt aga ggg ctg gag	101
Ala Ser Trp Pro Leu Leu Ala Ala Val Ser Gly Leu Arg Gly Leu Glu	
	-10 -5 1
tgg ccg ccg agt tgg agg cgg gtg gtg gca gca gta gga gtg tgt aga	149
Trp Pro Pro Ser Trp Arg Arg Val Val Ala Ala Val Gly Val Cys Arg	
5	10 15
gtg cgg gat tgg ggg ccc cgg g	171
Val Arg Asp Trp Gly Pro Arg	
20	25

<210> 180
 <211> 245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 177..245

<221> sig_peptide
 <222> 177..227
 <223> Von Heijne matrix
 score 7.19999980926514
 seq FLLLISVLTVIWF/WK

<400> 180
 tgtaattttc cttgccaaaa agcttagttt catcttttat aaatataccta taatgccaaag 60
 ttgattgcat ggtcagagtg aatctgtgct gtaccawat tcagtagcct tctctatatcc 120
 aacaaagtgt tttgtaaata ggaggtaaat gaatgagtgg atggatggag ggatga atg 179
 Met

aat gga att ttc ttg ctc ttg atc tct gtc tta aca gtg att tgg ttt 227
 Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp Phe
 -15 -10 -5
 tgg aag aca cac ccg ggg 245
 Trp Lys Thr His Pro Gly
 1 5

<210> 181
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..240
 <221> sig_peptide
 <222> 160..213
 <223> Von Heijne matrix
 score 7.19999980926514
 seq XLLCIIXLYLIRG/SE

<400> 181
 gttgactttt ctctctgctg aggcagaaaa atgcttccat agtccatgca gcaatgttta 60
 aaacaaggga ttctgttccc cctcvcctt ttgtgtaggc tggtaataa actctgtggt 120
 tywtgacatt gtcgtgaawa ttcagagtgc tccctgcga atg gtt ttc cta gta 174
 Met Val Phe Leu Val
 -15

kct ctg ttg tgt atc att kct ctt tat ttg att cgt ggt tct gag tgg 222
 Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile Arg Gly Ser Glu Trp
 -10 -5 1
 amc cta cca ccg aac tgg g 241
 Xaa Leu Pro Pro Asn Trp
 5

<210> 182
 <211> 263
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..261

<221> sig_peptide
 <222> 103..156
 <223> Von Heijne matrix
 score 7.19999980926514

seq LFFLLRIALASWA/LF

<400> 182

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gggttatcta acctgttcca ttgttccgtg tatcagtttc tgtaccgata ccatgctgtt      60
ttggttactg tagtcttgta gtatagttta aagtcagata gc atg atg act cta      114
                               Met Met Thr Leu
                               -15
gct ttg ttc ttt ttg ctt agg att gct ttg gct agt tgg gct ctc ttt      162
Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser Trp Ala Leu Phe
                               -10                               -5                               1
tgg atc cat atg aat ttt aga aga gct ttt ttc cac tta cgg tgg ttt      210
Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His Leu Arg Trp Phe
                               5                               10                               15
gat atc aat agc act gaa tct gta aat tgc ttt ggg cag tat ggc cta      258
Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly Gln Tyr Gly Leu
                               20                               25                               30
gcg gg                                                                263
Ala
35

```

<210> 183

<211> 170

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 60..170

<221> sig_peptide

<222> 60..146

<223> Von Heijne matrix
score 7.09999990463257
seq SLLVFCLNDLSNA/VX

<400> 183

```

ttccatgtgg agatgrraag aatatatatt ctgtggttat tgggtagagt gttctatag      59
atg tct att agg tct aat tgg tct agt gtc gaa tct aag tct aga att      107
Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile
                               -25                               -20                               -15
tct tta tta gtt ttc tgc ctc aat gat ctw tck aat gcw gtc arg wgg      155
Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa
                               -10                               -5                               1
ggm att gaa rtc ccc                                                                170
Gly Ile Glu Xaa Pro
5

```

<210> 184

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 83..442

<221> sig_peptide

<222> 83..130

<223> Von Heijne matrix

score 7.09999990463257

seq IPLFLGVLAYCTG/SV

<400> 184

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ctttccagca aggggataag agaggcctgg aagaacctgc ccagcctggg cctcaggaag      60
cagcatcgga ggtgcctcag cc atg gca tgg atc cct ctc ttc ctc ggc gtc      112
                               Met Ala Trp Ile Pro Leu Phe Leu Gly Val
                               -15                               -10
ctt gct tac tgc aca gga tcc gtg gcc tcc tat gag ctg act cac cca      160
Leu Ala Tyr Cys Thr Gly Ser Val Ala Ser Tyr Glu Leu Thr His Pro
   -5                               1                               5                               10
ccc tca gtg tcc gtg tcc cca gga cag aca gcc agc atc acc tgc tct      208
Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser
               15                               20                               25
gga gat aaa ttg ggg gat aaa tat gct tgc tgg tat cag cag aag cca      256
Gly Asp Lys Leu Gly Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro
               30                               35                               40
ggc cag tcc cct gtg ctg gtc atc tat caa gat agc aag cgg ccc tca      304
Gly Gln Ser Pro Val Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser
               45                               50                               55
ggg atc cct gag cga ttc tct ggc tcc aac tct ggg aac aca gcc act      352
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
               60                               65                               70
ctg acc atc agc ggg acc cag gct atg gat gag gct gac tat tac tgt      400
Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys
               75                               80                               85                               90
cag gcg tgg gac agc agc act gtg gta ttc ggc gga ggg acc a      443
Gln Ala Trp Asp Ser Ser Thr Val Val Phe Gly Gly Gly Thr
               95                               100
```

<210> 185

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 332..427

<221> sig_peptide

<222> 332..418

<223> Von Heijne matrix

score 7.09999990463257

seq FCFXLCFGRSSLC/CR

<400> 185

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taagtttata yhtctgaatc tgaatcaga atatatatat ttaatttttc aatttttaaaa      60
atgttaccct gtgtgagaca aaacaaaaca gtgactagaa ccctccttgt gggctaaatt      120
tgagtttgct tcttcataat gttttaaatg cttcacaaac atttttcttt ggtatatattga      180
```

gcaaaatgaa ttgaagtata tttactgagt gatgattatt gaggaanaac tcaaagatct 240
gctgtaagca ctagagttga aggactagcc caacagctcc tcaggcacct ttgggtatat 300
tgagttgccc cccctgactt tgaacacatc t atg gtc tgt gtc atc ttc aaa 352
Met Val Cys Val Ile Phe Lys

-25
gag ctc atg gaa ttt gaa ttc cct ggg ttt tgt ttt tgh ctt tgt ttt 400
Glu Leu Met Glu Phe Glu Phe Pro Gly Phe Cys Phe Xaa Leu Cys Phe
-20 -15 -10
gga cgg agc tcg ctc tgt tgc cga rac 427
Gly Arg Ser Ser Leu Cys Cys Arg Xaa
-5 1

<210> 186
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 130..363
<221> sig_peptide
<222> 130..219
<223> Von Heijne matrix
score 7.09999990463257
seq SCLALXTLAVVYA/AL

<400> 186
aacgagtcctt tgggaacgtg gtccacccag ggatgtaaaa ctgtgcttac cgatgcatcc 60
catacgaaat gcttatgtga tcgtctctct accttcgcca ttttggtctca gcaacctaga 120
gaaataatc atg gaa tcc tct ggc aca cct tca gtt acc cta ata gta ggc 171
Met Glu Ser Ser Gly Thr Pro Ser Val Thr Leu Ile Val Gly
-30 -25 -20
agt ggt ctt tct tgc ttg gcc ttg atb acc cta gca gtt gtc tat gca 219
Ser Gly Leu Ser Cys Leu Ala Leu Xaa Thr Leu Ala Val Val Tyr Ala
-15 -10 -5
gca tta tgg mgt tac ata cgc tct gag aga tcc ata ata cta att aac 267
Ala Leu Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile Ile Leu Ile Asn
1 5 10 15
ttc tgc ctg tct atc atc tca tcc aat atc ctc ata ctg gtt gga cag 315
Phe Cys Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile Leu Val Gly Gln
20 25 30
act cag aca cat aat aaa gag tat ctg cac aac cac cac tgc att ttt 363
Thr Gln Thr His Asn Lys Glu Tyr Leu His Asn His His Cys Ile Phe
35 40 45
gc 365

<210> 187
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 86..259

<221> sig_peptide

<222> 86..178

<223> Von Heijne matrix
score 7.09999990463257
seq LXFLASSFCFGEA/DS

<221> misc_feature

<222> 143

<223> n=a, g, c or t
Oligonucleotide

<400> 187

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ttttggaaca gggtaggcat tttgtttatt gtttgcttgc ttctaggtgt tttcgccatc    60
aggggtgtatt ggaggctgac actta atg ggt gtg tgt tgc gcc cag aac tgc    112
                               Met Gly Val Cys Cys Ala Gln Asn Cys
                               -30                               -25

tcg gtg tcg ggg ktc waa agr aat gcg ctg ntg ttc ttg gct tca agt    160
Ser Val Ser Gly Xaa Xaa Arg Asn Ala Leu Xaa Phe Leu Ala Ser Ser
          -20          -15          -10

ttc tgc ttt gga gaa gca gat tca gga agt agg tgt tgc tta aaa ata    208
Phe Cys Phe Gly Glu Ala Asp Ser Gly Ser Arg Cys Cys Leu Lys Ile
          -5          1          5          10

att ctt ggt ttt tat cta atc aga tat tca ttg att acc tac cag gtg    256
Ile Leu Gly Phe Tyr Leu Ile Arg Tyr Ser Leu Ile Thr Tyr Gln Val
          15          20          25

cgt g    260
Arg
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<210> 188

<211> 172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..171

<221> sig_peptide

<222> 52..105

<223> Von Heijne matrix
score 7.09999990463257
seq LFFFLKWSHPGWS/AT

<221> misc_feature

<222> 112

<223> n=a, g, c or t
Oligonucleotide

<400> 188

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ttaatggaat atattatagt acactagcat gctggaaaga atgaaaataa t atg aaa    57
                               Met Lys
att ctt tac ctt ttt ttc ttt ttg aaa tgg agt cac cca ggc tgg agt    105
```

Ile	Leu	Tyr	Leu	Phe	Phe	Phe	Leu	Lys	Trp	Ser	His	Pro	Gly	Trp	Ser		
-15						-10					-5						
gca	acg	ncg	tgg	tct	tgg	cac	act	gca	acc	tcc	gcc	tcc	ctg	att	caa		153
Ala	Thr	Xaa	Trp	Ser	Trp	His	Thr	Ala	Thr	Ser	Ala	Ser	Leu	Ile	Gln		
1			5					10					15				
gtg	att	ctc	ccg	cct	tgg	g											172
Val	Ile	Leu	Pro	Pro	Trp												
			20														

<210> 189
 <211> 150
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..148
 <221> sig_peptide
 <222> 47..124
 <223> Von Heijne matrix
 score 7.09999990463257
 seq LFLSGCFLFLSXC/XI

<400> 189																	
tatcacwtct	aagagatttc	tggtgaaact	tgtggatttt	ctatac	atg	aca	cca										55
						Met	Thr	Pro									
						-25											
tgt	ttt	ctg	caa	atg	gac	aat	ttg	act	cct	ctt	ttc	cta	tct	gga	tgc		103
Cys	Phe	Leu	Gln	Met	Asp	Asn	Leu	Thr	Pro	Leu	Phe	Leu	Ser	Gly	Cys		
		-20					-15				-10						
ttt	tta	ttt	ctc	tct	cwt	tgc	wtg	att	tat	ttg	gct	agg	att	ttg	gg		150
Phe	Leu	Phe	Leu	Ser	Xaa	Cys	Xaa	Ile	Tyr	Leu	Ala	Arg	Ile	Leu			
	-5					1				5							

<210> 190
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..338
 <221> sig_peptide
 <222> 195..314
 <223> Von Heijne matrix
 score 7
 seq ITCKLCLCEQSG/QD

<400> 190																	
agtcttgcaa	agtgtaaagc	tgctagccgc	agagcacgga	ggaaagacgg	agagaatgga												60
agagctcctg	tccggtgtgc	cagcagcccg	gactggcggt	gagcgcgagg	gaggctackg												120
agaagcccg	cgacggagga	acgcaggtct	gctgccagg	attgaggaga	ctgaagaacg												180

ctgaagacag gctg atg ggc tca gct ggt agg ctc cac tat ctc gsc atg	230
Met Gly Ser Ala Gly Arg Leu His Tyr Leu Xaa Met	
-40 -35 -30	
act gct gaa aat ccc act cct gga gac ctg gct ccg kcc ccc ctc atc	278
Thr Ala Glu Asn Pro Thr Pro Gly Asp Leu Ala Pro Xaa Pro Leu Ile	
-25 -20 -15	
act tgc aaa ctc tgc ctg tgt gag cag tct crt gga caa gat gac cac	326
Thr Cys Lys Leu Cys Leu Cys Glu Gln Ser Xaa Gly Gln Asp Asp His	
-10 -5 1	
act cca gga atg c	339
Thr Pro Gly Met	
5	

<210> 191
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..359
 <221> sig_peptide
 <222> 96..242
 <223> Von Heijne matrix
 score 7
 seq VTVLLSAAPCLLS/CF

<221> misc_feature
 <222> 340
 <223> n=a, g, c or t
 Oligonucleotide

<400> 191	
tacaagagtt ttgctgaaa gttttaagtt gataagatgc agagaattgg gggaatgtat	60
aataaatcag gtttcattgt tatattatatt accac atg aat cac ctt cct cct	113
Met Asn His Leu Pro Pro	
-45	
aac cat tat agg mgc cat gtg ttc aca tgt cat gtg gac cag tat tta	161
Asn His Tyr Arg Xaa His Val Phe Thr Cys His Val Asp Gln Tyr Leu	
-40 -35 -30	
act gtg gaa acc gcg ggt ggc atg gag aag gag gca gtg tcc gtg act	209
Thr Val Glu Thr Ala Gly Gly Met Glu Lys Glu Ala Val Ser Val Thr	
-25 -20 -15	
gtg ctg ctc tcc gca gcc ccc tgc ctg ctg tcc tgt ttc ctc ggc tcc	257
Val Leu Leu Ser Ala Ala Pro Cys Leu Leu Ser Cys Phe Leu Gly Ser	
-10 -5 1 5	
tcg gtg tct gga ctg gcg ttc tgg gtt tcc cag cag aaa act aaa ggg	305
Ser Val Ser Gly Leu Ala Phe Trp Val Ser Gln Gln Lys Thr Lys Gly	
10 15 20	
cca gag agg tgt aaa aac aca cac cac tbg gca gnt aat aat ttc ccc	353
Pro Glu Arg Cys Lys Asn Thr His His Xaa Ala Xaa Asn Asn Phe Pro	
25 30 35	
gcg agg	359

Ala Arg

<210> 192
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..263

<221> sig_peptide
<222> 138..257
<223> Von Heijne matrix
score 7
seq FLFMLPLWCSIGT/CT

<400> 192
ttgagcttaa ggccaggtat atgggctcac acttgtaatc tcagtgtttt gggaggctga 60
gggaaaagga tagcttgagt ccaggagttc gagatcatcc tgggcaacat agcaagatcc 120
tgtctctaca aaaccta atg aac aaa att aaa gaa aac aca cac aca cac 170
Met Asn Lys Ile Lys Glu Asn Thr His Thr His
-40 -35 -30
aca cac aca cac aca cac aaa aac aac acc aaa cta gtg tca aac cta 218
Thr His Thr His Thr His Lys Asn Asn Thr Lys Leu Val Ser Asn Leu
-25 -20 -15
ttc ott ttt atg tta cct ctc tgg tgc tcc att ggc act tgc aca g 264
Phe Leu Phe Met Leu Pro Leu Trp Cys Ser Ile Gly Thr Cys Thr
-10 -5 1

<210> 193
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..299

<221> sig_peptide
<222> 147..272
<223> Von Heijne matrix
score 7
seq LFLYSLFTENVLA/HP

<400> 193
tgtattgttt mmmmttattta ctagtatgca gatctggttt tcattctttt catattgaat 60
ttcgttatgg gtagaatcat ttgcaaacat ttctagacat ttttaaagat ctatttaatt 120
tgtttaagaa tggaaaacat aaaata atg cat gat tct tca ggc aag aat aat 173
Met His Asp Ser Ser Gly Lys Asn Asn
-40 -35
ttc aga aag ata cct gtt gta aat tta att tat ctc tat gta gac ata 221
Phe Arg Lys Ile Pro Val Val Asn Leu Ile Tyr Leu Tyr Val Asp Ile
-30 -25 -20

cat ata cat aaa tta ttt tta tat agt ctc ttt aca gaa aat gta ttg	269
His Ile His Lys Leu Phe Leu Tyr Ser Leu Phe Thr Glu Asn Val Leu	
-15 -10 -5	
gca cat cct tgc att gtt cta cgc cgc cta tg	301
Ala His Pro Cys Ile Val Leu Arg Arg Leu	
1 5	

<210> 194
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..215

<221> sig_peptide
 <222> 105..203
 <223> Von Heijne matrix
 score 7
 seq LFFLFVGPFSCLG/SY

<400> 194	
gctctgactg cagcctccca gggaatgcgc ggccgagga atgcgcgcag tcacaggccc	60
tgggagtgag ctggtgcccg gcgacctggc acccgcgctt ggat atg ggg cgt cta	116
Met Gly Arg Leu	
-30	

cat cgt ccc agg agc agc acc agc tac agg aac ctg ccg cat ctg ttt	164
His Arg Pro Arg Ser Ser Thr Ser Tyr Arg Asn Leu Pro His Leu Phe	
-25 -20 -15	
ctg ttt ttc ctc ttc gtg gga ccc ttc agc tgc ctc ggg agt tac agc	212
Leu Phe Phe Leu Phe Val Gly Pro Phe Ser Cys Leu Gly Ser Tyr Ser	
-10 -5 1	
cgg	215
Arg	

<210> 195
 <211> 209
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..209

<221> sig_peptide
 <222> 78..158
 <223> Von Heijne matrix
 score 7
 seq RLLLLLLLXLPLP/PP

<221> misc_feature
 <222> 73..74
 <223> n=a, g, c or t

Oligonucleotide

<400> 195

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tcattcactg attagatcca gcgctgagag gcagcactgc tccttctctc acgccaactg      60
agtctcttga tcnntac atg caa tcc cag gca gct cgc gaa cac aaa ccc      110
                Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro
                -25                -20

ggg ghc agc cgc cta ctg ctg ctg ctg ctg ctg cwg ctg ccg ctg cct      158
Gly Xaa Ser Arg Leu Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro
    -15                -10                -5

ccg ccg gkv ctg cga acc cgg gdy ttt tca wgc acc aca ctc acc gcm      206
Pro Pro Xaa Leu Arg Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala
1                5                10                15

ggg
Gly

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<210> 196

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 287..361

<221> sig_peptide

<222> 287..331

<223> Von Heijne matrix

score 7

seq LWSLACLSPPAVQ/LG

<400> 196

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ttacattgta atatataaat aattatacaa ctcaccataa cgtagaatca gtgggagccc      60
tgagcttggt ttcctgcaac tagatggtcc caactagacc aggtgatggg agacaatgac      120
agatcattag gcattagatt atcataagga gcatacaacc tagatccctt gcatgtgcag      180
ttaataatag gttttgcact tctatgagga tctaatagcgg cctctgatct gacaaggggc      240
ggastcaggc agtaatggga gcaatgggga gcgggttttca atacag atg agg ctt      295
                Met Arg Leu
                -15

tgg tca ctt gcc tgc ctt tca cct cct gct gtg cag ctt ggt tcc caa      343
Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu Gly Ser Gln
    -10                -5                1

cag gcc acg gac tgg tgg tc      363
Gln Ala Thr Asp Trp Trp
5                10

```

<210> 197

<211> 155

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..153

<221> sig_peptide
 <222> 58..132
 <223> Von Heijne matrix
 score 7
 seq IFSFFFFITLVRG/SI

<400> 197
 tagtggttatt catagtagta tctgaagacc tttgtattc ttgtgggata agttgta 57
 atg tca cct ttg ttt att ctg att gtg ctt att tgg atc ttc tct ttc 105
 Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe
 -25 -20 -15 -10
 ttt ttc ttt att act cta gtt agg ggg tct atc aat ctt ttt ttt ttt 153
 Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe
 -5 1 5
 tt 155

<210> 198
 <211> 135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..134

<221> sig_peptide
 <222> 60..125
 <223> Von Heijne matrix
 score 7
 seq STELFFLFFSVFC/FF

<400> 198
 ttgcctotta aaaggccaca cttcttaata ctatcaaatt ggctattaag tttcaacaa 59
 atg aat ttg ggg gga cat tca gat cat agc act ttt ctt ttc ttt ctt 107
 Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu
 -20 -15 -10
 ttt ttt tct gtt ttt tgt ttt ttt ttt t 135
 Phe Phe Ser Val Phe Cys Phe Phe Phe
 -5 1

<210> 199
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..318

<221> sig_peptide
 <222> 46..108
 <223> Von Heijne matrix
 score 6.90000009536743

seq VTFLALVGAVLY/LY

<221> misc_feature

<222> 9

<223> n=a, g, c or t
Oligonucleotide

<400> 199

```

gctggagcng ccgatccgag acgtggcthc ctgggaggca gaacc atg ttg gac ttc      57
                                   Met Leu Asp Phe
                                   -20
gcg atc ttc gcc gtt acc ttc ttg ctg gcg ttg gtg gga gcc gtg ctc      105
Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val Gly Ala Val Leu
      -15                               -10                               -5
tac ctc tat ccg gct tcc aga caa gct gca gga att cca ggg att act      153
Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile Pro Gly Ile Thr
      1                               5                               10                               15
cca act gaa gaa aaa gat ggt aat ctt cca gat att gtg aat agt gga      201
Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile Val Asn Ser Gly
      20                               25                               30
agt ttg cat gag tbc ctg gtt aat ttg cat gag aga tat ggg cct gtg      249
Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg Tyr Gly Pro Val
      35                               40                               45
gtc tcc ttc tgg ttt ggc agg cgc ctc gtg gtt agt ttg ggc act gtt      297
Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser Leu Gly Thr Val
      50                               55                               60
gat gta ctg aag cag cat cgg gg      320
Asp Val Leu Lys Gln His Arg
      65                               70

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<210> 200

<211> 125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 40..123

<221> sig_peptide

<222> 40..93

<223> Von Heijne matrix
score 6.90000009536743
seq LELLGSSSPPIISA/SQ

<400> 200

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cttcctcagt caccaggt ggagtacagt ggcataatc atg gct cac tgc agc      54
                                   Met Ala His Cys Ser
                                   -15
tta gaa ctc ttg ggc tca agc agt cct ccc atc tca gcc tcc caa agc      102
Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile Ser Ala Ser Gln Ser
      -10                               -5                               1
act gga att aca agc gtg agc ca      125
Thr Gly Ile Thr Ser Val Ser

```

5

10

<210> 201
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..209

<221> sig_peptide
 <222> 78..128
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LLLLSLSLFLFFW/RQ

<400> 201
 tcaggtttttc ctccttcccg ggtgctctga agtttcacca tgaatcacct tgcaggggct 60
 cttttttattt tttattg atg ccc agc cag ttg ttg ttg ttg tct ctt tct 110
 Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser
 -15 -10
 ctc ttt ttg ttt ttt tgg aga cag agt ctc gtt ttg tgg ccc agg ctg 158
 Leu Phe Leu Phe Phe Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu
 -5 1 5 10
 gag tgc agt tgt gtc att gcg gct cac tgc agc ctg acc tcc cag gct 206
 Glu Cys Ser Cys Val Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala
 15 20 25
 cgg g 210
 Arg

<210> 202
 <211> 338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..337

<221> sig_peptide
 <222> 89..226
 <223> Von Heijne matrix
 score 6.90000009536743
 seq CLFCCXFISSCNS/VF

<221> misc_feature
 <222> 291
 <223> n=a, g, c or t
 Oligonucleotide

<400> 202
 aattataata atatactaaa atatgtacga atatatacta ataattagta tataatgaat 60
 cagtataaaa tatataatat acactaat atg tat act aat aaa tat aca cta 112

```

Met Tyr Thr Asn Lys Tyr Thr Leu
-45 -40
ata tat aac ata cta ata tat aat ata tgt btk drg tat atg tgg ttg 160
Ile Tyr Asn Ile Leu Ile Tyr Asn Ile Cys Xaa Xaa Tyr Met Trp Leu
-35 -30 -25
ata ctc att tat atg tac cta cat att tgc ctc ttt tgt tgc wct ttt 208
Ile Leu Ile Tyr Met Tyr Leu His Ile Cys Leu Phe Cys Cys Xaa Phe
-20 -15 -10
att tct tcc tgc aat tct gtg ttt ccc tgt gtg att atb ttt ctt ctg 256
Ile Ser Ser Cys Asn Ser Val Phe Pro Cys Val Ile Xaa Phe Leu Leu
-5 1 5 10
cct gaa gaa ctt ctt twt gtd twt ctd wdw dtg tnt tty wtt gtg aga 304
Pro Glu Glu Leu Leu Xaa Val Xaa Leu Xaa Xaa Xaa Phe Xaa Val Arg
15 20 25
tgg agt ctc amt cwg tcc agg ctg gag tgc a 338
Trp Ser Leu Xaa Xaa Ser Ser Arg Leu Glu Cys
30 35

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<210> 203
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..188

<221> sig_peptide
 <222> 84..176
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LWSLIQAVHICLG/RK

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<400> 203
tattctctga ttckctgtct tggaatgcat ttaaaatctc tgcoctcgatt ctgacctacc 60
tggcatggga acaagaattt aca atg tta ctc acc cac aat gaa gat tac atg 113
Met Leu Leu Thr His Asn Glu Asp Tyr Met
-30 -25
cct ggc aat ttd grc ttw ard daw ttg tgg agc tta att cag gct gtt 161
Pro Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val
-20 -15 -10
cat atc tgc cta ggc agg aaa aaa aaa 188
His Ile Cys Leu Gly Arg Lys Lys Lys
-5 1

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<210> 204
 <211> 347
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..347

<221> sig_peptide

<222> 81..137

<223> Von Heijne matrix

score 6.90000009536743

seq WVFLVAIIKGVQC/QV

<400> 204

agctctggga gaagagcccc agccccagaa ttcccaggag ttccattcg gtgatacagca 60
ctgaacacag aggactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt 113

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val
-15 -10

gct att ata aaa ggt gtc cag tgt cag gtg caa ctg gtg gag tct ggg 161
Ala Ile Ile Lys Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly
-5 1 5

ggg ggc ttg gtc aag cct gga ggg tcc cta aga ctc tcc tgt gca gcc 209
Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
10 15 20

tct gga ttc acc ttc agt gay tac waw atr act kgg att cgc mag gcc 257
Ser Gly Phe Thr Phe Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala
25 30 35 40

cma ggg aag ggs ytg rak tgg att yca tam atw acg act agt ggg aat 305
Xaa Gly Lys Gly Leu Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn
45 50 55

acc gca awy tac gca gwc tct gta aag gsc cga ttc acc atc 347
Thr Ala Xaa Tyr Ala Xaa Ser Val Lys Xaa Arg Phe Thr Ile
60 65 70

<210> 205

<211> 440

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..440

<221> sig_peptide

<222> 276..326

<223> Von Heijne matrix

score 6.90000009536743

seq FLFVCLXFDESCS/VT

<400> 205

cagtaaattt ttttgwwcat tggttccttc dkcttggaact ctctgttagc acaoctgac 60
agagttggcc gtgttgtaat tctttccctc tctgtgcaa tgttggttac ttctacctgs 120
caactawkct ttatactttc cttttttgcc atgaaggga tacattttt ccttcttggt 180
gggctataca gtgatacctca tcaacaaatt atcaaagaac tgtatgagga aaaggtctct 240
ttttttaaaa gtgaatcagg gctggggagt tagga atg aag agg ttt ttt ttg 293

Met Lys Arg Phe Phe Leu
-15

ttt gtt tgt ttg tww ttt gac gag tct tgc tct gtc acc agg ctg ggg 341
Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys Ser Val Thr Arg Leu Gly
-10 -5 1 5

tgc tgt ggc gcg atc tca gcc cac tgc aam ctc cga ctc cct ggt tca 389

Cys	Cys	Gly	Ala	Ile	Ser	Ala	His	Cys	Xaa	Leu	Arg	Leu	Pro	Gly	Ser	
				10					15					20		
agc	rat	dyt	cct	gcc	tca	acc	tcc	cga	gta	gvy	ggg	att	aca	ggc	atg	437
Ser	Xaa	Xaa	Pro	Ala	Ser	Thr	Ser	Arg	Val	Xaa	Gly	Ile	Thr	Gly	Met	
			25					30					35			
cgc																440
Arg																

<210> 206
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..281
 <221> sig_peptide
 <222> 162..275
 <223> Von Heijne matrix
 score 6.90000009536743
 seq CMLFVSFLLLLLG/SR

<400> 206																
aataactccc	tttagcattt	cttgtaggac	aggtctgatg	ttgatgaaat	ctctcatctt											60
gtttgtcaga	gaaagtcttt	atttctcctt	catgcttgaa	ggatgtttcc	accggatata											120
ctatcctagg	gtaaaagttt	ttttccttca	gcactttaaa	t atg tca tgc cac tct												176
				Met Ser Cys His Ser												
				-35												
ctt ctg gcc tgt aag gtt ttc act	gaa aag tct cct acc aaa cat att															224
Leu Leu Ala Cys Lys Val Phe Thr	Glu Lys Ser Pro Thr Lys His Ile															
-30	-25															
aga gag cac cat tgt atg tta ttt	gtt tct ttt ctc ttg ctg ctt tta															272
Arg Glu His His Cys Met Leu Phe	Val Ser Phe Leu Leu Leu Leu															
-15	-10															
gga tcc cgg gg																283
Gly Ser Arg																
1																

<210> 207
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..262
 <221> sig_peptide
 <222> 113..190
 <223> Von Heijne matrix
 score 6.90000009536743
 seq LLSMLSCCQGACC/PS

<400> 207
gacggcggag agcagagagg gagcgcgcct tggctcgtg gccttggcgg cggctcctca 60
ggagagctgg ggcgcccacg agaggatccc tcacccgggt ctctcctcag gg atg aca 118
Met Thr
-25
tca tcc gtc cac ctc ctt gtc ttc aag gac cac ctc ctc tcc atg ctg 166
Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser Met Leu
-20 -15 -10
agc tgc tgc caa ggg gcc tgc tgc cca tct aca cct cac gag ggc act 214
Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu Gly Thr
-5 1 5
agg agc acg gtt tcc tgg atc cca cca aca tac aaa gca gcc aca cag 262
Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala Thr Gln
10 15 20
gg 264

<210> 208
<211> 422
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 352..420
<221> sig_peptide
<222> 352..408
<223> Von Heijne matrix
score 6.80000019073486
seq LLSMFCVSHTVQT/AT

<221> misc_feature
<222> 289..290
<223> n=a, g, c or t
Oligonucleotide

<400> 208
aaaataaaag tcttcttgat ttccagtgtg ttctcctgc acwttttggc ctgtttggac 60
cacagatttg tggcttttta tgaaatacac ctgtagatta atttwcagtt thtwhayggw 120
agtagacagt caaaggctag atcactgtra tgagtagggc ttccacattt aagaaaaagc 180
tgtaatgaag tgaattgaat cttgcttctt ttgggtcacc caaaagcagt gataagtgtc 240
gagtgtgtta ggcacttatt aacaaaagta actcagaatt gctgtctann cctccatata 300
ttttttcttc tctccgtgta gttctaaaaa tgaccatatg atattccttg a atg gta 357
Met Val
aga gcg tct att ctt ctt agc atg ttc tgt gtg tca cac act gtg cag 405
Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr Val Gln
-15 -10 -5
aca gca aca tac aca ca 422
Thr Ala Thr Tyr Thr
1

<210> 209
<211> 195
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..194

<221> sig_peptide

<222> 39..89

<223> Von Heijne matrix

score 6.80000019073486

seq ALSSFTWWAPACC/AP

<400> 209

agccactgca cctgggctca cagtttaa at ctgagta atg gag aaa aca gcc ttg 56
Met Glu Lys Thr Ala Leu
-15

tca tcc ttt acg tgg tgg gca cct gcc tgc tgt gct cca cgt aca tac 104
Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys Cys Ala Pro Arg Thr Tyr
-10 -5 1 5

gtg gtg tct gca aca act ctg tca gct gtg caa ggt cac tgt cct cta 152
Val Val Ser Ala Thr Thr Leu Ser Ala Val Gln Gly His Cys Pro Leu
10 15 20

cag agt aga aca tcg acc aaa gga aag tta tgg ccg ttt ggg g 195
Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu Trp Pro Phe Gly
25 30 35

<210> 210

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 212..361

<221> sig_peptide

<222> 212..280

<223> Von Heijne matrix

score 6.80000019073486

seq KLLLSGLTQECLG/AL

<400> 210

taattttcat catctaaact gaatgcaa ac agcgcttggc aattaaaatg aagctctcca 60
atgaagtata cttcatcagc tgctgtcaag tcatccattg atactgtttt gcggttttta 120
aattcctttt gtcactgtga ctgctcatca gcaggcaagg aagagcaggc aacaaaagtt 180
gaaaagtgca tgaaggaaaa ctttgaggaa t atg ata ttc aca ttc cag caa 232
Met Ile Phe Thr Phe Gln Gln
-20

att ggg gga aaa ctg cta tta tct ggt tta aca cag gag tgc ctt ggt 280
Ile Gly Gly Lys Leu Leu Ser Gly Leu Thr Gln Glu Cys Leu Gly
-15 -10 -5

gcc ctg cct gag gct aat gtg ttc tgt agg ggt ggc tgc aca gcc aca 328
Ala Leu Pro Glu Ala Asn Val Phe Cys Arg Gly Gly Cys Thr Ala Thr
1 5 10 15

gtc ctg aaa cat ggg aaa gca tct cct gag tcc ag 363
 Val Leu Lys His Gly Lys Ala Ser Pro Glu Ser
 20 25

<210> 211
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 230..367

<221> sig_peptide
 <222> 230..322
 <223> Von Heijne matrix
 score 6.80000019073486
 seq LLALSPDLQAARG/LM

<400> 211
 acagagaacc ctgcttcaaa gcagaagtag cagttccgga gtccagctgg ctaaaactca 60
 tccchygat aatggcaacc catgccttag aaatcgctgg gctgtttctt ggtggtgttg 120
 gmatgggtgg gsacmrkgw ggbkgyvack gtcatgcctc agtggdrrag tgcggcctt 180
 cattgaaaac aacatcgtgg ttttgaaaaa cttctgggaa ggactgttg atg aat tgc 238
 Met Asn Cys
 -30

gtg agg cag gct aac atc agg atg cag tgc aaa atc tat gat tcc ctg 286
 Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu
 -25 -20 -15
 ctg gct ctt tct ccg gac cta cag gca gcc aga ggr ctg atg tgt gct 334
 Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala
 -10 -5 1
 gct tcc gtg atg tcc ttc ttg gct ttc atg atg g 368
 Ala Ser Val Met Ser Phe Leu Ala Phe Met Met
 5 10 15

<210> 212
 <211> 448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 316..447

<221> sig_peptide
 <222> 316..435
 <223> Von Heijne matrix
 score 6.80000019073486
 seq LLKLLISLRSFWA/ET

<400> 212
 ttgtcttggc tatacgggat ctttttttgt cccatatgaa atttaagtag cttttcctaa 60
 ttctgtgaag gaagtcaatg gtagcttgat gggaatagca ttgaatctat aaattacttt 120

```

gggcggtatg gcatttgggc aatattgatt ctctctattc atgagcatgg aatgtttttc 180
catttggtca tgctctctct tattttgttg agcagtgggt tgtagttctc cttgaagggg 240
ttcttcacat cccttgtaag ttgtattccc aggtatttta ttctctttgt agcaattttg 300
aatgggagtt cactc atg att tgg ctc tct ttt tgt cta tta ttg gtg tat 351
          Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr
          -40          -35          -30
agg aat gct tgt gat ttt tgc aca ttg act tta tat cct ggg act ttg 399
Arg Asn Ala Cys Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu
          -25          -20          -15
ctg aag ttg ctt atc agc tta agg agt ttt tgg gct gag acg acg ggg g 448
Leu Lys Leu Leu Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly
          -10          -5          1

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<210> 213
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..156

<221> sig_peptide
<222> 28..102
<223> Von Heijne matrix
score 6.69999980926514
seq LVGSLHLFLSVLA/SK

```

<400> 213
gcgctgggag ttctcttttt cacttga atg ttt tct tct cca ggg ctg agg acg 54
          Met Phe Ser Ser Pro Gly Leu Arg Thr
          -25          -20
ctc ttt gta ttg gta ggc agc ctg cac ttg ttc ctt tca gtc ctg gca 102
Leu Phe Val Leu Val Gly Ser Leu His Leu Phe Leu Ser Val Leu Ala
          -15          -10          -5
agt aaa agc agg aat tct aaa aag caa cga tta ttc ctc cta gtt cct 150
Ser Lys Ser Arg Asn Ser Lys Lys Gln Arg Leu Phe Leu Leu Val Pro
1          5          10          15
ttg tac ag 158
Leu Tyr

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<210> 214
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..191

<221> sig_peptide
<222> 39..107
<223> Von Heijne matrix
score 6.69999980926514

seq NVCSLPAPGLCSG/QP

<400> 214

```

aagaaaagct ttgggtcaac tcagcatcat gtttgcag atg ctg aca gac ggg atc      56
                                Met Leu Thr Asp Gly Ile
                                -20
cta atg aga gtc aat gtg tgc tca ctg cca gct cct ggg ctg tgc tct      104
Leu Met Arg Val Asn Val Cys Ser Leu Pro Ala Pro Gly Leu Cys Ser
      -15                      -10                      -5
ggg cag cca ggt gtg agg gcc tgg cct ggg gtc aca cag ctg act car      152
Gly Gln Pro Gly Val Arg Ala Trp Pro Gly Val Thr Gln Leu Thr Gln
      1                      5                      10                      15
bta gag gaa tgc cca tgg ttc tca gca ttg gaa gga ctg gg      193
Xaa Glu Glu Cys Pro Trp Phe Ser Ala Leu Glu Gly Leu
      20                      25

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<210> 215

<211> 214

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..213

<221> sig_peptide

<222> 67..165

<223> Von Heijne matrix

score 6.69999980926514

seq ILLLSLIFGPCIL/NS

<400> 215

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aaagttcgag aaaatchaga taggcaccaa caagaacgag aaaataacat cccctggtat      60
caaagc atg ttt aac tgg aac cca tgg cta act act tta atc act ggg      108
      Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly
      -30                      -25                      -20
wta gch gga cct ctc ctc atc cta cta tta agt tta att ttt ggg cct      156
Xaa Ala Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro
      -15                      -10                      -5
tgt ata tta aat tcg ttt ctk aat tkt ata aaa caa cgc ata gct tct      204
Cys Ile Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser
      1                      5                      10
ggc aaa cgg g      214
Gly Lys Arg
      15

```

<210> 216

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..327

<221> sig_peptide

<222> 22..108

<223> Von Heijne matrix

score 6.69999980926514

seq FCALLLSLXXXXP/XX

<400> 216

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ctccgcgttc cagaatccaa g atg gcg gga tcc agg caa agg ggt ctc cgg      51
                               Met Ala Gly Ser Arg Gln Arg Gly Leu Arg
                               -25                               -20
gcc aga gtt cgg ccg ctg ttc tgc gcc ttg ctg ctg tca ctm sgw hsv      99
Ala Arg Val Arg Pro Leu Phe Cys Ala Leu Leu Leu Ser Leu Xaa Xaa
-15                               -10                               -5
mty ckt ccg rkg cka cgs cgt gkg agg aga ccc cgc ggt cgc gtt gcc      147
Xaa Xaa Pro Xaa Xaa Arg Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala
1                               5                               10
aca tcg ccg ttt cga gta saa ata cag ctt caa ggg gcc gca cct ggt      195
Thr Ser Pro Phe Arg Val Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly
15                               20                               25
gca gag cga cgg gac cgt gcc ctt ctg ggm cca cgc ggg gaa tgc tat      243
Ala Glu Arg Arg Asp Arg Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr
30                               35                               40                               45
tcc aag ttc aga tca aat tcg agt agc acc atc ttt aaa aag cya aag      291
Ser Lys Phe Arg Ser Asn Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys
50                               55                               60
agg ctc agt gtg gvm aam gac aav agc gga cct ggg      327
Arg Leu Ser Val Xaa Xaa Asp Xaa Ser Gly Pro Gly
65                               70
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<210> 217

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..357

<221> sig_peptide

<222> 70..126

<223> Von Heijne matrix

score 6.69999980926514

seq WVFLVAILKGVHC/DV

<400> 217

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aggagcccca gccctgggat tcccagctgt ttctgcttgc tgatcaggac tgcacacaga      60
gaactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt gct att tta      111
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
-15                               -10
aaa ggt gtc cac tgt gac gtg cag ctg gtg gag tcc ggg gga ggt tta      159
Lys Gly Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu
-5                               1                               5                               10
gtt cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ctc      207
```

Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Leu		
			15					20					25				
acc	ctc	agt	aac	gac	tgg	atg	cac	tgg	gtc	cgc	caa	gcc	cca	ggg	aag	255	
Thr	Leu	Ser	Asn	Asp	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys		
			30				35				40						
ggg	ctg	gtg	tgg	gtc	tca	cac	att	gat	agt	tct	rgg	act	atc	aca	aat	303	
Gly	Leu	Val	Trp	Val	Ser	His	Ile	Asp	Ser	Ser	Xaa	Thr	Ile	Thr	Asn		
			45			50				55							
tac	gcg	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aac	gcc	351	
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala		
60					65				70					75			
aag	tgg															357	
Lys	Trp																

<210> 218
 <211> 189
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..187

<221> sig_peptide
 <222> 74..118
 <223> Von Heijne matrix
 score 6.69999980926514
 seq LFLGFLACSVAYQ/CH

<400> 218																	
ttatcaagga	cactgtcttt	tcgccatcat	gtgttcttgg	cccctctggt	gaaattcaat	60											
ctatcataga	caa atg ggt tta ttt ctg ggc ttt cta gcc tgt tct gtt	109															
	Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val																
	-15	-10	-5														
gca tac cag tgc cat tct gct ttt gtt act gta gct tca cag tac act	157																
Ala Tyr Gln Cys His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr																	
	1	5	10														
ttg aaa tca gag act ttg atg ccc gca gcg gg	189																
Leu Lys Ser Glu Thr Leu Met Pro Ala Ala																	
	15	20															

<210> 219
 <211> 353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..352

<221> sig_peptide
 <222> 41..187
 <223> Von Heijne matrix
 score 6.69999980926514

seq FLGLIFFLELATG/IL

<400> 219

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agttgacttg ccatctgcct tgcaggatgg catccagccc atg tgg gag gac agc      55
                                   Met Trp Glu Asp Ser
                                   -45
agg aat aaa cgg ggt ggc cgc tgg ctg gtc agc ctg gcc aag cag cag      103
Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser Leu Ala Lys Gln Gln
                                   -40                                   -35                                   -30
cgc cac att gag ctg gac cgg ctg tgg ctg gag acg ttc tcc gtg ttc      151
Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu Thr Phe Ser Val Phe
                                   -25                                   -20                                   -15
ctc ggt ctc atc ttc ttc ctg gag ctg gca aca ggg atc ctg gcc ttt      199
Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr Gly Ile Leu Ala Phe
                                   -10                                   -5                                   1
gtc ttc aag gac tgg att cga gac cag ctc aac ctc ttc atc aac aac      247
Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn Leu Phe Ile Asn Asn
5                                   10                                   15                                   20
aac gtc aag gcc tac cgg gac gac att gac ctc cag arc ctc att gac      295
Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu Gln Xaa Leu Ile Asp
                                   25                                   30                                   35
ttt gct cag gaa tac tgg tct tgc tgc gga scc gag gcc cca ata rdt      343
Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa Glu Ala Pro Ile Xaa
                                   40                                   45                                   50
gga acc ggg g
Gly Thr Gly
                                   55

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<210> 220

<211> 115

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..113

<221> sig_peptide

<222> 12..53

<223> Von Heijne matrix

score 6.59999990463257

seq FLSLSTAFWVYA/MI

<400> 220

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actagcattt c atg ttt tta tct ctc tct act goa ttc tgg gta gtt tat      50
                                   Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr
                                   -10                                   -5
gcc atg ata att tat tca gct ctc tct gct gga ttt att att ttc ttt      98
Ala Met Ile Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe
1                                   5                                   10                                   15
tta gtt gtg ttt aat ct
Leu Val Val Phe Asn
                                   20

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<210> 221
 <211> 142
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..142

<221> sig_peptide
 <222> 29..130
 <223> Von Heijne matrix
 score 6.59999990463257
 seq FFLFFCFETGSHS/VT

<400> 221
 cctgccatt gcttcaacct gcacctct atg tac att gtg atg gat cta cct 52
 Met Tyr Ile Val Met Asp Leu Pro
 -30
 cta tgg ctc tcc cat gag gtc caa tct tat att cct tct ttc ttc ctt 100
 Leu Trp Leu Ser His Glu Val Gln Ser Tyr Ile Pro Ser Phe Phe Leu
 -25 -20 -15
 ttt ttt tgc ttt gag act ggg tct cac tct gtc acc cac ggg 142
 Phe Phe Cys Phe Glu Thr Gly Ser His Ser Val Thr His Gly
 -10 -5 1

<210> 222
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 209..370

<221> sig_peptide
 <222> 209..289
 <223> Von Heijne matrix
 score 6.59999990463257
 seq LAFSFSFFPSSFS/SF

<400> 222
 ttttggatcac atatgactca tgtgacatta gatcacagca tttttgtttt tattattaat 60
 atattgcctt agaactacat tgctaaacct ggtcttttgta tctgcgaagt tctaaccatct 120
 tgccacagct tagttagctt tgagagggaa agggtagaat ccatttaagg agacagggtta 180
 aaaaatgata tatttaagca tataggca atg gta gca cat gat tac caa aac 232
 Met Val Ala His Asp Tyr Gln Asn
 -25 -20
 ata att agc ctt ttc ttt ctt gct ttt tca ttt tct ttc ttt cct tct 280
 Ile Ile Ser Leu Phe Phe Leu Ala Phe Ser Phe Ser Phe Phe Pro Ser
 -15 -10 -5
 tca ttt tct tct ttc ttt ctt ktc ttt ctt tct ttt ttc tct tct ttc 328
 Ser Phe Ser Ser Phe Phe Leu Xaa Phe Leu Ser Phe Phe Ser Ser Phe
 1 5 10

<221> CDS
 <222> 132..281
 <221> sig_peptide
 <222> 132..215
 <223> Von Heijne matrix
 score 6.5
 seq LVFLHLFLXVYLG/LV

<400> 224
 atttttaaagt gtttctgtta atgtattcta cttcagtc ccacaaattcc aactaacgac 60
 atacatgaat aacagatcat gactgctgtt tctacaagcc tttctgctca ctgtgcttcc 120
 acttacaact c atg tta ata tgg tct tcc tct tct ttt cct gca ccc cct 170
 Met Leu Ile Trp Ser Ser Ser Ser Phe Pro Ala Pro Pro
 -25 -20
 ctc ttt ctt gtc ttt ctt cat ctt ttc ctt mwt gtc tat ttg ggt ctt 218
 Leu Phe Leu Val Phe Leu His Leu Phe Leu Xaa Val Tyr Leu Gly Leu
 -15 -10 -5 1
 gtc atg ccc act caa cag tat ctc ctc ctg cag agt cca ttg atg ttc 266
 Val Met Pro Thr Gln Gln Tyr Leu Leu Leu Gln Ser Pro Leu Met Phe
 5 10 15
 aca gac aaa gcc cag c 282
 Thr Asp Lys Ala Gln
 20

<210> 225
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..196
 <221> sig_peptide
 <222> 26..163
 <223> Von Heijne matrix
 score 6.5
 seq WLFFLMLSLCTPP/DR

<400> 225
 acttttgctt tatgttcagg ggtcc atg tgt agg atg tgc agg ttt gtt aca 52
 Met Cys Arg Met Cys Arg Phe Val Thr
 -45 -40
 tgg ata aac gtg tgc cat ggt gat ttg ctg cac aga tca tcc cgt cgc 100
 Trp Ile Asn Val Cys His Gly Asp Leu Leu His Arg Ser Ser Arg Arg
 -35 -30 -25
 ctg ggt gtg aag ccg agc acg cat tgg cta ttc ttc ctg atg ctc tcc 148
 Leu Gly Val Lys Pro Ser Thr His Trp Leu Phe Phe Leu Met Leu Ser
 -20 -15 -10
 ctt tgc acc cct cct gac aga ccc tgg tgt gtg ttg ttc ccc ccg ctg 196
 Leu Cys Thr Pro Pro Asp Arg Pro Trp Cys Val Leu Phe Pro Pro Leu
 -5 1 5 10
 gg 198

<210> 226
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..140

<221> sig_peptide
 <222> 21..113
 <223> Von Heijne matrix
 score 6.5
 seq LSLSLPLSLXLLX/XP

<400> 226
 gcagttgagr dsacttggtg atg tsa acg caa gaa gca ggc ttg aty ttt ttt 53
 Met Xaa Thr Gln Glu Ala Gly Leu Ile Phe Phe
 -30 -25
 tct ccc ccc ttc tct ctc tct ctc tct ctc tct cty cct ctc tcc ctc 101
 Ser Pro Pro Phe Ser Leu Ser Leu Ser Leu Ser Leu Pro Leu Ser Leu
 -20 -15 -10 -5
 tyt ctc ctc tst sac cca cac tca cgc aca cct caa agg g 141
 Xaa Leu Leu Xaa Xaa Pro His Ser Arg Thr Pro Gln Arg
 1 5

<210> 227
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..205

<221> sig_peptide
 <222> 77..115
 <223> Von Heijne matrix
 score 6.5
 seq MEFLLLWSLXSNG/KR

<400> 227
 awcaartact tgttaagcrt ttacgatgtg ccaggttctg tgctaggtgc tgagtgtaca 60
 ttgttgargc aaacag atg gag ttc ctg cta ttg tgg agt ttg cmg tct aat 112
 Met Glu Phe Leu Leu Trp Ser Leu Xaa Ser Asn
 -10 -5
 ggg aag aga ggc cag gca tgg cgg ctc atg cct gtw gtc cca gca gtt 160
 Gly Lys Arg Gly Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val
 1 5 10 15
 tgg gag cct gag gca ggt gga ttg ctt cag ctc ggg ggt tct agg g 206
 Trp Glu Pro Glu Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg
 20 25 30

<210> 228
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 216..479

<221> sig_peptide
 <222> 216..326
 <223> Von Heijne matrix
 score 6.5
 seq LLVFFLIVRTLSC/RS

<400> 228
 gcatccccck ktagctcaga gaagtttggt rdgaccgatc ttctgaagcc tactttctgtc 60
 aactcatcaa agtcattctc catccagctt tgttccatta tgggtgagga gctacgatcc 120
 ttggaggag aagaggcact ctgattttta gaattttcag cttttctgct ctgggttcgc 180
 cccatctttg tggttttatc taccttcggt ctttg atg atg gtg acc tac aga 233
 Met Met Val Thr Tyr Arg
 -35
 tgg ggt ttt ggt gtg gat gtc mtt ttt gtt gct gtt gat gct att cct 281
 Trp Gly Phe Gly Val Asp Val Xaa Phe Val Ala Val Asp Ala Ile Pro
 -30 -25 -20
 ttc tgt ttg tta gtt ttc ttt cta ata gtc agg acc ctc agc tgc agg 329
 Phe Cys Leu Leu Val Phe Phe Leu Ile Val Arg Thr Leu Ser Cys Arg
 -15 -10 -5 1
 tct gtt gga gta tgc tgg agg tcc act cca gac cct gtt tgc cta ggt 377
 Ser Val Gly Val Cys Trp Arg Ser Thr Pro Asp Pro Val Cys Leu Gly
 5 10 15
 atc acc agc aga ggc tgc aga aca gaa ata ttg cag aac agc aaa tgt 425
 Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile Leu Gln Asn Ser Lys Cys
 20 25 30
 tgc tcc ctg atc ctt cct ctg gaa gct tgc tct caa agg ggc act gaa 473
 Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser Ser Gln Arg Gly Thr Glu
 35 40 45
 tgt atg a 480
 Cys Met
 50

<210> 229
 <211> 144
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..144

<221> sig_peptide
 <222> 43..99
 <223> Von Heijne matrix
 score 6.5

seq EIFLPFSLSPANA/QS

<400> 229

tccagatgtg atttgggtatt tcatactttg ttgcttttgt aa atg ctg tac cca	54
Met Leu Tyr Pro	
ctg cct gag ata ttc tta cct ttt tct ttg tcc cca gca aat gcc cag	102
Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro Ala Asn Ala Gln	
-15 -10 -5 1	
tca aaa ttt agc ctt tat ttt ttt ccc ttg gtg aag ccg ggg	144
Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys Pro Gly	
5 10 15	

<210> 230

<211> 457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 314..457

<221> sig_peptide

<222> 314..394

<223> Von Heijne matrix
score 6.40000009536743
seq RLLCLXFXRLLLG/TS

<221> misc_feature

<222> 118,258..259,303,440

<223> n=a, g, c or t
Oligonucleotide

<400> 230

agctccgcgg taatggaggc tagggatggg tgctgaagta tcaggctctg gctctagctt	60
tagctctggc actggaactg cgtcggagtc tgggtctgag tctggcagcc cgaagcentg	120
grmcaccttt tcttgattct ctaaggcggg ggctgcctgc gtccaagcag ctggtttgca	180
gcgttccaac gctgggaggg agttccctta cctgggggtcc agtctgtaaa gttgtcgccg	240
ctttctaggg acccgccnnd scggctggga ctcttccatg cgtgagtatt actgarstgc	300
tsnaagggtcc ggc atg tcc ctg gaa cct gcc tcg gsc ctc ttg ggt gtg	349
Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val	
-25 -20	
cgg cgg aga ctg ctt tgt cta mct ttc tsc cga ctt ctc tta ggr acc	397
Arg Arg Arg Leu Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr	
-15 -10 -5 1	
agt ctg ttg aag ttt gtg gkc tcc tgs agy cca ccc ama ccg nat act	445
Ser Leu Leu Lys Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr	
5 10 15	
ctc acc tct tcc	457
Leu Thr Ser Ser	
20	

<210> 231

<211> 112

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..110

<221> sig_peptide

<222> 12..83

<223> Von Heijne matrix

score 6.40000009536743

seq LSVLILCVCVCVC/VY

<400> 231

ctgattttkc t atg ytg att ttg tat ctk gca act tta cta aat tta tca 50

Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser

-20 -15

gtt cta ata ctt tgt gtg tgt gtg tgt gtg tgt gtg tat gat tta tat 98

Val Leu Ile Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr

-10 -5 1 5

ata waa agg gga gt 112

Ile Xaa Arg Gly

<210> 232

<211> 359

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..358

<221> sig_peptide

<222> 8..55

<223> Von Heijne matrix

score 6.40000009536743

seq LGTTVLLWSLLRS/SP

<221> misc_feature

<222> 326

<223> n=a, g, c or t

Oligonucleotide

<400> 232

gataatc atg gcg ccc ctc gga aca act gta ttg ctg tgg agc ctc ttg 49

Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu

-15 -10 -5

agg agt tct ccg ggc gtg gaa cgg gtc tgt ttc cgg gct cga atc cag 97

Arg Ser Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln

1 5 10

ccc tgg cac ggt ggc ctg ctc caa ccg cta cct tgc tct ttc gag atg 145

Pro Trp His Gly Gly Leu Glu Pro Leu Pro Cys Ser Phe Glu Met

15 20 25 30

ggg ctg cca cgc cgc cgg ttc agc tcc gag gcc gca gaa tct ggt agc 193

Gly Leu Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser

	35	40	45	
cca gag acc aag aaa cct aca ttt atg gat gag gaa gtt caa agc ata				241
Pro Glu Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile				
	50	55	60	
ctc acg aaa atg aca ggc ttg aac ttg cag aag act ttt aag cca gct				289
Leu Thr Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala				
	65	70	75	
ata caa gaa ctg aag cca cca acc tat aag cta atg nct cag gca cag				337
Ile Gln Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln				
	80	85	90	
ttg gaa gag gct aca aga cag g				359
Leu Glu Glu Ala Thr Arg Gln				
	95	100		

<210> 233

<211> 301

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..300

<221> sig_peptide

<222> 4..105

<223> Von Heijne matrix

score 6.40000009536743

seq LLFVVLLPPPPGS/VX

<221> misc_feature

<222> 124,129,162

<223> n=a, g, c or t

Oligonucleotide

<400> 233

gcg atg ctc ctc act ttc agc tcc agc tcc cgc cac cgc cgc ctc tat	48
Met Leu Leu Thr Phe Ser Ser Ser Ser Arg His Arg Arg Leu Tyr	
cgc cgc cgc cgc cac cac ctc ctc ttc gtt gtc ctc ctt cct cct ccg	96
Arg Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro	
cct ggc agc gtt gkt ctc tgc agc sgg nrm grn smv raa gtg ctr vbg	144
Pro Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Xaa Val Leu Xaa	
kma sga aag ttc cgg gan gga cta cat gga gcc atg ctc cct ggg ctc	192
Xaa Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu	
ttc cgc ggg cgc ccg cgc gct gcc ctt cgc ttg aga gtc tca ccg wgt	240
Phe Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa	
tgc cca ggc tgg aaa gtg gcg cga tct cgg ctc aca gca acc tcc gcc	288
Cys Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala	
tcm cgg gmc cgg g	301

Ser Arg Xaa Arg
65

<210> 234
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..247

<221> sig_peptide
<222> 152..190
<223> Von Heijne matrix
score 6.40000009536743
seq MLLLLQLNLKTLS/SS

<400> 234
acaagttggg tgctgtcgcc tgcgcacg cgggccggga ggctgagcag tactgttgag 60
agcgggtgtga ggtgcttggt agcgcgccgt agctgcttcc acgtccttgc ttcacctcag 120
gtaaagagag aagtaatgga aggcctgtct g atg ttg ctt ctt ttg caa cta 172
Met Leu Leu Leu Leu Gln Leu
-10
aac tta aaa aca ctc tca tcc agt acc ata gca ttg aag aag ata agt 220
Asn Leu Lys Thr Leu Ser Ser Ser Thr Ile Ala Leu Lys Lys Ile Ser
-5 1 5 10
ggc gag ttg cta aga aaa cga aag agg g 248
Gly Glu Leu Leu Arg Lys Arg Lys Arg
15

<210> 235
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 339..392

<221> sig_peptide
<222> 339..383
<223> Von Heijne matrix
score 6.40000009536743
seq LFVLLIITQLLYG/GI

<400> 235
gttcacaaagt gagctgtctc tggcagcatt catatagaat agaatttgaa tgggtgcaccc 60
agatttgaac aacatggtaa tcatgtgatg gacatggaaa agtgractaa cbtkrgggat 120
cwtgggtargg tcaytaagaa taactckaatt cawgatgtta aaaggctttc ctttacattc 180
acaaaacaat ttrsttcccta gaagtagttt attcttgccct gtgggtcattt ttgctccttt 240
ataatactac atctaaatca atttgtaaa tatagtagag aaatgaaata aatttcttcc 300
agttaaacca ctgcacttaa agagtagaaa ccctctct atg tca ctc ttt gtt ttg 356
Met Ser Leu Phe Val Leu

atc ggg agt tcg gga ccg gcc gca cca aca tgg aga agc ccc gtc cag 152
 Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val Gln
 5 10 15

gg 154

<210> 238
 <211> 439
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 255..437

<221> sig_peptide
 <222> 255..341
 <223> Von Heijne matrix
 score 6.30000019073486
 seq LGCLLLAVRSSAT/VN

<221> misc_feature
 <222> 359..360,381
 <223> n=a, g, c or t
 Oligonucleotide

<400> 238
 tcaccacaat caatttttaga acatttttcat catcccgaaa ataagccctg ttccctttag 60
 ctgtcactcc ccactcctac cccccagccc tgtgcaataa tctactttct gtctttgaag 120
 ctttgccctat tctggacatt ttgtataaaa gggtttgtgg aggatgtggg cttttgtgac 180
 tggcttcttg aacttggcat agtgttttca aggttcaacc atgtttagac acgtacgttc 240
 ctttttatgg ccaa atg tac gga gag tcc aca ttg ttt atc cat tca tca 290
 Met Tyr Gly Glu Ser Thr Leu Phe Ile His Ser Ser

-25 -20
 gtt cat ggg cat ttg ggt tgt ctc ctc ttg gct gtt agg agt agt gct 338
 Val His Gly His Leu Gly Cys Leu Leu Leu Ala Val Arg Ser Ser Ala
 -15 -10 -5

act gtg aac att acg tac chn nkw gtk tgt gtg gac att cak ntt cat 386
 Thr Val Asn Ile Thr Tyr Xaa Xaa Val Cys Val Asp Ile Xaa Xaa His
 1 5 10 15

ttc cat atg ctt atg tct gga att act ggg tca tat ggc aac tct ctt 434
 Phe His Met Leu Met Ser Gly Ile Thr Gly Ser Tyr Gly Asn Ser Leu
 20 25 30

tca ct 439
 Ser

<210> 239
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..228

<221> sig_peptide
 <222> 7..159
 <223> Von Heijne matrix
 score 6.30000019073486
 seq WLYLLEVVAPLSG/IH

<400> 239
 gtcaag atg gcg gcg tct gta tta aac acc gtg ctg agg cgg ctt cct 48
 Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro
 -50 -45 -40
 atg cta tct ctc ttc cga ggt tct cac aga gtt cag gta act ctt cga 96
 Met Leu Ser Leu Phe Arg Gly Ser His Arg Val Gln Val Thr Leu Arg
 -35 -30 -25
 aag aca ttt tgc aca acc tca agt tgg tta tac ctt ctc gag gtt gtc 144
 Lys Thr Phe Cys Thr Thr Ser Ser Trp Leu Tyr Leu Leu Glu Val Val
 -20 -15 -10
 gct cca ctg tca gga atc cac gag tgg aga cct tcc cac gtg tgt ctt 192
 Ala Pro Leu Ser Gly Ile His Glu Trp Arg Pro Ser His Val Cys Leu
 -5 1 5 10
 agc tgt cta ggc agt act tcc tgc aac ccc cct gag g 229
 Ser Cys Leu Gly Ser Thr Ser Cys Asn Pro Pro Glu
 15 20

<210> 240
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..316
 <221> sig_peptide
 <222> 65..259
 <223> Von Heijne matrix
 score 6.30000019073486
 seq LMVVAETSQGSWS/AP

<221> misc_feature
 <222> 259
 <223> n=a, g, c or t
 Oligonucleotide

<400> 240
 ctcttcgggtt gtccagccct tctcccagcc ctggtccctc agaaggaggg taactccctt 60
 ccag atg tta cgg tcc gcc tgc gtc tct cag cac gcc ggt ggc att tgg 109
 Met Leu Arg Ser Ala Cys Val Ser Gln His Ala Gly Gly Ile Trp
 -65 -60 -55
 gtt gac cgc gga ggc ccc cag tgc cag agg gtg ttc acg ttc tgc cgt 157
 Val Asp Arg Gly Gly Pro Gln Cys Gln Arg Val Phe Thr Phe Cys Arg
 -50 -45 -40 -35
 ggg ctc agc cca aac ttt gga cgc tca gag acc caa cgg gag cgc tgg 205
 Gly Leu Ser Pro Asn Phe Gly Arg Ser Glu Thr Gln Arg Glu Arg Trp
 -30 -25 -20

ata agg cca gga cag ctg atg gtt gtg gca gaa aca tct caa ggt agc	253
Ile Arg Pro Gly Gln Leu Met Val Val Ala Glu Thr Ser Gln Gly Ser	
-15 -10 -5	
tgg tcn gcc ccc act tcc cca tst acc tct tgt cct ccc ccc aac acc	301
Trp Ser Ala Pro Thr Ser Pro Xaa Thr Ser Cys Pro Pro Pro Asn Thr	
1 5 10	
asc acc aca ccg gyt cc	318
Xaa Thr Thr Pro Xaa	
15	

<210> 241
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 123..404

<221> sig_peptide
 <222> 123..257
 <223> Von Heijne matrix
 score 6.30000019073486
 seq GFVSLLVVHAADA/WV

<400> 241	
tagctggacc cgtctgggag gtaggtttgt gagcgtgaga gaks gatctg taccgcgggg	60
atccgaagta tgcttatcca ggtgggctgc ctcaagcctc gatccccacc cgcgctdvt	120
ag atg gtg tca agg tcc ttg cgt ggg aga agg act tgg gtg aga tgc	167
Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys	
-45 -40 -35	
atg cgg aga ttg ccc cca att ccg gcc tgg agc caa ggg aaa ggg atg	215
Met Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met	
-30 -25 -20 -15	
cct gga ttt gtg tct cta ttg gtg gtc cac gct gcg gat gcc tgg gta	263
Pro Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val	
-10 -5 1	
gcc cag agg ttr tct acg cca tac ttc tca ctg ttt ttg agc ata cct	311
Ala Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro	
5 10 15	
aga tgt tcc ttt cct agg cgg agt ata gat cgc acg tgt tct agc stc	359
Arg Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa	
20 25 30	
tta gac tca gag ggt tcg agc tct ata asc ccc tcc act ccc ttc a	405
Leu Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe	
35 40 45	

<210> 242
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 129..242

<221> sig_peptide

<222> 129..191

<223> Von Heijne matrix

score 6.30000019073486

seq SLLPCSLISDCCA/SN

<400> 242

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cttttgtttt gcaatgccct gccccagag gtggagtcta cagaggcagg caggcctcct    60
tgagctgagg tgggtccac ccagttcgag ctcccagct gctttgttta cctactcaag    120
cctgggca atg gtg ggc gcc ctt ccc cca gcc tcg ctt ctg cct tgc agt    170
      Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser
      -20          -15          -10
ttg atc tca gac tgc tgt gct agc aat gag cga ggc tcc atg ggc gta    218
Leu Ile Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val
      -5          1          5
gga ccc tct gag cca cgg cgy ggg    242
Gly Pro Ser Glu Pro Arg Arg Gly
10          15
```

<210> 243

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 298..363

<221> sig_peptide

<222> 298..357

<223> Von Heijne matrix

score 6.30000019073486

seq LGSLIASLAPSTG/LG

<400> 243

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accactctga ggagacggt gacagataag aagggctggt gggatcagtc ctggtggttag    60
ctcaggaagc agagcctgga gcatctccac tatggcctgg gctccactac ttctcacct    120
cctcgctcac tgcacaggtt cttgggcaa ctttatgctg actcagccgc actctgtgtc    180
ggagtgcgag gssgaagacg gtaaccatct cctgcacccg cagcagtggc agctttgtca    240
gcaactatgt tcagtggtag cagcggcgcc cggacagtgc cccaccact gtgatct    297
atg agg atg aca aaa gac cct ctg ggg tct ctg atc gct tct ctg gct    345
Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala
-20          -15          -10          -5
cca tcg aca ggt ctt ggg    363
Pro Ser Thr Gly Leu Gly
      1
```

<210> 244

<211> 324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 153..323

<221> sig_peptide

<222> 153..236

<223> Von Heijne matrix

score 6.30000019073486

seq FFLFLFFXEXXX/XX

<400> 244

aattgatact gcttttagatg tttctgtctc attttacaaa aatgtaagaa aaaagaaaaa 60

tcaaactata ctgttaccta tttcttgat attcttaaca gaatgttctg tacacataag 120

tgtatgtgtg ttaatcctct tgtttaaatg cc atg aaa ctt cag ttt gcc ttt 173

Met Lys Leu Gln Phe Ala Phe

-25

tgt tat ttt ctt tat tta gat acc ttt ttt ctt ttt ctt ttt ttt ttt 221

Cys Tyr Phe Leu Tyr Leu Asp Thr Phe Phe Leu Phe Leu Phe Phe Xaa

-20

-15

-10

gag ama gyc tkg cyc kgt kgc hta ggm agg agt gca gtg gca maa cct 269

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg Ser Ala Val Ala Xaa Pro

-5 1 5 10

cag ctc ayt gca gcc tcc acc ttc kgg tty caa gca att tty ctg ccc 317

Gln Leu Xaa Ala Ala Ser Thr Phe Xaa Phe Gln Ala Ile Phe Leu Pro

15

20

25

cag ckg g 324

Gln Xaa

<210> 245

<211> 280

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..278

<221> sig_peptide

<222> 27..233

<223> Von Heijne matrix

score 6.30000019073486

seq GILKVLLFSVVSG/LE

<400> 245

gttgcgggggc ggggccttcg cagagc atg gcg gcg ggc gag ctt gag ggt ggc 53

Met Ala Ala Gly Leu Glu Gly Gly

-65

aaa ccc ctg agc ggc ctg ctg aat gcg ctg gcc cag gac act ttc cac 101

Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr Phe His

-60

-55

-50

-45

ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta tat cca 149

Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu Tyr Pro

-40

-35

-30

gag gtg cca ccc gag gag ttc cac ccc ttt ctg gca aag atg agg ggc 197

Glu	Val	Pro	Pro	Glu	Glu	Phe	His	Pro	Phe	Leu	Ala	Lys	Met	Arg	Gly	
			-25					-20					-15			
att	ott	aag	gta	ctg	ctc	ttt	tct	gta	gtc	tcc	ggc	ttg	gag	cag	aac	245
Ile	Leu	Lys	Val	Leu	Leu	Phe	Ser	Val	Val	Ser	Gly	Leu	Glu	Gln	Asn	
		-10					-5					1				
ccc	ttg	gcc	gct	ggc	ttc	aga	ctc	tcc	cac	ccg	gg					280
Pro	Leu	Ala	Ala	Gly	Phe	Arg	Leu	Ser	His	Pro						
5					10				15							

<210> 246
 <211> 211
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..210

<221> sig_peptide
 <222> 70..162
 <223> Von Heijne matrix
 score 6.30000019073486
 seq SLILSPSPRPVLG/FF

<400>	246															
ttt	ggc	tggg	gag	acc	catc	tgg	act	acca	agg	aga	agct	ata	gact	tact	tcc	acc
cag	ga	agg	t	atg	atg	atg	tca	aac	gtg	atg	ctg	atg	cta	cag	tta	cag
				Met	Met	Met	Ser	Asn	Val	Met	Leu	Met	Leu	Gln	Leu	Gln
				-30				-25				-20				
ctg	ctg	gog	cas	tct	ctg	att	ctc	tct	ccc	tct	ccg	cgt	cca	gtg	ctg	159
Leu	Leu	Ala	Xaa	Ser	Leu	Ile	Leu	Ser	Pro	Ser	Pro	Arg	Pro	Val	Leu	
		-15				-10					-5					
ggc	ttt	ttc	aga	caa	gtg	cat	ctc	cta	acc	agg	tca	cat	ttc	agc	cgc	207
Gly	Phe	Arg	Gln	Val	His	Leu	Leu	Thr	Arg	Ser	His	Phe	Ser	Arg		
1				5				10				15				
tgg	g															211
Trp																

<210> 247
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 249..359

<221> sig_peptide
 <222> 249..308
 <223> Von Heijne matrix
 score 6.19999980926514
 seq LLFICPPPPPIISA/SS

<400> 247

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tttcagaatt ttgtgcagga atatctgagt atttctaatt agattagaat gtcagaatac    60
attcatggac atatgagggg ttttttaaaa ttttttttag atatccttca ccttgaacat    120
ttattatttc ttgtgttgg gaacaatcca aatctctcct agatgttttg aaatgtgcaa    180
tgtattgta gctgtagtca cctactgtg ctattgaata ctagagcttg ttccttctgt    240
ctaactgt atg att ata ctc att aac caa ctt ctc ttc atc tgt ccc cca    290
      Met Ile Ile Leu Ile Asn Gln Leu Leu Phe Ile Cys Pro Pro
      -20                -15                -10

cct cca ccc atc tca gcc tct agt aac tac cat ttt act ctc tac ctc    338
Pro Pro Pro Ile Ser Ala Ser Ser Asn Tyr His Phe Thr Leu Tyr Leu
      -5                1                5                10

cat gac att aac ttt ttt agc    359
His Asp Ile Asn Phe Phe Ser
      15

```

```

<210> 248
<211> 236
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 182..235

```

```

<221> sig_peptide
<222> 182..226
<223> Von Heijne matrix
      score 6.19999980926514
      seq DVLLQLLLRVCSP/RT

```

```

<400> 248
attgggttaa tttcactgca ctgactatatt ttagatatat attctttgtg ccttcaactag    60
aactcctott acttcatgat atcttaacta taaaatcatc caaccatgaa aacaagcaca    120
caagaaacag aaacaaaaca gtcacaaaaa agcataaaact gttagcattg atccatgatg    180
a atg act gat gta tta ctt caa ttg cta tta aga gtg tgt tct ccc agg    229
      Met Thr Asp Val Leu Leu Gln Leu Leu Arg Val Cys Ser Pro Arg
      -15                -10                -5                1

acc agg g    236
Thr Arg

```

```

<210> 249
<211> 342
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 266..340

```

```

<221> sig_peptide
<222> 266..304
<223> Von Heijne matrix
      score 6.19999980926514
      seq MGLFLCCSLIFC/LV

```



```

<400> 249
taggctatatt ctttaattttc cttctaggat tcttatagtt tgaagtttta catttagatc      60
gtcaatccat cttgagttca tttttgtata tgatgaaaag taggggtctg attttattct      120
tctgcataag accagttatc ccagaaccgt ttgttgaata ggaagttctt ttctcattgc      180
ttgtttgtgg ggactttgtc aaagatcaaa tagttatagg tgtgtggctg tatttcaggg      240
tttctttatt ccatttcact gatct atg ggt ctg ttt ttg tgc tgc tct tta      292
                               Met Gly Leu Phe Leu Cys Cys Ser Leu
                               -10                               -5

ctg ata ttc tgt ctg gtt gtt cta atc ata act gaa ctg ggc tat ggg      340
Leu Ile Phe Cys Leu Val Val Leu Ile Ile Thr Glu Leu Gly Tyr Gly
              1              5              10

gg      342

```

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<210> 250
<211> 382
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 291..380

<221> sig_peptide
<222> 291..332
<223> Von Heijne matrix
      score 6.19999980926514
      seq GSWALTWLHPAEA/GT

<221> misc_feature
<222> 264..265,279..280
<223> n=a, g, c or t
      Oligonucleotide

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<400> 250
atacagcggc ctctgacacc agcacagcaa acccgccggg atcaaagtgt accagtcggc      60
agcatgggta aggagagggg tttccaatca cccattgcct gctctgtctg cccctaattt      120
ggaaaggccc tcctccagaa aatgctagaa aacctgagtg gggagctggg gagggagtag      180
tggaactctgc ttcattgtcc ccagtctgca caccctctcc cccaccaccc caactgcattt      240
cccagctcag ccaaactttc tgannaagac gggcagaggn ctgctgggag atg gga      296
                               Met Gly

tcc tgg gcc ctg act tgg ctc cat cca gca gag gct ggg acc agg gtg      344
Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr Arg Val
      -10      -5      1

cct ttc tgc agc tgg gaa aaa tca gat ggg cgc tct ta      382
Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser
      5      10      15

```

```

<210> 251
<211> 303
<212> DNA
<213> Homo sapiens

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```

<220>
<221> CDS

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<222> 108..302

<221> sig_peptide

<222> 108..233

<223> Von Heijne matrix
score 6.19999980926514
seq LSVLSLVINFSWS/RK

<221> misc_feature

<222> 279

<223> n=a, g, c or t
Oligonucleotide

<400> 251

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aaaagctgtg aggttgtaac tcagttcagt agtatattata aatatttggt ttccactttt      60
gtgcatatta tacaaatgat ggatataaaa tttgtttwga ccatwta atg atg ctt      116
                                         Met Met Leu
                                         -40
rmw wwr rra aga gga tat cct cat aga act gaa cgt tat gat gga ttt      164
Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr Asp Gly Phe
          -35                -30                -25
tta aaa tat tct gac cca aat gat att gca ttg tca gta ctg tcc ctg      212
Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val Leu Ser Leu
          -20                -15                -10
gtt att aat ttc tcc tgg agt aga aaa tgc ttt gtt cct tac tat atc      260
Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro Tyr Tyr Ile
          -5                1                5
cca ttt aaa cct tac cgv nta cct tac ccc acc gcg gcc cgg g      303
Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala Arg
10                15                20
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<210> 252

<211> 259

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 106..258

<221> sig_peptide

<222> 106..222

<223> Von Heijne matrix
score 6.19999980926514
seq CFVCXLFFVLLSG/LN

<221> misc_feature

<222> 134

<223> n=a, g, c or t
Oligonucleotide

<400> 252

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attttaaagg attttttaaa ggacctctat agttataagt cagcttaatt aaaaatggat      60
attccatagt catatttata tatatataca cacacatata tatgt atg tat gtg tgt      117
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<400> 254
aaacgttttc ttttatctaa tttatattaa atttaattaa aataagccag gaggctagt 60
gctaccatgt tagcagcaca gtcctatata ttctttcact ttgtttacat ttgttatcaa 120
ttttaactac tattattatt acatacaata caattttaac aataggagat tgctattaga 180
tgaggcttta acagaaaarv attaav atg ara ata tgc tat aac att ttt caa 233
Met Xaa Ile Cys Tyr Asn Ile Phe Gln

-25 -20
aac att ctc ggc ctc ttg ctt att ttc ctg tat ctt tct ttg aat ctt 281
Asn Ile Leu Gly Leu Leu Leu Ile Phe Leu Tyr Leu Ser Leu Asn Leu
-15 -10 -5
ttt tgt att ttc ttt tct gtc cct gcc ctt caa cct aga aga ctg gg 328
Phe Cys Ile Phe Phe Ser Val Pro Ala Leu Gln Pro Arg Arg Leu
1 5 10

<210> 255
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 233..319

<221> sig_peptide
<222> 233..310
<223> Von Heijne matrix
score 6.09999990463257
seq MLTLLGFPSKALT/FI

<221> misc_feature
<222> 129
<223> n=a, g, c or t
Oligonucleotide

<400> 255
caagttgtct cctgcgtagt gtctattagc tcttgaattt cttcaagatc catatactga 60
aacacttcac tctccaactt ttttgccata ttgacaatca ctttcataat ttcacttatt 120
gacyctgynw haaatcmtgt gaagyhatgc agahcatctg gacacagctt tctccagcag 180
ggatyyatdg ttttgggctt gaagggggtt cacggctttt tctataacaa cg atg gca 238
Met Ala
-25

tct tca atg ctg waa tcc ttc cag act ttc atg atg ttg act cta ttg 286
Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr Leu Leu
-20 -15 -10
ggc ttc cct tcc aaa gct ttg aca ttc att tcc a 320
Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser
-5 1

<210> 256
<211> 305
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 205..303

<221> sig_peptide
 <222> 205..264
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LLSLPGSFIPGNC/RP

<400> 256
 ttgttttat ttggttattt gttttgtttt gtttctctga ggccaatggg tgggaggaag 60
 tataaagaag tgtaaacagg aaagccagct gggcctggag ttccaagtgc ccatatttca 120
 tcagcttctc ctccataact gtggcaggga cacttaaccc ttccctggct gtgagaagtt 180
 attctctgag ggctggtgag caga atg gga aga tct aag agg cag ctc ctt 231
 Met Gly Arg Ser Lys Arg Gln Leu Leu
 -20 -15
 tcc ttg cct ggt tcc ttt atc cct ggg aat tgc agg cca agg att ctg 279
 Ser Leu Pro Gly Ser Phe Ile Pro Gly Asn Cys Arg Pro Arg Ile Leu
 -10 -5 1 5
 agc aat ggw gaa gwc aga agg aag gg 305
 Ser Asn Gly Glu Xaa Arg Arg Lys
 10

<210> 257
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..180

<221> sig_peptide
 <222> 37..111
 <223> Von Heijne matrix
 score 6.09999990463257
 seq CFFLIFLLPPLPA/MI

<400> 257
 tttctaattgc tattatcctg mtagtgamta agtctc atg aga tct gat ggg ttt 54
 Met Arg Ser Asp Gly Phe
 -25 -20
 atc agg ggt ttc tgc ttc tgc ttc ttc cta att ttt ctc ctg cca ccg 102
 Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu Ile Phe Leu Leu Pro Pro
 -15 -10 -5
 ctt cct gcc atg ata ctg agg cct ctg cag cca tgt gga att ata agt 150
 Leu Pro Ala Met Ile Leu Arg Pro Leu Gln Pro Cys Gly Ile Ile Ser
 1 5 10
 cca att aaa cct ctt ttt cct ttt ttt ttt t 181
 Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe
 15 20

<210> 258

<211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..235

<221> sig_peptide
 <222> 119..166
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LWTASSLPLSTHS/QR

<400> 258
 caaaaaaatc agtctttaag catttgcttg gtaagggttc ttaagattag gtttataata 60
 caaccatctg taatgtatct stcgtttgag cttgtgggcc atacaattca ttaactag 118
 atg aat aca ttg tgg aca gca tcc tca cta ccc ctc tct act cac tca 166
 Met Asn Thr Leu Trp Thr Ala Ser Ser Leu Pro Leu Ser Thr His Ser
 -15 -10 -5
 caa aga acc atg ata cac tgg aat gtt ttt ctc tgg aat tct ttc tac 214
 Gln Arg Thr Met Ile His Trp Asn Val Phe Leu Trp Asn Ser Phe Tyr
 1 5 10 15
 tct tgt att aaa att ttt ccc c 236
 Ser Cys Ile Lys Ile Phe Pro
 20

<210> 259
 <211> 265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 128..265

<221> sig_peptide
 <222> 128..220
 <223> Von Heijne matrix
 score 6.09999990463257
 seq CLIGLLVPLLGWG/NQ

<400> 259
 gacttaggat ttgagcatct ttctgttatg ctgttgcccc actcctattg caatactccc 60
 cttcttaaga aagtttttct agactaatgt ctagattaaa cttcttttct ttgacaataa 120
 tgatgcc atg act tgg aca aaa tgc cca ttg cct ctg ggt cct gct ttc 169
 Met Thr Trp Thr Lys Cys Pro Leu Pro Leu Gly Pro Ala Phe
 -30 -25 -20
 ttc acc cag tgc tgc ctt att gga ctc ctt gtg cct ctc ctt ggc tgg 217
 Phe Thr Gln Cys Cys Leu Ile Gly Leu Leu Val Pro Leu Leu Gly Trp
 -15 -10 -5
 gga aat cag aat aca cag tgg tat ccc act tct aag atg cct gat ggg 265
 Gly Asn Gln Asn Thr Gln Trp Tyr Pro Thr Ser Lys Met Pro Asp Gly
 1 5 10 15

<210> 260
 <211> 272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 162..272

<221> sig_peptide
 <222> 162..257
 <223> Von Heijne matrix
 score 6.09999990463257
 seq IVYFLVLLRVLYT/LQ

<400> 260
 cacaagggttg attttaaatt cttaaaaaat ttttcaaaat ctttccaaat gaaacaagat 60
 ttattgttaa tctacagaaa tatcctccat tcactttgat atttaaata catcgta cat 120
 tttaggtaga gcatttttat gaccactcat tgcttagtct g atg ggg agg agc aat 176
 Met Gly Arg Ser Asn
 -30
 gat ttt agg ttt gcc ttt cta aca tgc ttt ctt gga tgg gaa ata gta 224
 Asp Phe Arg Phe Ala Phe Leu Thr Cys Phe Leu Gly Trp Glu Ile Val
 -25 -20 -15
 tat ttc ttg gtg ctt ctt cgt gtt tta tac act tta caa tgg ggt ggg 272
 Tyr Phe Leu Val Leu Leu Arg Val Leu Tyr Thr Leu Gln Trp Gly Gly
 -10 -5 1 5

<210> 261
 <211> 98
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..97

<221> sig_peptide
 <222> 26..79
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LTSFLTYMPLISS/SC

<400> 261
 tttctaggta tacaatcata ttata atg aaa aca gat aat ttg act tct ttt 52
 Met Lys Thr Asp Asn Leu Thr Ser Phe
 -15 -10
 ctt aca tat atg cct ctt att tct tcc tct tgc tca att gct ccc t 98
 Leu Thr Tyr Met Pro Leu Ile Ser Ser Cys Ser Ile Ala Pro
 -5 1 5

<210> 262
 <211> 419

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..417

<221> sig_peptide
<222> 28..264
<223> Von Heijne matrix
score 6.09999990463257
seq ATVAVLSFILSSA/AK

<400> 262
attcccgggc cctggcttct tggcgcg atg agg ttc cgg ttc tgt ggt gat ctg 54
Met Arg Phe Arg Phe Cys Gly Asp Leu
-75
gac tgt ccc gac tgg gtc ctg gca gaa atc agc acg ctg gcc aag atg 102
Asp Cys Pro Asp Trp Val Leu Ala Glu Ile Ser Thr Leu Ala Lys Met
-70 -65 -60 -55
tcc tct gtg aag ttg cgg ctg ctc tgc agc cag gta cta aag gag ctg 150
Ser Ser Val Lys Leu Arg Leu Leu Cys Ser Gln Val Leu Lys Glu Leu
-50 -45 -40
ctg gga cag ggg att gat tat gag aag atc ctg aag ctc acg gct gac 198
Leu Gly Gln Gly Ile Asp Tyr Glu Lys Ile Leu Lys Leu Thr Ala Asp
-35 -30 -25
gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca gtg ctg agt 246
Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala Val Leu Ser
-20 -15 -10
ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc gaa tcc ttg 294
Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly Glu Ser Leu
-5 1 5 10
tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac gcg gcc agc 342
Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His Ala Ala Ser
15 20 25
ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag aag cac ttg 390
Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln Lys His Leu
30 35 40
cgg gtc tgc agc cta cgc atg aat agg tt 419
Arg Val Cys Ser Leu Arg Met Asn Arg
45 50

<210> 263
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..369

<221> sig_peptide
<222> 133..174
<223> Von Heijne matrix

score 6.09999990463257
seq FLAALFTVAKIWK/QP

<400> 263

cactatggag aactgtatgg cgggtcctca aaaaactaaa aatagaactc ccatatgatac	60
cagcaatccc attgctaggt atataccccc ccaaaaaagg aaatcagtat atgaaagaga	120
tatctgaatc cc atg ttt ctt gca gca ctg ttt aca gta gct aag att tgg	171
Met Phe Leu Ala Ala Leu Phe Thr Val Ala Lys Ile Trp	
-10 -5	
aag caa cct aag tgt tca tca aca aac aaa tgg aca aag aaa atg tgg	219
Lys Gln Pro Lys Cys Ser Ser Thr Asn Lys Trp Thr Lys Lys Met Trp	
1 5 10 15	
tac ata tac aca atg gag tac tat tca gcc ata aaa aaa gat gat atc	267
Tyr Ile Tyr Thr Met Glu Tyr Tyr Ser Ala Ile Lys Lys Asp Asp Ile	
20 25 30	
ctg tca ttt gca aca ata tgg atg gaa ctg gag agc att aca tta agt	315
Leu Ser Phe Ala Thr Ile Trp Met Glu Leu Glu Ser Ile Thr Leu Ser	
35 40 45	
gaa ata agt ggg sca cca aaa gac aaa ctt ctc atg ttc tca ctc att	363
Glu Ile Ser Gly Xaa Pro Lys Asp Lys Leu Leu Met Phe Ser Leu Ile	
50 55 60	
tgt gga ag	371
Cys Gly	
65	

<210> 264

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 194..283

<221> sig_peptide

<222> 194..274

<223> Von Heijne matrix

score 6.09999990463257
seq LSILQSLVPAAGA/XS

<400> 264

ctcattccct gtcctcggat cacagtctct tctcactaca gtgtcgcgcgc ctctgcctgc	60
gtascccggc catggctctg tagcctcgac ccctttgtgc ccccgggcccg tctccgcgct	120
caccacgcct gcgctctccg ctcccacatt ctttcttcag ccgagggcgc cgccgcctct	180
ccctgtctgca gcc atg gag tct tcc act ttc gcc ttg gtg cct gtc ttc	229
Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe	
-25 -20	
gcc cac ctg agc atc ctc cag agc ctc gtg cca gct gct ggt gca gyc	277
Ala His Leu Ser Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa	
-15 -10 -5 1	
tct cct	283
Ser Pro	

<210> 265

<211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..368

<221> sig_peptide
 <222> 117..350
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LLWFLQTFFFGIA/SL

<400> 265
 aaagcgcgct cccggggagg tgttcagcc atggctacgg cagccggcgc gacctacttt 60
 cagcgaggca gtctgttctg gttcacagtc atcaccctca gctttggcta ctacac atg 119
 Met
 ggt tgt ctt ctg gcc tca gag tat ccc tta tca gaa cct tgg gcc cct 167
 Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala Pro
 -75 -70 -65
 ggg ccc ttc act cag tac ttg gtg gac cac cat cac acc ctc ctg tgc 215
 Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys
 -60 -55 -50
 aat ggg tat tgg ctt gcc tgg ctg att cat gtg gga gag tcc ttg tat 263
 Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr
 -45 -40 -35 -30
 gcc ata gta ttg tgc aag cat aaa ggc atc aca agt ggt cgg gct cag 311
 Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln
 -25 -20 -15
 cta ctc tgg ttc cta cag act ttc ttc ttt ggg ata gcg tct ctc asc 359
 Leu Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Xaa
 -10 -5 1
 atc ttg att gc 370
 Ile Leu Ile
 5

<210> 266
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..273

<221> sig_peptide
 <222> 178..225
 <223> Von Heijne matrix
 score 6.09999990463257
 seq WIWVASILLRIFA/SV

<400> 266
 tatcgtgaaa gaattattgaa ttttatcaaa tctttttttg tatctgttga gatgattaca 60

tggttattat ccttcattct gttgatgtga tgtatcacat ttattgattt gcatatgttg	120
aaccctcctt gcatccctgg aatgattcct acttcattat agtgtataat ctttttg	177
atg tgc tgt tgg att tgg gtt gct agt att ttg ttg aga att ttt gca	225
Met Cys Cys Trp Ile Trp Val Ala Ser Ile Leu Leu Arg Ile Phe Ala	
-15 -10 -5	
tct gtg tta atc agg gat att tac ctg tgg ttt tct ttt ttt ttt ttt t	274
Ser Val Leu Ile Arg Asp Ile Tyr Leu Trp Phe Ser Phe Phe Phe Phe	
1 5 10 15	

<210> 267
 <211> 342
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 232..342
 <221> sig_peptide
 <222> 232..300
 <223> Von Heijne matrix
 score 6.09999990463257
 seq LLFFXLWLRYS/GR

<221> misc_feature
 <222> 158
 <223> n=a, g, c or t
 Oligonucleotide

<400> 267	
caagttatct caatttcttc tgagaagaaa tatagtttca aaatcaatca ataaagataa	60
tcctctgata aagtaagatc tgaatataca aatcatgggt acagtaatct taccattata	120
tataaattac ctctcaaaca aatgggcat tcagaarnrg gctcagagtg aattagctgg	180
aggggtgtgc aagggtcata gtttttactg ctttgaagag attatcactg g atg att	237
	Met Ile
tcc tca cat tta tat aac ttc agt ctc ctg ttc ttt kta ctc tgg ctg	285
Ser Ser His Leu Tyr Asn Phe Ser Leu Leu Phe Phe Xaa Leu Trp Leu	
-20 -15 -10	
agg tac aag gaa tca gga aga gag ggc aac tgt gag gaa gga gca ttc	333
Arg Tyr Lys Glu Ser Gly Arg Glu Gly Asn Cys Glu Glu Gly Ala Phe	
-5 1 5 10	
tcc agg tgg	342
Ser Arg Trp	

<210> 268
 <211> 427
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..427
 <221> sig_peptide

<222> 62..112

<223> Von Heijne matrix

score 6.09999990463257

seq RLLLLPRPPASTG/AS

<400> 268

agttgagtgg aaatgggcaa cggcgggagg agcggcctgc agcaggggaa ggggaacgtg 60

g atg ggg tgg cag cga ctc cta ctg ctg cct cgg cct cct gcc agt aca 109

Met Gly Trp Gln Arg Leu Leu Leu Leu Pro Arg Pro Pro Ala Ser Thr

-15 -10 -5

ggt gca tcg aat gca acc agg rrg cca aag agk ttg tac cga grc tat 157

Gly Ala Ser Asn Ala Thr Arg Xaa Pro Lys Xaa Leu Tyr Arg Xaa Tyr

1 5 10 15

aac cac ggt gtg ctg aag ata acc atc tgt aaa tcc tgc cag aaa cct 205

Asn His Gly Val Leu Lys Ile Thr Ile Cys Lys Ser Cys Gln Lys Pro

20 25 30

gta gac aaa tat atc gag tat gat cct gtt atc atc ttg awk aat gct 253

Val Asp Lys Tyr Ile Glu Tyr Asp Pro Val Ile Ile Leu Xaa Asn Ala

35 40 45

ata ttg tgc aaa gct cad gcc tac agr cat att ctt ttc aat act caa 301

Ile Leu Cys Lys Ala Xaa Ala Tyr Arg His Ile Leu Phe Asn Thr Gln

50 55 60

ata aat aac aaa ctg cct att tta ttg gca ttt tta cct tcc tgt ggv 349

Ile Asn Asn Lys Leu Pro Ile Leu Leu Ala Phe Leu Pro Ser Cys Gly

65 70 75

dga acg gcc cat gac ggc aaa aaa aag ccc aac ttc att ttg ctg ctg 397

Xaa Thr Ala His Asp Gly Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu

80 85 90 95

aaa sat tat tat tat cta gct acg gaa aac 427

Lys Xaa Tyr Tyr Tyr Leu Ala Thr Glu Asn

100 105

<210> 269

<211> 143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 20..142

<221> sig_peptide

<222> 20..76

<223> Von Heijne matrix

score 6

seq LLALVVRVILSTA/IL

<400> 269

ctttctttgc ggaatcacc atg gcg gct ggg gta agt ttg ctg gct ctg gtg 52

Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val

-15 -10

gtt cgg gtc atc cta tcc acc gcc atc ctt tgc ccg agt ggg gcc agt 100

Val Arg Val Ile Leu Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser

-5 1 5

cgg cgc cag agg agt tct gag gtt gag tgg gga act gat tcg g 143
 Arg Arg Gln Arg Ser Ser Glu Val Glu Trp Gly Thr Asp Ser
 10 15 20

<210> 270
 <211> 79
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..79

<221> sig_peptide
 <222> 23..67
 <223> Von Heijne matrix
 score 6
 seq PLFWLILCSGLLC/NK

<221> misc_feature
 <222> 2..3
 <223> n=a, g, c or t
 Oligonucleotide

<400> 270
 tnngctaatac ttgcttgtac tt atg aat cct tta ttc tgg ttg att ctc tgc 52
 Met Asn Pro Leu Phe Trp Leu Ile Leu Cys
 -15 -10
 tct ggg tta tta tgt aac aag tca ttt 79
 Ser Gly Leu Leu Cys Asn Lys Ser Phe
 -5 1

<210> 271
 <211> 121
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..120

<221> sig_peptide
 <222> 61..114
 <223> Von Heijne matrix
 score 6
 seq ISIFLSSLSLSL/LF

<400> 271
 cttccttaag aagcggtttc tctccctct tttctctctc tcacctgggt ttgtttgtcc 60
 atg aga ggg gct tgg ata agt ata ttt ctt tct tct cta tct ctc tct 108
 Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
 -15 -10 -5
 ctc tct ctt ttt t 121
 Leu Ser Leu Phe

1

<210> 272
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..291

<221> sig_peptide
<222> 196..267
<223> Von Heijne matrix
score 6
seq LFVLLPHFFLSFL/SP

<400> 272
ctcatggact gtggctgtct tattttatgt ctctaatacc agattatgaa aatcacagaa 60
aaaaggaaaa aatattattt ccaaagagta agttatgaag ccatgttaga aacccatatg 120
acaatatgaa ttctttttat ctgtcaatct caaggtagaa ttctcatat ttctgataat 180
gccaaatacc atgaa atg tct caa aaa aga ctt gac ttt ata tac cag ttg 231
Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu
-20 -15
ttt gtc ttg ctg cct cac ttc ttc ctt tct ttt ctt tct ccc ttt tat 279
Phe Val Leu Leu Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr
-10 -5 1
ctg cac cca tgg g 292
Leu His Pro Trp
5

<210> 273
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..157

<221> sig_peptide
<222> 2..100
<223> Von Heijne matrix
score 6
seq LAHFLIGLTVCFG/EG

<400> 273
c atg tac ctg tac ctg ttg tcc att tgt atg tct tct ttg aag aaa tgt 49
Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
-30 -25 -20
cta ttc aag ttc tta gcc cac ttt tta atc ggg tta aca gtt tgt ttt 97
Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
-15 -10 -5
ggg gag ggr wgg cta atg agt tat agg agt tct tat tta tta ctt aaa 145

Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
 1 5 10 15
 gga cca ccg ggg g 158
 Gly Pro Pro Gly

<210> 274
 <211> 113
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..111

<221> sig_peptide
 <222> 31..96
 <223> Von Heijne matrix
 score 6
 seq CLLVFLLTEWTSS/KL

<400> 274
 ccttttggtct ttgatgatgg tgacatacag atg ggg ttt tgg tgt gaa tgt cct 54
 Met Gly Phe Trp Cys Glu Cys Pro
 -20 -15
 ttc tgt ttg tta gtt ttc ctt cta aca gag tgg acc tct agc aaa ctc 102
 Phe Cys Leu Leu Val Phe Leu Leu Thr Glu Trp Thr Ser Ser Lys Leu
 -10 -5 1
 caa aag acg gg 113
 Gln Lys Thr
 5

<210> 275
 <211> 254
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 182..253

<221> sig_peptide
 <222> 182..247
 <223> Von Heijne matrix
 score 6
 seq VLHLFPLTPASTG/HW

<400> 275
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 ctcttcacac accctttgag gaggacaagg gaacttttcc tgtttcagaa agttgtgttg 120
 agaagaatgg caaggctaac agggcaggtg tccgggcgga ggggcggaac tggctgttgg 180
 c atg tgg tgg ggg aga tgc ttc atc cgg gtc ttg cat ttg ttc cct ctg 229
 Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu
 -20 -15 -10
 aca cca gcc tcg aca gga cac tgg g 254

Thr Pro Ala Ser Thr Gly His Trp
 -5 1

<210> 276
 <211> 364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 189..362

<221> sig_peptide
 <222> 189..275
 <223> Von Heijne matrix
 score 6
 seq LFMALPPVLSSHG/SR

<400> 276
 acttgcactt gcttgttggg gtcagagccc gtccctaaac cagggctcca tatgggctgc 60
 ctgtctgccg caacacagcc tagcggggaa acagtagaaa tgccacttct atgtatttat 120
 catattttatt ttgagataat taacgaagac gttaaataaaa gccagactgc actgaccctt 180
 ggggcgcc atg cga gac ccc ctc gcg gac atg gta cac agt tat tta tca 230
 Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser
 -25 -20
 tcg tct ttg ttc atg gcc ctt cca cca gtg ctg agc tca cat ggc agc 278
 Ser Ser Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser
 -15 -10 -5 1
 agg aac ctg aga atc tgg ggg agt cca ttt ggt gga gcg ctg act aag 326
 Arg Asn Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys
 5 10 15
 ggc aaa gca ccc cca acc cca gca caa cca gcc ctg gg 364
 Gly Lys Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu
 20 25

<210> 277
 <211> 130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..129

<221> sig_peptide
 <222> 46..96
 <223> Von Heijne matrix
 score 6
 seq WLCLPCSLCVSQL/LP

<400> 277
 gtctttgcag gmvgtgttgg gctccaacag ggagctgagt ttgtc atg agc agt gcc 57
 Met Ser Ser Ala
 -15

tgg ctg tgt ctg cca tgc tcc ctg tgt gtg tcc cag ctc ctt ccc tct	105
Trp Leu Cys Leu Pro Cys Ser Leu Cys Val Ser Gln Leu Leu Pro Ser	
-10 -5 1	
tat tcc ctg ttg atc cca gcc ccg g	130
Tyr Ser Leu Leu Ile Pro Ala Pro	
5 10	

<210> 278
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..183

<221> sig_peptide
 <222> 103..165
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSLGGLXPPMRA/CS

<400> 278	
cattatgttg acatttctag ctacaaggcc agtatTTTtac aaaataaggc cttttccctt	60
aattaagggtt gtgacagata aaagtatatt cccagctgac tc atg tca ccc atg	114
Met Ser Pro Met	
-20	

tgg gca ggc cta tta tcc cta ctt ggc ccg ctc wgt ccg cct atg agg	162
Trp Ala Gly Leu Leu Ser Leu Leu Gly Pro Leu Xaa Pro Pro Met Arg	
-15 -10 -5	
gct tgc tct gtg tgc gta ctc t	184
Ala Cys Ser Val Cys Val Leu	
1 5	

<210> 279
 <211> 265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..265

<221> sig_peptide
 <222> 149..202
 <223> Von Heijne matrix
 score 5.90000009536743
 seq LSIADLLPSSSFA/NP

<400> 279	
tgagcatttc ocaacatatc tgttgagttt ttaactcttt ttatgatctt ttttatttct	60
aggagttcta tttggttctt ttccaagtca gctatgtcat gttttaawag tttccwgtcc	120
ttdgcrtrwc twttctawct tgaggttt atg tct tta aac gag tta agc ata	172
Met Ser Leu Asn Glu Leu Ser Ile	

-15

gct gat tta tta ccc agc tca tcc ttt gct aat ccc aag ctg agt ggg	220
Ala Asp Leu Leu Pro Ser Ser Ser Phe Ala Asn Pro Lys Leu Ser Gly	
-10 -5 1 5	
ccg att tct atc tcg gtc act tca gct ggt tct cct ccc ggg gcg	265
Pro Ile Ser Ile Ser Val Thr Ser Ala Gly Ser Pro Pro Gly Ala	
10 15 20	

<210> 280
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..187

<221> sig_peptide
 <222> 110..154
 <223> Von Heijne matrix
 score 5.90000009536743
 seq DLLGTAFLEGLA/AY

<400> 280	
taataataat aataataaat ttttctgtta gattagtaga tgtaagatt atggacaaaa	60
tccaacgtag attggagtat agagaagtgg acctttctgt gtggtcttg atg aaa gac	118
Met Lys Asp	
-15	
tta ctt ggc act gcc ttt ctg gag gga agt tta gca gca tat ctc acc	166
Leu Leu Gly Thr Ala Phe Leu Glu Gly Ser Leu Ala Ala Tyr Leu Thr	
-10 -5 1	
atg gcc aat ata acc cat gtg g	188
Met Ala Asn Ile Thr His Val	
5 10	

<210> 281
 <211> 177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..177

<221> sig_peptide
 <222> 91..147
 <223> Von Heijne matrix
 score 5.90000009536743
 seq HLFMCLLTICISS/LE

<400> 281	
gccaaactgt tttttgctgt agttttgatt agagccattc tactgggtgt gaagtgatat	60
tttcatgttg ttttgatttg catttccttg atg gct aat gac att aag cat ctt	114
Met Ala Asn Asp Ile Lys His Leu	

-15

ttc	atg	tgc	tta	ttg	acc	ata	tgt	ata	tct	tct	ttg	gag	aaa	ctt	cca	162
Phe	Met	Cys	Leu	Leu	Thr	Ile	Cys	Ile	Ser	Ser	Leu	Glu	Lys	Leu	Pro	
-10						-5					1				5	
ttc	ttt	ttt	ttt	ttt												177
Phe	Phe	Phe	Phe	Phe												
					10											

<210> 282
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..335
 <221> sig_peptide
 <222> 42..113
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ATLVGFTVGSVLG/QI

<400> 282

ttgcctatta	ctcttatatc	tacagtgtgg	tggacctggg	c	atg	tac	cag	aaa	gtc	56						
					Met	Tyr	Gln	Lys	Val							
									-20							
aca	agt	tac	tgt	cga	agt	gcc	act	ttg	gtg	ggc	ttt	aca	gtg	ggc	tct	104
Thr	Ser	Tyr	Cys	Arg	Ser	Ala	Thr	Leu	Val	Gly	Phe	Thr	Val	Gly	Ser	
			-15					-10					-5			
gtc	cta	ggg	caa	atc	ctt	gtc	tca	gtg	gca	ggc	tgg	tgc	ctg	ttc	agc	152
Val	Leu	Gly	Gln	Ile	Leu	Val	Ser	Val	Ala	Gly	Trp	Ser	Leu	Phe	Ser	
		1				5					10					
ctg	aat	gtc	atc	tct	ctt	acc	tgt	gtt	tca	gtg	gct	ttt	gct	gtg	gcc	200
Leu	Asn	Val	Ile	Ser	Leu	Thr	Cys	Val	Ser	Val	Ala	Phe	Ala	Val	Ala	
	15					20				25						
tgg	ttt	tta	cct	atg	cca	cag	aag	agc	ctc	ttc	ttt	cac	cac	att	cct	248
Trp	Phe	Leu	Pro	Met	Pro	Gln	Lys	Ser	Leu	Phe	Phe	His	His	Ile	Pro	
30					35				40					45		
tct	acc	tgc	cag	aga	gtg	aat	ggc	atc	aag	gta	caa	aat	ggg	ggc	att	296
Ser	Thr	Cys	Gln	Arg	Val	Asn	Gly	Ile	Lys	Val	Gln	Asn	Gly	Gly	Ile	
			50						55					60		
gtt	act	gac	acc	cag	ctt	cta	aca	cct	tcc	tgg	ctg	gga	g			336
Val	Thr	Asp	Thr	Gln	Leu	Leu	Thr	Pro	Ser	Trp	Leu	Gly				
			65						70							

<210> 283
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 238..294

<221> sig_peptide
 <222> 238..288
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ALFFLLRIAWLLG/LF

<221> misc_feature
 <222> 227
 <223> n=a, g, c or t
 Oligonucleotide

<400> 283
 acatacacgt caattaatct gattcatccc ataaacaaaa ctaaagataa aaaccatgtg 60
 attatctcaa tatatgcaga aaaggctttc aataaaattc aaggcctctc catattaaaa 120
 actctaaaaa atctgggtat tgaggaarca tagctcaaaa gtgatgrgct gttttgtac 180
 cagtatcatg ctgttttggg tactgtagcc ctgtagtata gtttgangtt gggtaac 237
 atg atg cct cca gct ttg ttc ttt ttg ctg agg att gct tgg cta tta 285
 Met Met Pro Pro Ala Leu Phe Phe Leu Leu Arg Ile Ala Trp Leu Leu
 -15 -10 -5
 ggg ctc ttt 294
 Gly Leu Phe
 1

<210> 284
 <211> 203
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..203

<221> sig_peptide
 <222> 90..152
 <223> Von Heijne matrix
 score 5.90000009536743
 seq ALSLWASVSPSWM/CR

<400> 284
 catctttcgg cctagatgga ggaaccgtgt gctggctggg caggctgctg gcagaggtca 60
 ggagggctct tccctgagcc ctgccatcc atg aac tgt gta act ttg atc cag 113
 Met Asn Cys Val Thr Leu Ile Gln
 -20 -15
 gcc ttg tcc ctc tgg gcc tca gtt tcc cca agc tgg atg tgt cgt ccc 161
 Ala Leu Ser Leu Trp Ala Ser Val Ser Pro Ser Trp Met Cys Arg Pro
 -10 -5 1
 cct gct tca ttc ata atc acc acc acc acc acc tgc ggg 203
 Pro Ala Ser Phe Ile Ile Thr Thr Thr Thr Thr Cys Gly
 5 10 15

<210> 285
 <211> 297
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 240..296

<221> sig_peptide

<222> 240..287

<223> Von Heijne matrix

score 5.90000009536743

seq LLSLMARTDLVFC/SP

<221> misc_feature

<222> 107

<223> n=a, g, c or t

Oligonucleotide

<400> 285

aggcattgtc taggctgctg ggcacatgag ctccgggatg cccatgtcct ctggccaggc 60

agacacagac ctggggcagc accagcttct tgatggcagc ctgctcnttc caacagttcc 120

ctaccagaat cctgcctcac tggagcagag gatgccagca tcagccggga accactcctg 180

tgctaaaacc gccttggtgg cctgtggctt gaggtcttga tgcggatgaa gccggagga 239

atg ttg tct ctc ctc agt ctc atg gca agg act gat ctt gtt ttc tgt 287

Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys

-15 -10 -5

tcc cca cgg g 297

Ser Pro Arg

1

<210> 286

<211> 774

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..772

<221> sig_peptide

<222> 8..109

<223> Von Heijne matrix

score 5.90000009536743

seq MAVLAPLIALVYS/VP

<221> misc_feature

<222> 486,565

<223> n=a, g, c or t

Oligonucleotide

<400> 286

agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca 49

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala

-30 -25

gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct 97

Val	Ala	Val	Thr	Ala	Glu	Lys	Met	Ala	Val	Leu	Ala	Pro	Leu	Ile	Ala		
-20					-15					-10					-5		
ctc	gtg	tat	tcg	gtg	ccg	cga	ctt	tca	cga	tgg	ctc	gcc	caa	cct	tac		145
Leu	Val	Tyr	Ser	Val	Pro	Arg	Leu	Ser	Arg	Trp	Leu	Ala	Gln	Pro	Tyr		
			1				5						10				
tac	ctt	ctg	tcg	gcc	ctg	ctc	tct	gct	gcc	ttc	cta	ctc	gtg	agg	aaa		193
Tyr	Leu	Leu	Ser	Ala	Leu	Leu	Ser	Ala	Ala	Phe	Leu	Leu	Val	Arg	Lys		
	15						20					25					
ctg	ccg	ccg	ctc	tgc	cac	ggt	ctg	ccc	acc	caa	cgc	gaa	gac	ggt	aac		241
Leu	Pro	Pro	Leu	Cys	His	Gly	Leu	Pro	Thr	Gln	Arg	Glu	Asp	Gly	Asn		
	30					35				40							
ccg	tgt	gac	ttt	gac	tgg	aga	gaa	gtg	gag	atc	ctg	atg	ttt	ctc	agt		289
Pro	Cys	Asp	Phe	Asp	Trp	Arg	Glu	Val	Glu	Ile	Leu	Met	Phe	Leu	Ser		
45					50				55				60				
gcc	att	gtg	atg	atg	aag	aac	cgc	aga	tcc	atc	act	gtg	gag	caa	cat		337
Ala	Ile	Val	Met	Met	Lys	Asn	Arg	Arg	Ser	Ile	Thr	Val	Glu	Gln	His		
			65					70				75					
ata	ggc	aac	att	ttc	atg	ttt	agt	aaa	gtg	gcc	aac	aca	att	ctt	ttc		385
Ile	Gly	Asn	Ile	Phe	Met	Phe	Ser	Lys	Val	Ala	Asn	Thr	Ile	Leu	Phe		
			80					85				90					
ttc	cgc	ttg	gat	att	cgc	atg	ggc	cta	ctt	tac	atc	aca	ctc	tgc	ata		433
Phe	Arg	Leu	Asp	Ile	Arg	Met	Gly	Leu	Leu	Tyr	Ile	Thr	Leu	Cys	Ile		
	95						100					105					
gtg	ttc	ctg	atg	acg	tgc	aaa	ccc	ccc	cta	tat	atg	ggc	cct	gag	tat		481
Val	Phe	Leu	Met	Thr	Cys	Lys	Pro	Pro	Leu	Tyr	Met	Gly	Pro	Glu	Tyr		
	110					115					120						
atc	ang	tac	ttc	aat	gat	aaa	acc	att	gat	gag	gaa	cta	gaa	cgg	gac		529
Ile	Xaa	Tyr	Phe	Asn	Asp	Lys	Thr	Ile	Asp	Glu	Glu	Leu	Glu	Arg	Asp		
125					130					135				140			
aag	agg	gtc	act	tgg	att	gtg	gag	ttc	ttt	gcc	aan	tgg	tct	aat	gac		577
Lys	Arg	Val	Thr	Trp	Ile	Val	Glu	Phe	Phe	Ala	Xaa	Trp	Ser	Asn	Asp		
			145					150					155				
tgc	caa	tca	ttt	gcc	cct	atc	tat	gct	gac	ctc	tcc	ctt	aaa	tac	aac		625
Cys	Gln	Ser	Phe	Ala	Pro	Ile	Tyr	Ala	Asp	Leu	Ser	Leu	Lys	Tyr	Asn		
			160					165					170				
tgt	aca	ggg	cta	aat	ttt	ggg	aag	gtg	gat	gtt	gga	cgc	tat	act	gat		673
Cys	Thr	Gly	Leu	Asn	Phe	Gly	Lys	Val	Asp	Val	Gly	Arg	Tyr	Thr	Asp		
	175						180					185					
gtt	agt	acg	cgg	tac	aaa	gtg	agc	aca	tca	ccc	ctc	acc	aag	caa	ctc		721
Val	Ser	Thr	Arg	Tyr	Lys	Val	Ser	Thr	Ser	Pro	Leu	Thr	Lys	Gln	Leu		
	190					195					200						
cct	acc	ctg	atc	ctg	ttc	caa	ggt	ggc	aag	gag	gca	atg	cgg	cgg	cca		769
Pro	Thr	Leu	Ile	Leu	Phe	Gln	Gly	Gly	Lys	Glu	Ala	Met	Arg	Arg	Pro		
205					210					215					220		
cag	at																774
Gln																	

<210> 287

<211> 614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 155..613

<221> sig_peptide

<222> 155..205

<223> Von Heijne matrix

score 5.80000019073486

seq LWLKLAFGFAFL/DT

<400> 287

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agggtaacag aggaggaaat tggtcctcgt ctgataagac aacagtggag aaaggacgca      120
tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt      175
                               Met Thr Met Tyr Leu Trp Leu
                               -15
aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg      223
Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
-10                               -5                               1                               5
aca ggg caa agc cca aca cct tcc ccc act gga ttg act aca gca aag      271
Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys
                               10                               15                               20
atg ccc agt gtt cca ctt tca agt gac ccc tta cct act cac acc act      319
Met Pro Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr
                               25                               30                               35
gca ttc tca ccc gca agc acc ttt gaa aga gaa aat gac ttc tca gag      367
Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu
                               40                               45                               50
acc aca act tct ctt agt cca gac aat act tcc acc caa gta tcc ccg      415
Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro
55                               60                               65                               70
gac tct ttg gat aat gct agt gct ttt ark acc aca ggt gtt tca tca      463
Asp Ser Leu Asp Asn Ala Ser Ala Phe Xaa Thr Thr Gly Val Ser Ser
                               75                               80                               85
gta cag acg cct cas ctt ccc acg cac gca gac tcg cag acg ccc tct      511
Val Gln Thr Pro Xaa Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser
                               90                               95                               100
gct gga act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac      559
Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn
                               105                               110                               115
tca acc cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga      607
Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg
                               120                               125                               130
gga gta c                                                                614
Gly Val
135
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<210> 288

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 124..249

<221> sig_peptide
 <222> 124..174
 <223> Von Heijne matrix
 score 5.80000019073486
 seq LWLKLLAFGFAFL/DT

<400> 288
 atttttattt actttttacat ttttgattcg tttttacaga gaaaaacttc tacagagata 60
 acaattattt tgcttttcag aaggacgcat gctgtttctt agggacacgg ctgacttcca 120
 gat atg acc atg tat ttg tgg ctt aaa ctc ttg gca ttt ggc ttt gcc 168
 Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala
 -15 -10 -5
 ttt ctg gac aca gaa gta ttt gtg aca ggg caa agc cca aca cct tcc 216
 Phe Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser
 1 5 10
 ccc act ggt gtt tca tca gta cag acg ccc cag gg 251
 Pro Thr Gly Val Ser Ser Val Gln Thr Pro Gln
 15 20 25

<210> 289
 <211> 416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 155..415
 <221> sig_peptide
 <222> 155..205
 <223> Von Heijne matrix
 score 5.80000019073486
 seq LWLKLLAFGFAFL/DT

<400> 289
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 agggtaacag aggaggaaat tgttctctgt ctgataagac aacagtggag aaaggacgca 120
 tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
 Met Thr Met Tyr Leu Trp Leu
 -15
 aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
 Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
 -10 -5 1 5
 aca ggg caa agc cca aca cct tcc ccc act ggt gtt tca tca gta cag 271
 Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Val Ser Ser Val Gln
 10 15 20
 acg cct cac ctt ccc acg cac gca gac tcg cag acg ccc tct gct gga 319
 Thr Pro His Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser Ala Gly
 25 30 35
 act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac tca acc 367
 Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn Ser Thr
 40 45 50
 cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga gga gta c 416
 Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg Gly Val

55

60

65

70

<210> 290
 <211> 309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..308

<221> sig_peptide
 <222> 183..290
 <223> Von Heijne matrix
 score 5.80000019073486
 seq LFLLSGTIWIAIC/KP

<400> 290
 gaggcctttt ggtcacttag aagaggtgcc aaagatcaag gagaggaaag tgggtgggcta 60
 caaatgtaaa ttctgtgtgg aagtgcaccc aacgctccga gccatctgca atcacctccg 120
 wwagcacgtc cagtatggca atgtcccagc tgtgtcagct gctgtgaagg ggctgcgttc 180
 tc atg aga gga gcc acc tgg ccc tgg cca tgt tta ccc gcg agg aca 227
 Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr
 -35 -30 -25
 agt aca gct gcc agt att gct cgt ttg ttt ctg ott tca ggc aca att 275
 Ser Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile
 -20 -15 -10
 tgg atc gcc ata tgc aaa ccc acc acg aac ggg g 309
 Trp Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
 -5 1 5

<210> 291
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 142..357

<221> sig_peptide
 <222> 142..333
 <223> Von Heijne matrix
 score 5.80000019073486
 seq SALLRSLLLPXLX/QI

<221> misc_feature
 <222> 282..283
 <223> n=a, g, c or t
 Oligonucleotide

<400> 291
 caagtccaca gcgctgggtg cagtacctcc ggcttcttca ggagtccatc tggcctgggtg 60
 gagttttgcc taagtttcca cggcccshta aggaccaag agcagaaaact ggctgctgag 120

```

aaacaggctt tgcagagcct g atg gga gtc ctc cca gat ctc gta gta gaa 171
                        Met Gly Val Leu Pro Asp Leu Val Val Glu
                        -60 -55
att ttt ggg gtg aac aaa tgc cgg ctg agc tgg ggt cta gtc ctg gag 219
Ile Phe Gly Val Asn Lys Cys Arg Leu Ser Trp Gly Leu Val Leu Glu
                        -50 -45 -40
tca cta caa caa ccc ctc atc aac agg cat ttg att tac tgc ctt ggg 267
Ser Leu Gln Gln Pro Leu Ile Asn Arg His Leu Ile Tyr Cys Leu Gly
                        -35 -30 -25
gac atc atc ctg grn ntc ttg gat ctc agt gct ctg ttg agg agt ctg 315
Asp Ile Ile Leu Xaa Xaa Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu
                        -20 -15 -10
ctg cta cca sct ctg sct cag ata ccc cag gca act cta aga gg 359
Leu Leu Pro Xaa Leu Xaa Gln Ile Pro Gln Ala Thr Leu Arg
                        -5 1 5

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<210> 292
 <211> 254
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..254

<221> sig_peptide
 <222> 129..173
 <223> Von Heijne matrix
 score 5.80000019073486
 seq ALGFVLLAPRGWG/SL

```

<400> 292
gtttttcagc tcgccattca cttcgctgtg aagatggcgt cgggcagcgg gacaaaaaac 60
ttggactttc gccgaaagtg ggatgtggga agtgggcag ggaccagatc aaaggagaca 120
gccaggag atg aca gca ctg ggg ttt gtt ctg tta gct cca cgt ggc tgg 170
      Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp
      -15 -10 -5
ggg agc ctc aca gtc atg gtg gaa ggc aag gaa gag caa gtc acg tct 218
Gly Ser Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser
      1 5 10 15
tac acg gat ggc agc agg caa aga gac agc aat ttt 254
Tyr Thr Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe
      20 25

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<210> 293
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 221..412

<221> sig_peptide

<222> 221..337

<223> Von Heijne matrix
score 5.80000019073486
seq LISFLHTLQVVCS/VI

<400> 293

```
gtcagagcac atccggtgtt agaagcgctg gtaggccttg gagaggcggg ttaggaagag      60
tgagagactgc tgcacggact ctggaaccat gaacatatatt gatcgaaaga tcaactttga    120
tgcgcttttta aaattttctc atataacccc gtcaacgcag cagsrccctga agaagatttc    180
attactgtctc tcagaaaact catgatgatc ctggccatga atg aaa agg ata aga      235
                                   Met Lys Arg Ile Arg
                                   -35
aga aag aga aga aat gaa gtg acc atc cag cct ttc cca att aga ctt      283
Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro Phe Pro Ile Arg Leu
                                   -30      -25      -20
cct ctc ctt cca ccc ctc att tcc ttt ttg cac aca tta cag gtg gtg      331
Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His Thr Leu Gln Val Val
                                   -15      -10      -5
tgt tct gtg ata atg aaa agc atc aga aaa gct ttt gta ctt tgt ggt      379
Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala Phe Val Leu Cys Gly
                                   1      5      10
ttc ctc tat ttt gaa ttt ttt gat caa aaa ctg at      414
Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu
15      20      25
```

<210> 294

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..332

<221> sig_peptide

<222> 156..221

<223> Von Heijne matrix
score 5.80000019073486
seq XVXLFXXVXVXXA/AL

<400> 294

```
catgtgtttc tcatctttca accaccaaac ttacataaaa ttcattccacc ttcccattct      60
tcctattata gtacaggaaa ggtccttcct gtcaaaggca aaatcactta tgattgtgtc    120
cccattctctc ttgccttttc aaggactttg agcct atg ctg cca ctg ctt cat      173
                                   Met Leu Pro Leu Leu His
                                   -20
tgt ttt ttt ttk gtt kgt ttg ttt kgt ttk gtt ttk gtt twa ama gca      221
Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa Val Xaa Val Xaa Xaa Ala
                                   -15      -10      -5
gct tta ttg aga tat aat yca agt ata cag kgt ggc cgg gca cag kgg      269
Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln Xaa Gly Arg Ala Gln Xaa
1      5      10      15
ctc ama cct gwa atc cca gma ctt tgg gag act aag gma ggc aga tta      317
Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu Thr Lys Xaa Gly Arg Leu
```



```

                                -25
cga agt act cta aca tgg aca gaa gtc gtg ggc tgg tgg agt gtt gcg      163
Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp Trp Ser Val Ala
                                -20          -15          -10
tcg ctg ctt agt gat gtg gca gca tgg tgg cca ccg cac tcc acc tca      211
Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro His Ser Thr Ser
                                -5          1          5
aca cgg gga ggg gta      226
Thr Arg Gly Gly Val
10

```

```

<210> 297
<211> 232
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 90..230

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<221> sig_peptide
<222> 90..221
<223> Von Heijne matrix
      score 5.80000019073486
      seq LVCVFTCSLLAFF/SP

```

```

<400> 297
ctgaactttt tatttttcta tttttataac caggagaaag taaacacata cacacacatg      60
gatggagaga gggacagagg gatggacgg atg aat gca ttr gta gat ggg aaa      113
                                Met Asn Ala Leu Val Asp Gly Lys
                                -40
cgg ctt asa krg tgc ata cgc tat ttc gat tct atc tca cta tat tct      161
Arg Leu Xaa Xaa Cys Ile Arg Tyr Phe Asp Ser Ile Ser Leu Tyr Ser
      -35          -30          -25
aag gca agt tta agt tgt tgt tta gtg tgt gtg ttt act tgt tca ttg      209
Lys Ala Ser Leu Ser Cys Cys Leu Val Cys Val Phe Thr Cys Ser Leu
      -20          -15          -10          -5
cta gct ttc ttc agc cca tgc ac      232
Leu Ala Phe Phe Ser Pro Cys
1

```

```

<210> 298
<211> 258
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 7..258

```

```

<221> sig_peptide
<222> 7..63
<223> Von Heijne matrix
      score 5.80000019073486

```

seq WVFLVAILKGVQC/EL

```

<400> 298
ccaacc atg gag ttt ggg ctt agc tgg gtt ttc ctt gtt gct att ttg      48
      Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
            -15                                -10

aaa ggt gtc caa tgt gaa ctg cag gtg gtg gag tct ggg gga ggc ttg      96
Lys Gly Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu
-5              1              5              10

gta cag cca ggg cgg tcc ctc aga ctc tcc tgt cga act tct gga ttc      144
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe
            15              20              25

gcc ttt gat gat tat aat ttg agt tgg gtc cgc cag gct cca ggg aag      192
Ala Phe Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys
            30              35              40

ggg ctg gag tgg gta ggt ttc att aga agc aaa cct tat ggt gag aca      240
Gly Leu Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr
            45              50              55

aca acg tac gcc gcg tgg      258
Thr Thr Tyr Ala Ala Trp
60              65

```

<210> 299
 <211> 139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..139
 <221> sig_peptide
 <222> 83..124
 <223> Von Heijne matrix
 score 5.80000019073486
 seq SLFXLXXLRQSFT/XX

```

<400> 299
tttgggagct ccagtgttag gcgcatatat atttyagaat tgtgacaatt tcctgttggt      60
ttagtctctyt tatkattata ta atg tcc ctc ttt gwc ctt yyt yyt ttg aga      112
            Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg
                        -10                                -5

cag agt ttc act cht gwt gcc cag gca      139
Gln Ser Phe Thr Xaa Xaa Ala Gln Ala
            1              5

```

<210> 300
 <211> 286
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 196..285

<221> sig_peptide
 <222> 196..252
 <223> Von Heijne matrix
 score 5.80000019073486
 seq SFYFLASSSLSTS/AS

<221> misc_feature
 <222> 16,286
 <223> n=a, g, c or t
 Oligonucleotide

<400> 300
 asatcgcgct gggganasgc cacgtcgcta tgagtgtggt tcagtctacc tggattaaac 60
 gtttgcttct ctctgtctac cttgattaa cgtgcacttc gcagtcctcg gttctccata 120
 cccgtgacct ggggatcgct acggacctta aaataccgcg aacascccct tcgtsccaag 180
 ctggagagca gtggc atg atc tcg gct cac tgc agc ttc tac ttc ctg gcc 231
 Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala
 -15 -10
 tca agc agt ctt tcc acc tca gcs tct saa cgc act gga att aca gat 279
 Ser Ser Ser Leu Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp
 -5 1 5
 gtg agc n 286
 Val Ser
 10

<210> 301
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..241

<221> sig_peptide
 <222> 113..184
 <223> Von Heijne matrix
 score 5.69999980926514
 seq CLFVFLYTTPCNC/FG

<400> 301
 tgcaatgggt ggtgttttat aatgctctct tccctaataca tgttaatacag gagattttcc 60
 ttttggaact cctgactgaa agcttcttag tttacacaca tgttcctcca gg atg aac 118
 Met Asn
 gct gaa aat aac ttt ttc ggt ttt gtt tgt ttg ttt gtt ttc ctc tat 166
 Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe Leu Tyr
 -20 -15 -10
 aca acc cct tgc aat tgc ttt ggt tta gaa cac ctt tgg att cta agt 214
 Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile Leu Ser
 -5 1 5 10
 ttc atg gtt gtt ctg gga gwy acc agg g 242
 Phe Met Val Val Leu Gly Xaa Thr Arg
 15

<210> 302
 <211> 136
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..134

<221> sig_peptide
 <222> 42..110
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LPCCCHLLTCVSS/LR

<400> 302
 agtcacagtg acacagcctt ccaaccaggc cgccccctgg c atg acc atg gct gtg 56
 Met Thr Met Ala Val
 -20
 ggt gca gct gmy cam ctc ccc tgc tgc tgc cat ttr ctc acc tgc gtm 104
 Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His Leu Leu Thr Cys Val
 -15 -10 -5
 tcc agc ctt cgc amt gac att tac cca cat gg 136
 Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His
 1 5

<210> 303
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..174

<221> sig_peptide
 <222> 73..147
 <223> Von Heijne matrix
 score 5.69999980926514
 seq SILLAALSRNISP/GQ

<400> 303
 aagaggaagc ggaakdgcct caggtgggag gtagtgccaa aagcccaggg cgcccgcgca 60
 aaccgaggcg tc atg cgg aga aaa agg cga gaa aga aaa gag agg aag agc 111
 Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser
 -25 -20 -15
 atc ctc ctg gcc gcc ctt tcg agg aac ata agt cct ggt cag aca tac 159
 Ile Leu Leu Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr
 -10 -5 1
 cga aca tcc ccc gcg g 175
 Arg Thr Ser Pro Ala
 5

<210> 304
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 402..491

<221> sig_peptide
 <222> 402..470
 <223> Von Heijne matrix
 score 5.69999980926514
 seq LELLTSSDPPSLA/SQ

<400> 304
 ttagggtgttc tgatagttaa gtggtagtat catgggtctta atttttcctt gaagtggcctt 60
 ttgatttgca tttccttaat gactaattag gttagagcatc ttttcatgta cttactggcc 120
 ttctttggag aaataacctt tccaaatcca atgggttggtc tttttttatt gttgatctta 180
 agggttctta ggtgttctgg gtaccagttt cttgtgagat gtgtgacttg taaatacttt 240
 cttccattct ccatgttggtc tttttattct cttgatggta ttctttgaaa taaaaaartk 300
 tttatatttg acaaagttca gtttatttat ttatttattg ccattcgtgc ttttggtttt 360
 gataatccat ttttwtgtt tttattttta tttacttaga g atg ggg tct ccc tat 416
 Met Gly Ser Pro Tyr
 -20
 gtt gcc cac gtt ggt ctt gaa ctc ttg acc tca agt gat cct ccc tcc 464
 Val Ala His Val Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ser
 -15 -10 -5
 ttg gcc tcc caa gtg ctg gga ata cat tm 493
 Leu Ala Ser Gln Val Leu Gly Ile His
 1 5

<210> 305
 <211> 214
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..213

<221> sig_peptide
 <222> 79..135
 <223> Von Heijne matrix
 score 5.69999980926514
 seq VCWLTLTLAHSLS/LT

<400> 305
 cacacacgca ccaaatacac acagasaccc tggccctcac tcacgcacav tctctcacac 60
 tcgtggacac acccccag atg cat ctt tac act cat gta tgc tgg ctc act 111
 Met His Leu Tyr Thr His Val Cys Trp Leu Thr
 -15 -10
 ctc aca ctg gca cac tca cac agc ttg acc cac acg cac aca ctc aca 159
 Leu Thr Leu Ala His Ser His Ser Leu Thr His Thr His Thr Leu Thr

```

      -5              1              5
ccc agt cac aca cgt aca cac tca cat acg tgt gct tgc cta cac gca      207
Pro Ser His Thr Arg Thr His Ser His Thr Cys Ala Cys Leu His Ala
      10              15              20
cac aag g      214
His Lys
25

```

```

<210> 306
<211> 458
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 306..458

<221> sig_peptide
<222> 306..350
<223> Von Heijne matrix
      score 5.69999980926514
      seq LSLTFYHFPLCWG/HQ

```

```

<221> misc_feature
<222> 286,448
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 306
atcagagagc gccggaagcg gtccgagaat gaagcagtgat gatctaccat gcattgtctc      60
agaaagaggc gaatgactcc gatgtccagg tcagttcttg gcagggagtc caggagcaac      120
agaggtgatg gcaaagatgg ctacgtagct tctgagcccc cagcactgat tgagatgtcc      180
tttcccatat catactctc atttttctgg cagacatcta aggctggatc aaagtctgta      240
gttctcatta cctgttccca cgtgccagcc tccttttctg ttgtgnummaa gtcaagtttg      300
gtaaa atg agg ctt tcc tta acc ttt tat cat ttc oca ctg tgt tgg gga      350
      Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly
      -15              -10              -5
cac cag gct gtg ccc acg tgg tgg saa rgc atc att caa cct tgt cac      398
His Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His
      1              5              10              15
tgt gcc ctg tgc act tct gca gaa ggt gtg caa tca cat atc ata agt      446
Cys Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser
      20              25              30
gna att tac aga      458
Xaa Ile Tyr Arg
      35

```

```

<210> 307
<211> 328
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS

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<222> 87..326

<221> sig_peptide

<222> 87..128

<223> Von Heijne matrix

score 5.69999980926514

seq NVLIIVFVAFAG/FL

<400> 307

tatcttctct ccagtctaaa gcctcaactga acaaactgtc ottgactgtc agtgctcagg 60
gaactgctct gccacccttc tcctca atg aat gtg tta atc att gtt ttt gtt 113

Met Asn Val Leu Ile Ile Val Phe Val

-10

gca ttt gct ttt ggg ttc ytg gtc atg aag tct ttg ctt aag cca atg 161

Ala Phe Ala Phe Gly Phe Leu Val Met Lys Ser Leu Leu Lys Pro Met

-5 1 5 10

tcg aga agg gtt ttt ctg atg tta tct tct agg att ttt atg gtt tca 209

Ser Arg Arg Val Phe Leu Met Leu Ser Ser Arg Ile Phe Met Val Ser

15 20 25

ggc ctt aga ttt aag tcc ttg atc cat ctt gag ttg att ttt gta tat 257

Gly Leu Arg Phe Lys Ser Leu Ile His Leu Glu Leu Ile Phe Val Tyr

30 35 40

aag ttg aga gat gag gat cca gtt tca ttc ttc tac atg tgg ctt gcc 305

Lys Leu Arg Asp Glu Asp Pro Val Ser Phe Phe Tyr Met Trp Leu Ala

45 50 55

aat tat ccc agc acc att tgt tg 328

Asn Tyr Pro Ser Thr Ile Cys

60 65

<210> 308

<211> 380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 33..380

<221> sig_peptide

<222> 33..92

<223> Von Heijne matrix

score 5.69999980926514

seq LAWALPSLLRLGA/AQ

<221> misc_feature

<222> 326

<223> n=a, g, c or t

Oligonucleotide

<400> 308

agcgggtctcc cggccctctgc cgccctgccca ct atg tcc cgc cgc tct atg ctg 53

Met Ser Arg Arg Ser Met Leu

-20 -15

ctt gcc tgg gct ctg ccc agc ctg ctt cga ctg gga gcg gct cag gag 101

Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	
			-10					-5					1			
aca	gaa	gac	ccg	gcc	tgc	tgc	agc	ccc	ata	gtg	ccc	cgg	aac	gag	tgg	149
Thr	Glu	Asp	Pro	Ala	Cys	Cys	Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	
	5					10					15					
aag	gcc	ctg	gca	tca	gag	tgc	gcc	cag	cac	ctg	agc	ctg	ccc	tta	cgc	197
Lys	Ala	Leu	Ala	Ser	Glu	Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	
20					25					30					35	
tat	gtg	gtg	gta	tcg	cac	acg	gcg	ggc	agc	agc	tgc	aac	acc	scc	gcc	245
Tyr	Val	Val	Val	Ser	His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Xaa	Ala	
				40					45						50	
tcg	tgc	cag	cag	cag	gcc	cgg	aat	gtg	cag	cac	tac	cac	atg	aag	aca	293
Ser	Cys	Gln	Gln	Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	
				55				60					65			
ctg	ggc	tgg	tgc	gac	gtg	ggc	tac	aac	tkc	ctn	gat	tgg	aga	aga	cgg	341
Leu	Gly	Trp	Cys	Asp	Val	Gly	Tyr	Asn	Xaa	Leu	Asp	Trp	Arg	Arg	Arg	
		70					75					80				
gct	cgt	ata	cra	ggg	ccg	tgg	mtg	gaa	ctt	cac	ggg	tsc				380
Ala	Arg	Ile	Xaa	Gly	Pro	Trp	Xaa	Glu	Leu	His	Gly	Xaa				
	85					90					95					

<210> 309
 <211> 284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 228..284

<221> sig_peptide
 <222> 228..269
 <223> Von Heijne matrix
 score 5.69999980926514
 seq VFLFLMISVFAGC/QI

<400>	309															
aaaagaagaa	agctgaatca	tactcgatga	ttattgatca	tttgtataca	gctcaagccc											60
tcaagtagcc	tgctgtaata	tttactagtt	acaaagaaaa	gattcgtttt	gtcacagtta											120
catgaaaggt	gcttatat	ttt gcaa	aatatgg	agacaaagtt	catcttaaaa	gattaaaatg										180
agaatctcct	aatgaagca	tttgg	aatat	tgattagtat	accagaa	atg gtt ttt										236
						Met Val Phe										
ctt ttt	ctt atg	atc agc	gtt ttt	gcc ggt	tgt caa	atc cct	tcc ggg									284
Leu Phe	Leu Met	Ile Ser	Val Phe	Ala Gly	Cys Gln	Ile Pro	Ser Gly									
	-10			-5		1	5									

<210> 310
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 243..356

<221> sig_peptide
 <222> 243..305
 <223> Von Heijne matrix
 score 5.59999990463257
 seq AGLELLASSNSSA/LP

<400> 310
 ttgagatcac ctgaggcaac atagtgaac cctgtatcta gaataaatta gagaaagaaa 60
 aatagtctgg gcatgatggt gtgcacctat agtctccagc tabtcasgag cctgaggcag 120
 gaggwtcact tgagctkagg agttcaagga tgcagtsacc tgtgattgca cactgcatt 180
 ccagcttgga caacagagtg agaccctgtc ttaaaattta aattttktgt yttwtggtag 240
 ag atg ggg tct cgc cct gtt tcc gak gct ggt ctc gaa ctc ctg gcc 287
 Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala
 -20 -15 -10
 tcg agc aat tct tct gcc ttg ccc ttc caa tgt tct ggg att aca ggc 335
 Ser Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly
 -5 1 5 10
 atg agc crc cac acc cta gcg g 357
 Met Ser Xaa His Thr Leu Ala
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<210> 311
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<221> sig_peptide
 <222> 413..451
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 score 5.59999990463257
 seq MLCHLSLVFLGXG/QF

<221> misc_feature
 <222> 30
 <223> n=a, g, c or t
 Oligonucleotide

<400> 311
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 aatcaaatatt aataatatca agcttgcttg gtgagcatgg atttataaga tagaatgggt 120
 tgtgggggrg artatagtkc cgaaaaagrk tattgtttcc cataatgcct ggtattgtat 180
 taagtacttt gcatacagta gggcatttca ttgtccagc gatcctcctg caaagtaggt 240
 acaattatct tcaattttaca aatgaggaaa ccaagctctc ttcaagctga taagatgctg 300
 aactgagatt tgaaccaagt ccctctgccc ctaagagccc ctaccctag ctgctactat 360
 atgctgtacc catctaagct ttgtgaaata rccttggtcc actgcagaga ag atg ttg 418
 Met Leu
 tgt cac cta tct cta gta ttt ctt ggc ktt ggg cag ttc tgg agt caa 466
 Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp Ser Gln
 -10 -5 1 5

aat g
Asn

470

<210> 312
<211> 187
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<220>
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<221> sig_peptide
<222> 98..148
<223> Von Heijne matrix
score 5.59999990463257
seq FMCLFAICISSNA/KC

<400> 312
aagtttggtt ttgttggtgg tggatagat ttcttatatt ctattccata aagtatgaaa 60
tggaggctcc ttgtgatttt taatttgcac ttctgta atg act aat ctt ttc atg 115
Met Thr Asn Leu Phe Met
-15
tgc ttg ttt gcc atc tgt ata tct tct aat gcg aag tgt ctg ttt agt 163
Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn Ala Lys Cys Leu Phe Ser
-10 -5 1 5
ctt ttt cct ttt ttt att gag ggg 187
Leu Phe Pro Phe Phe Ile Glu Gly
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<210> 313
<211> 237
<212> DNA
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<221> CDS
<222> 93..236

<221> sig_peptide
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<223> Von Heijne matrix
score 5.59999990463257
seq CVLFTLLVSTRSG/RS

<221> misc_feature
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Oligonucleotide

<400> 313
ttgcttagga ttttctaaaa gattacataa aatactgttg aaaagatgat tgcatacaaa 60
acataatctg ttcatgttta aacgtatacg aa atg ttg gga tac atc tgg naa 113
Met Leu Gly Tyr Ile Trp Xaa

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                                -25
caa gac aaa gtc ttt gct aat tgt gtt cta ttt acg ctc tta gtg tct      161
Gln Asp Lys Val Phe Ala Asn Cys Val Leu Phe Thr Leu Leu Val Ser
-20                -15                -10                -5
aca aga tcc ggg aga tcg cgs gcg ggt tgt gcc tgg agg tgg agg gga      209
Thr Arg Ser Gly Arg Ser Arg Ala Gly Cys Ala Trp Arg Trp Arg Gly
                1                5                10
aga tgg tca gta gga cag aag ggc hgg g      237
Arg Trp Ser Val Gly Gln Lys Gly Xaa
                15                20
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<210> 314
<211> 356
<212> DNA
<213> Homo sapiens

<220>
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<221> sig_peptide
<222> 272..316
<223> Von Heijne matrix
score 5.59999990463257
seq LILSLQVCRPATL/DQ

<221> misc_feature
<222> 275..276
<223> n=a, g, c or t
Oligonucleotide

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ggatttgctt tctttttctc caaaagggga ggaaattgaa actgagtggc ccacgatggg      60
aagaggggaa agcccagggg tacaggaggc ctctgggtga aggcagaggc taacatgggg      120
ttcggagcga ccttgccgtg tggcctgacc atctttgtgc tgtctgtcgt cactatcatc      180
atctgcttca cctgctcctg ctgctgcctt tacaagacgt gccgccgacc acgtccgggt      240
gtcaccacca ccacatccac cactgtggtg c atg nnc ctt atc ctc agc ctc      292
                                Met Xaa Leu Ile Leu Ser Leu
                                -15                -10
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caa gtg tgc cgc cca gct acc ctg gac caa gct acc agg gct acc aca      340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
                -5                1                5
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cca tgc cgc cta cgg g      356
Pro Cys Arg Leu Arg
                10
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<210> 315
<211> 162
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
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 <223> Von Heijne matrix
 score 5.59999990463257
 seq VLMLSLPLPPTPQ/QA

<400> 315
 tacatgtgca gaatgtgcag atttgtcaca taggtgtgt atg tgc cac agg cgt 54
 Met Cys His Arg Arg
 -35
 tgg ctg cac cta tca acc cgt cat cta ggt ttt aag ccc cgc atc cat 102
 Trp Leu His Leu Ser Thr Arg His Leu Gly Phe Lys Pro Arg Ile His
 -30 -25 -20
 tac gta ttt gtc tta atg ctg tcc ctc ccc ttg ccc ccc acc ccc caa 150
 Tyr Val Phe Val Leu Met Leu Ser Leu Pro Leu Pro Pro Thr Pro Gln
 -15 -10 -5
 cag gcc ctc ggg 162
 Gln Ala Leu Gly

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 <210> 316
 <211> 404
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 297..404
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 <221> sig_peptide
 <222> 297..353
 <223> Von Heijne matrix
 score 5.59999990463257
 seq FVIFPAALLLCWG/GL

<400> 316
 taagctgaaa aagaatataa aaattaaaga gaaattgaaa atctaagtct tgcagtgaga 60
 atgaccagaa atcgtttccc tctctggggg gttcctgttt aatatgaaag tcctcttaac 120
 aagcgtggac agaggaagtt ttaggtttga ttggaacttc atgtacatga catatttcat 180
 ttttttttct tccctcacia atttcaaccc aggccacttg tttgcagaga ctgccaaacc 240
 ttccattgct gcttccaaga tactcctgga atctgagatt accttttata ctcttg atg 299
 Met
 gac cat gtt gtt att ttt gtc att ttc cct gca gct ctt ctg ctt tgc 347
 Asp His Val Val Ile Phe Val Ile Phe Pro Ala Ala Leu Leu Leu Cys
 -15 -10 -5
 tgg gga gga ctc atc ccc cta tgc atc atc tac ccc ccg ata gct gac 395
 Trp Gly Gly Leu Ile Pro Leu Cys Ile Ile Tyr Pro Pro Ile Ala Asp
 1 5 10
 aca gtt ggg 404
 Thr Val Gly
 15

<210> 317

<211> 450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 359..448

<221> sig_peptide
 <222> 359..433
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LIIILXFDIYSLA/FI

<221> misc_feature
 <222> 323,410
 <223> n=a, g, c or t
 Oligonucleotide

<400> 317
 tatgtctttt gaatttgtga tgtacatatt aacagtagat taagttgaaa taataaaaatc 60
 tgtattgttt atgatttatc agttatatga tgagtagaat atagtctatt gtggscmagt 120
 gtgtatatat aacataaaca atacattaac ccaattttgt gtgaaaatta ttttgggacc 180
 tagtagcttt cttgggcaca acctttcaaa caaacaattt ttttttaaata taattttttc 240
 ccttaataaa gaaaacaatt cctcaatgtg taatagcaaa taccttttaa caggtcatat 300
 atcatcaatg ctttctttga aancgtactg atgcttacaa gatgctttac gagtaaag 358
 atg ctt aca aat ctt ttc ttt caa gta gct cat cct ctg atc att att 406
 Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile
 -25 -20 -15 -10
 ctg ntg ttt gat atc tac tcc cta gca ttt atc cat gac gtg gg 450
 Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val
 -5 1 5

<210> 318
 <211> 395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 313..393

<221> sig_peptide
 <222> 313..354
 <223> Von Heijne matrix
 score 5.59999990463257
 seq LFGLRGMLPLTQQ/AP

<400> 318
 aatcgaaaac agcaaatacac acaactgtta aaaatatattt vtgtttacaa agccaagcca 60
 aaattttatg ttttctctcc caaactttga tataaacact aacatttttt agcatgtata 120
 aacatcatta ttaaccagtg tcctattaaa actccttttc tatgatagaa tgtctgttrc 180
 ttttaggtgg ataaggccta gatgattggc ctctaccagc atcctcatct ctgtccctga 240
 tgcccagctt carcctcgct cctgyatgct ggaccgcttc agtghagctc tcagacttgc 300

tctgtgtctc ac atg cty ttt ggc tta cgt gga atg ctc cca ctc acc cag 351
Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln
-10 -5
caa gct ccc att cct cat tta aga tgt aaa ttg agt gtc acc tc 395
Gln Ala Pro Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr
1 5 10

<210> 319
<211> 257
<212> DNA
<213> Homo sapiens

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<222> 20..256

<221> sig_peptide
<222> 20..82
<223> Von Heijne matrix
score 5.59999990463257
seq ACVYACVCASVSA/CV

<400> 319
catctgtgtg tgcgtgtgt atg cgt gtg tgt atg cgt ctg tgt gca tgt gtg 52
Met Arg Val Cys Met Arg Leu Cys Ala Cys Val
-20 -15
tat gcg tgt gtg tgc gca tca gtg tct gca tgt gtg tat rtg tgt gta 100
Tyr Ala Cys Val Cys Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val
-10 -5 1 5
tgt atg tst gtg cgc gcg cat ctg tgt gtg tgc atg tgt gta tgt atg 148
Cys Met Xaa Val Arg Ala His Leu Cys Val Cys Met Cys Val Cys Met
10 15 20
tgt gtg cat ctc tgt gtg tgc atg tgt gta tgt gtg tgt gca tct gtg 196
Cys Val His Leu Cys Val Cys Met Cys Val Cys Val Cys Ala Ser Val
25 30 35
tgt gtg tgc atg tgt gca tgc gtg tgt atg tgt gtg tgc gtg cgt gca 244
Cys Val Cys Met Cys Ala Cys Val Cys Met Cys Val Cys Val Arg Ala
40 45 50
tct gtg tgt gtg c 257
Ser Val Cys Val
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<210> 320
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 256..324

<221> sig_peptide
<222> 256..318
<223> Von Heijne matrix

score 5.59999990463257
seq LIANLVLFIISIAA/LR

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<400> 320
accacgcctc ctccaagtcc cagcgaaccc gcgtgcaacc tgtccctaaa aaagccaaag      60
cagtcactct ttacctccca ctttcctccc tcccagcctt tggcaaccac taatctactt      120
tccgtgtata tggatttacc tattcaggac atttcatatg tcctttggtg actggcttct      180
ttcactttgc acaatgtttt taaggttcat tcctgtcata gtgtgtgtca gtacgaaccc      240
ctccttaacc atcta atg gtt atc acc tct aat agt tat ctc ata gcc aat      291
                Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn
                -20                -15                -10
ctt gtt tta ttt ata tct atc gcc gcc ctc cgg g      325
Leu Val Leu Phe Ile Ser Ile Ala Ala Leu Arg
                -5                1
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<210> 321
<211> 201
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 31..201
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<221> sig_peptide
<222> 31..183
<223> Von Heijne matrix
      score 5.5
      seq LSLHASLVTKAFS/IN
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<400> 321
catcacaaga acccagagtg gaattctggg atg gaa gag ctg gac aga aag tgg      54
                Met Glu Glu Leu Asp Arg Lys Trp
                -50                -45
aga gag aag gtc ctc cca gcg gca aag cta att aaa agg aga aac ctg      102
Arg Glu Lys Val Leu Pro Ala Ala Lys Leu Ile Lys Arg Arg Asn Leu
                -40                -35                -30
ttt tcc aca tgc act cct caa tat ggy aca cat gct gct ttc ttg tca      150
Phe Ser Thr Cys Thr Pro Gln Tyr Gly Thr His Ala Ala Phe Leu Ser
                -25                -20                -15
tta cat gcc tca ctt gtc acc aaa gca ttt tca atc aat tcc tgg gag      198
Leu His Ala Ser Leu Val Thr Lys Ala Phe Ser Ile Asn Ser Trp Glu
                -10                -5                1                5
tgg      201
Trp
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<210> 322
<211> 159
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 77..157
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<221> sig_peptide
 <222> 77..151
 <223> Von Heijne matrix
 score 5.5
 seq PLLLCPLSSGSPC/PR

<400> 322
 aacaaaggga cagaatggtc ccagggttcc ttcttcttcc ttccagttaa gagctcagag 60
 tggaagtggg ctgggg atg gtg tgc ggg gcc caa gct ccc agc tcc caa agg 112
 Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg
 -25 -20 -15
 ccc ctg ctt cta tgc cct ttg agc tca ggt agc ccc tgc ccc cgg gg 159
 Pro Leu Leu Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg
 -10 -5 1

<210> 323
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<221> sig_peptide
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 <223> Von Heijne matrix
 score 5.5
 seq SFLPSLLSSFLLS/LP

<221> misc_feature
 <222> 117
 <223> n=a, g, c or t
 Oligonucleotide

<400> 323
 catgcaggat agtaatacgt tagaatcaaa aataagggtta tacttagaaa atattgattt 60
 gcctttttga ttttgcattg gtataatctg gctctgaaat cagtgcacag aagtganctt 120
 cgaaacaagc ctgagcaata gaagtagatg tggaaataac ttcggtttct caaggcaaat 180
 actttgatag gaacaaacaa ccgttttagat atagaagatg tgatacatte ctttaaaaag 240
 aatttgacct tatgtcattg taggcacacc tcatatttca attattcata tagtttttct 300
 tgagcaattg ctggtttaag aata atg tca tgt ctt ttg cgt gct tat atc 351
 Met Ser Cys Leu Leu Arg Ala Tyr Ile
 -25 -20
 att tgg ata ttt cct tcc ttc ctt cct tcc ctg ctt tct tcc ttc ctt 399
 Ile Trp Ile Phe Pro Ser Phe Leu Pro Ser Leu Leu Ser Ser Phe Leu
 -15 -10 -5
 ctt tcc ctg ccc cct tcc ggg 420
 Leu Ser Leu Pro Pro Ser Gly
 1 5

<210> 324
 <211> 210

<212> DNA
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<220>
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 <222> 9..209

<221> sig_peptide
 <222> 9..116
 <223> Von Heijne matrix
 score 5.5
 seq LHFVYCFLCCAEA/FL

<400> 324
 ctcccttat atg ttt cag tta ctg atc ctt tgt cag atg aat agt ttg aaa 50
 Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys
 -35 -30 -25
 ata ttt tct ccc att ctt gga tgg tct ctt cat ttt gtt tat tgt ttc 98
 Ile Phe Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe
 -20 -15 -10
 ctt tgc tgt gca gaa gcc ttt tta ctt gat atg atc cca ttt atg caa 146
 Leu Cys Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln
 -5 1 5 10
 ttt tac ttt ggt tac ctg tgc ttg tgg ggt att act tta aaa atc ttt 194
 Phe Tyr Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe
 15 20 25
 gcc cag tcc aat tgg g 210
 Ala Gln Ser Asn Trp
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<210> 325
 <211> 192
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 31..192

<221> sig_peptide
 <222> 31..174
 <223> Von Heijne matrix
 score 5.5
 seq VCLRLHVLSAVQT/ER

<400> 325
 aggctgctgc agttggcgma tgaggcgacc atg gcc ttg ctg ggt aag cgc tgt 54
 Met Ala Leu Leu Gly Lys Arg Cys
 -45
 gac gtc ccc acm aac ggc tgc gga ccc gac cgc wgg aam wac ggc gwy 102
 Asp Val Pro Thr Asn Gly Cys Gly Pro Asp Arg Xaa Xaa Xaa Gly Xaa
 -40 -35 -30 -25
 aac ccg caa ara cga gat cat cac cag cmt mgt gtc tgc ctt aga ctc 150
 Asn Pro Gln Xaa Arg Asp His His Gln Xaa Xaa Val Cys Leu Arg Leu

score 5.5
seq ILLISTLFYSLLS/GS

```
<400> 329
acacttaacc catctgtttt ctctaatacg cgacagattc ctttcagaca ggacaactgt      60
gatatctcag ttcctgattg taaatacctc ctaagcctga agcttctgtt actagccatt      120
gtgrgcttca gktctttcak yckgcaaa atg ggc ata ata car kct att ctt      172
                               Met Gly Ile Ile Gln Xaa Ile Leu
                               -45                               -40
gcc aca tca agg gat tgt tat tcc ttt aaa aaa aaa cca ata cca aag      220
Ala Thr Ser Arg Asp Cys Tyr Ser Phe Lys Lys Lys Pro Ile Pro Lys
                               -35                               -30                               -25
aag cct aca atg ttg gcc tta gcc aaa att ctg ttg att tca acg ttg      268
Lys Pro Thr Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu
                               -20                               -15                               -10
ttt tat tca ctt cta tcg ggg agc cat gga aaa gra aat caa gac gtg      316
Phe Tyr Ser Leu Leu Ser Gly Ser His Gly Lys Xaa Asn Gln Asp Val
                               -5                               1                               5                               10
gg                                                                 318
```

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<210> 330
<211> 223
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 135..221

<221> sig_peptide
<222> 135..203
<223> Von Heijne matrix
score 5.5
seq LPFVCLLLRNVS/DL
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<400> 330
aacagtgtgt gagagttccc ttctctccac atcctcgcca gcactctgtta ttgcctgtct      60
ttttgatacg agccttttta acaggggtaa gatgatatct cattgtagtt ttgatttgca      120
ttctctgatg atca atg atg ttg agc acc ttt tca tat gcc tgt ttg cca      170
                               Met Met Leu Ser Thr Phe Ser Tyr Ala Cys Leu Pro
                               -20                               -15
ttt gta tgt ctt ctt ttg aga aat gtc tat tca gat ctt ttg ccc aat      218
Phe Val Cys Leu Leu Leu Arg Asn Val Tyr Ser Asp Leu Leu Pro Asn
                               -10                               -5                               1                               5
cgg gg                                                                 223
Arg
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<210> 331
<211> 362
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
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<222> 272..361

<221> sig_peptide

<222> 272..343

<223> Von Heijne matrix

score 5.5

seq LIVVLVCISLVII/DD

<400> 331

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aatggacacc taggttgctt ccatactctga gctattgtga ataatgctgc aatgaacatg      60
ggagtggaga catctcctaa gcatactgat ttcagttcct ttgggtatat acccagaagt      120
gggatcatgt ggtaatcttg tttttacttt tttgaggaac ctccatacca ttatccatga      180
tggctatagt aatttacatt cataccagca gtgcacaagg gtctcctttt ctgtatacac      240
ttgccaacac ttgttatctt tcattttttt g atg cta gcc att cta aca ggt      292
                                   Met Leu Ala Ile Leu Thr Gly
```

-20

```
ggg agg tgg tat ctc ata gtg gtt tta gtt tgc att tcc ttg gtg att      340
Gly Arg Trp Tyr Leu Ile Val Val Leu Val Cys Ile Ser Leu Val Ile
-15                               -10                               -5
```

```
att gat gat gat gag cac ggg g      362
Ile Asp Asp Asp Glu His Gly
1                               5
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<210> 332

<211> 89

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 34..87

<221> sig_peptide

<222> 34..75

<223> Von Heijne matrix

score 5.5

seq LLPLGLKVLGLQA/RG

<400> 332

```
cccagaccgg tcttgaactc ctggcctcaa ctg atg ctc ctg cct ctg ggt ctc      54
                                   Met Leu Leu Pro Leu Gly Leu
                                   -10
```

```
aaa gtg ctg gga tta cag gcg aga ggc acc acg ct      89
Lys Val Leu Gly Leu Gln Ala Arg Gly Thr Thr
-5                               1
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<210> 333

<211> 399

<212> DNA

<213> Homo sapiens

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<221> sig_peptide
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 <223> Von Heijne matrix
 score 5.5
 seq PTLVVMWLSPQMA/SS

<400> 333
 ttcaactgcaa ggcggcgcca ggagaggttg tgggtgctagt ttctctaagc catccagtgc 60
 catcctcgtc gctgcagcga cacacgtctt cgccgccgcc atgactgagc agatgaccct 120
 tcgtggcacc ctcaagggcc acaacggctg ggtaaccag atcgctacta ccccgagtt 180
 cccggacatg atcctctccg cctctcgagg tacggactaa gataagacca tcatcatgtg 240
 gaaactgacc aggg atg aga cca act atg gaa ttc cac agc gtg ctc tgc 290
 Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys
 -25 -20
 ggg gtc act ccc act ttg tta gtg atg tgg tta tct cct cag atg gcc 338
 Gly Val Thr Pro Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala
 -15 -10 -5
 agt tcg ccc tct cag gct cct ggg atg gaa ccc tgc gcc tct ggg atc 386
 Ser Ser Pro Ser Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile
 1 5 10 15
 tca caa cgg gca a 399
 Ser Gln Arg Ala
 20

<210> 334
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 33..188

<221> sig_peptide
 <222> 33..131
 <223> Von Heijne matrix
 score 5.5
 seq SLCLLTAVLVLT/FK

<400> 334
 aatgaaggggt actagaacac ctgcccattcc at atg gga aaa aaa aaa atc tgg 53
 Met Gly Lys Lys Lys Ile Trp
 -30
 acc cct agc tca tat ccc atg ccc agt cat aaa cat gta tcc cta tgt 101
 Thr Pro Ser Ser Tyr Pro Met Pro Ser His Lys His Val Ser Leu Cys
 -25 -20 -15
 ctt cta acg gtt gca gtt tta gtt ctt aca ttt aag tct tta att cat 149
 Leu Leu Thr Val Ala Val Leu Val Leu Thr Phe Lys Ser Leu Ile His
 -10 -5 1 5
 ttt gag tda att ttt gca tat gag ata ggg gtc cag ggg 188
 Phe Glu Xaa Ile Phe Ala Tyr Glu Ile Gly Val Gln Gly
 10 15

<210> 335
 <211> 115
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 23..115

<221> sig_peptide
 <222> 23..94
 <223> Von Heijne matrix
 score 5.5
 seq CPSLLSPIPSQA/CP

<400> 335
 ccaatacaca tcactcagtg gc atg agc cct gtc ctc tgc ttc cat cgc tgc 52
 Met Ser Pro Val Leu Cys Phe His Arg Cys
 -20 -15
 tcc tgt ccc tcc ctc ctc agc ccc atc tcc cca tcc cag gcc tgt cct 100
 Ser Cys Pro Ser Leu Leu Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro
 -10 -5 1
 gag ccc ctc ctt ggg 115
 Glu Pro Leu Leu Gly
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<210> 336
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 197..298

<221> sig_peptide
 <222> 197..268
 <223> Von Heijne matrix
 score 5.5
 seq IMFVCMCVVCVC/VY

<400> 336
 catgcttggt gtaacgtgtc aaacaatata gaggtgtagg gaaaatacct agtgccaccc 60
 tccactccaa aaccccatgt cgccagagat aaccatttat tcagacagtg agtatctatt 120
 aagtatctat tgctaggctt tggagatagc ataatgaaca aaatggatgt gctctctgcc 180
 cttgtgattt ggacag atg ctt cag tta tct ttt tct gtg ttt ata ttg att 232
 Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile
 -20 -15
 atg ttt gta tgt atg tgc gtg tgt gtg tgt gtg tat cga ctg 280
 Met Phe Val Cys Met Cys Val Cys Val Cys Val Cys Val Tyr Arg Leu
 -10 -5 1
 ttt tct tcc tcc tcc ccg gg 300
 Phe Ser Ser Ser Ser Pro
 5 10

<210> 337
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..307

<221> sig_peptide
 <222> 5..277
 <223> Von Heijne matrix
 score 5.5
 seq RVLLGAGIPPVSS/AP

<400> 337
 caca atg aag tcg act gtt tcg tcg agg gaa gtg gcc acc gtt gat aaa 49
 Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys
 -90 -85 -80
 atg aaa aga cgc cat gca gaa tac tgt gca cag ggt ctc cag aga ttt 97
 Met Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe
 -75 -70 -65
 aaa gcc caa ctt tct caa gat acc ctt ccc cav cat cca cat ctg gag 145
 Lys Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu
 -60 -55 -50 -45
 awa gag aag ggg ctt gaa ggc ttg gag gaa aat gtg cct cta aag gga 193
 Xaa Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly
 -40 -35 -30
 gag aaa cct gga gaa ggg ggt cca gag tct cct aag aag aga aga agg 241
 Glu Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg
 -25 -20 -15
 gtg ctt ctc gga gcg ggc atc cca cca gta agc tca gct ccc agg aga 289
 Val Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg
 -10 -5 1
 cag agc cag cag gca aca 307
 Gln Ser Gln Gln Ala Thr
 5 10

<210> 338
 <211> 123
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..123

<221> sig_peptide
 <222> 16..75
 <223> Von Heijne matrix
 score 5.5
 seq VHLFFFFFFXETGS/RS

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<400> 338
ttaaattaaac tgtgg atg cac aac agt tgt aga cct gtg cac ctt ttt ttc 51
Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe
-20 -15 -10
ttt ttt ttt yct gag aca ggt tct cgt tct aat ycc tgg ctg gag tsc 99
Phe Phe Phe Xaa Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa
-5 1 5
agt ggt gcg atc ata gct aac tcc 123
Ser Gly Ala Ile Ile Ala Asn Ser
10 15

<210> 339
<211> 451
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 318..449

<221> sig_peptide
<222> 318..443
<223> Von Heijne matrix
score 5.40000009536743
seq TFRLLSLPVSQA/GP

<221> misc_feature
<222> 310..311,394
<223> n=a, g, c or t
Oligonucleotide

<400> 339
gtcacaaaag gagcactaag agcctgcttt actttcttcc tcagttgagt cgtggggaca 60
gcttgaagga gccaacctca attgcagaga gcagcgtca cccagctac cgctcagagc 120
ccagcttgga accagagagc ttccgttctc ctacctttgg caaaagtgtt cacttcgac 180
cactatccag tggetcaagc tctccagcc tcaagtcagc ccagggcaca ggctttgagc 240
tgggccagtt gcaatccatt cgttcagagg gcaccacctc cacctcctaa taagagcctg 300
gccaccagn nacgcaa atg gaa gcc tat ctt aat gac agc ttg ctc aca 350
Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr
-40 -35
cct tca gac agc cct gat ttt gag tca gtg cag gca ggg cct gna gcc 398
Pro Ser Asp Ser Pro Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala
-30 -25 -20
aga ccc acc ttt agg cta tac ctc tcc ctt cct gtc agc cag gct ggc 446
Arg Pro Thr Phe Arg Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly
-15 -10 -5 1
cca gc 451
Pro

<210> 340
<211> 304
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 94..303

<221> sig_peptide
 <222> 94..135
 <223> Von Heijne matrix
 score 5.40000009536743
 seq PALGPALLQGSLX/RV

<221> misc_feature
 <222> 244..245
 <223> n=a, g, c or t
 Oligonucleotide

<400> 340
 gcgcagggga gaaacaaggc gccttggagt tcaggtgact cccacacggg tcatgctgtt 60
 gtctcctgat ccagccggcc ctgccaggtg acc atg cct gct ctg ggc cca gct 114
 Met Pro Ala Leu Gly Pro Ala
 -10
 ctt ctc cag ggc tct ctg kgc cgv gtg ggt cct cac cct cca gcs cct 162
 Leu Leu Gln Gly Ser Leu Xaa Arg Val Gly Pro His Pro Pro Ala Pro
 -5 1 5
 toc acc aac tgc att cac tcc caa tgg cac gta tct gca gca csk ggc 210
 Ser Thr Asn Cys Ile His Ser Gln Trp His Val Ser Ala Ala Xaa Gly
 10 15 20 25
 aag gga ccc cac ctc agg cac cct ctr sct ggg nns tac caa ctt cct 258
 Lys Gly Pro His Leu Arg His Pro Leu Xaa Gly Xaa Tyr Gln Leu Pro
 30 35 40
 gtt cca gct gag ccc tgg gct gca gct gga ggc cac agt gtc cac c 304
 Val Pro Ala Glu Pro Trp Ala Ala Gly Gly His Ser Val His
 45 50 55

<210> 341
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 315..377

<221> sig_peptide
 <222> 315..371
 <223> Von Heijne matrix
 score 5.40000009536743
 seq LCCSGCVPSLCCS/SY

<400> 341
 gtagccgccg ccgaaacttc cgccgccgcg tccgccgcct ccggaactaa acggggtgag 60
 gtcacattcg gttatctcta acgttggaaa acgatggagc taacacccat tatggagatt 120
 aamcvacttt tcatcaggtt tttaacttaa gtcgtgagga atacaacggt gaacacaaga 180
 ttcattttat tttcatcacc atgggacgta tcctgttggt gagttctctg ggtcagacct 240
 ctgaagactt ctcagatgga tcctagtctc wrrgcttgcc ctgaaattac tcgctgctca 300

gggagagagt tgaa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt 350
Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys
-15 -10

gtc ccc tcg ctc tgt tgt tcc agc tat gt 379
Val Pro Ser Leu Cys Cys Ser Ser Tyr
-5 1

<210> 342
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..288

<221> sig_peptide
<222> 223..264
<223> Von Heijne matrix
score 5.40000009536743
seq AHSILLIASQAGC/LR

<400> 342
gggacccttt tagctatgaa atattttgga ttgcgtaggg tcttgcgag cgcgaaaagt 60
agcgtggggcc aggacagcgg gaggtaagtc gccaagaaaa gggttgggaa ragctcagaa 120
tcggacggct aggaagaaat gacccaaagg agcctgatag cccctattc tgcacgctgt 180
tcctggaaac cgcctttgca aagacagtga gagaaatcta ac atg gct cac tcc 234
Met Ala His Ser
atc ttg ctt cta gcc tcg cag gcc ggc tgt ctt cgc tca ttc ctg ggc 282
Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg Ser Phe Leu Gly
-10 -5 1 5
aat tgg g 289
Asn Trp

<210> 343
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..167

<221> sig_peptide
<222> 78..137
<223> Von Heijne matrix
score 5.40000009536743
seq WVFLVAIFKGVHC/EG

<400> 343
agctctggga gaggagcccc cgccctggga ttcccaggtg ttttcatttg gtgatcagca 60
ctgaacacag aagagtc atg acg gag ttt ggg ctg agc tgg gtt ttc ctt 110
Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu
-20 -15 -10

gtt gct att ttt aaa ggt gtc cac tgt gaa ggt cma att ggt gga gtc 158
 Val Ala Ile Phe Lys Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val
 -5 1 5

ggg ggg gcg gg 169
 Gly Gly Ala
 10

<210> 344
 <211> 112
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..110

<221> sig_peptide
 <222> 63..104
 <223> Von Heijne matrix
 score 5.40000009536743
 seq NTVFLLLLFFGCFF/FE

<400> 344
 tgtgttttct ctgtcccaaa ttaaattgcat tggggaagtt tataattaca ggaattccac 60
 gc atg aac act gtt ttt ttg ttg ttg ttt ttt ggt tgt ttt ttt ttt 107
 Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe
 -10 -5 1

gag ac 112
 Glu

<210> 345
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 207..347

<221> sig_peptide
 <222> 207..278
 <223> Von Heijne matrix
 score 5.40000009536743
 seq SCCCLSSSSFIAG/RR

<400> 345
 tcatcgtcta cgtggacggc agctggagcc cgtggagcaa gtggtcggcc tgtgggctgg 60
 actgcaccca ctggcggacc gtgagtgtc tgaccagca ccccgcaacg gaggggagga 120
 gtgccagggc actgacctgg acaccgcaa ctgtaccagt gacctctgtg tacacactgc 180
 ttctggccct gaggacgtgg cctct atg tgg gcc tca tcg ccg tgg ccg tct 233
 Met Trp Ala Ser Ser Pro Trp Pro Ser
 -20

gcb tgg tcc tgc tgc tgc ttg tcc tca tcc tcg ttt att gcc gga aga 281
 Ala Trp Ser Cys Cys Cys Leu Ser Ser Ser Ser Phe Ile Ala Gly Arg

-15		-10		-5		1	
agg	agg	ggc	tgg	act	cag	atg	tgg
Arg	Arg	Gly	Trp	Thr	Gln	Met	Trp
		5					10
							15
gct	tcc	agc	ccg	tca	gca	tc	
Ala	Ser	Ser	Pro	Ser	Ala		
		20					

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349

<210> 346
<211> 191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..191

<221> sig_peptide
<222> 45..143
<223> Von Heijne matrix
score 5.40000009536743
seq FMLIILSAILLNS/FI

<400> 346	
cottocatag	gtggtgtacc
gttttgcatt	cccatcagca
ctgt	atg
aca	atg
ccc	
	Met
	Thr
	Met
	Pro
	-30

56

att	tct	tca	tat	tcc	cag	aat	gtg	tig	tca	aac	ttt	cac	gat	ggc	tat
Ile	Ser	Ser	Tyr	Ser	Gln	Asn	Val	Leu	Ser	Asn	Phe	His	Asp	Gly	Tyr
			-25						-20				-15		
ttt	atg	tta	att	ata	ctt	tct	gcc	att	tta	cta	aat	tct	ttt	att	ggg
Phe	Met	Leu	Ile	Leu	Ser	Ala	Ile	Leu	Leu	Asn	Ser	Phe	Ile	Gly	
			-10					-5			1				
tgt	gtc	agc	ttt	tat	cat	tgc	ttt	tct	tgg	ggg	tca	ggg			
Cys	Val	Ser	Phe	Tyr	His	Cys	Phe	Ser	Trp	Gly	Ser	Gly			
	5					10				15					

104
152
191

<210> 347
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..227

<221> sig_peptide
<222> 144..203
<223> Von Heijne matrix
score 5.40000009536743
seq LSLVIFLLTVKHC/FR

<400> 347	
tttcatatag	ccacctcttc
ttggtagcca	gaagaccott
cggatgatgc	cccaggtgta

60

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aaactctctg gggcccgccc cactcggaag gattactgaa atgagtcatt tccgggacgc 120
cttttttact gttgaatgaa agg atg cta aca cat ggg gct tcc ctg tct tta 173
                               Met Leu Thr His Gly Ala Ser Leu Ser Leu
                               -20                               -15

gtc ata ttt ctg tta aca gtg aag cat tgc ttt aga tac aga gta tac 221
Val Ile Phe Leu Leu Thr Val Lys His Cys Phe Arg Tyr Arg Val Tyr
-10                               -5                               1                               5
aag act tt 229
Lys Thr

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<210> 348
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..210
 <221> sig_peptide
 <222> 106..171
 <223> Von Heijne matrix
 score 5.40000009536743
 seq FWTSIPILPLSSG/RQ

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<400> 348
aaagaatcca gttgagccta tcgggacttt tgacctacag aactgtgaga taaaaaatgg 60
gtgtcgtttt agataacca tggcagcatt ccctcctctg ctgga atg tcg tca gtg 117
                               Met Ser Ser Val
                               -20

gag act gac tgg gga ttc tgg act tcc atc ccc atc ctc cca ctc agc 165
Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile Leu Pro Leu Ser
-15                               -10                               -5

agt ggt agg cag ctc ccc ctc ccc act aga gaa tgg gga atg tgg 210
Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp Gly Met Trp
1                               5                               10

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<210> 349
 <211> 431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 184..429
 <221> sig_peptide
 <222> 184..282
 <223> Von Heijne matrix
 score 5.40000009536743
 seq LSAILSMLSLSFS/TT

<221> misc_feature
 <222> 214

<223> n=a, g, c or t
Oligonucleotide

<400> 349

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aggacatcct ctccaatcca ccacacacca ccttaccctt ctgctggcaa gaggggacct      60
gattcatcct cagcctaaac actcattcta cccaactgat tgagacagaa cagaagataa      120
ctgaaacttc tctgccttcc cgctgcaaga agtgaatgag cgatccctct caactgactk      180
raa atg ttt gcc tca ccc agg aga tgg agc tct ncg aag gcc ttc tct      228
    Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser
          -30                -25                -20
ggc cag cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc      276
Gly Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser
          -15                -10                -5
ttc tcc aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag      324
Phe Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln
          1                5                10
aag gtg ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt      372
Lys Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe
          15                20                25                30
gac atg cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag      420
Asp Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu
          35                40                45
gtg gta mma ta      431
Val Val Xaa
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<210> 350

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 197..385

<221> sig_peptide

<222> 197..244

<223> Von Heijne matrix

score 5.40000009536743

seq HSVFLCAPALVFP/RP

<400> 350

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aaagtaaagc ggaggcagcg ggggaagatg gcggcggccg ttccacagcg ggcgtggacc      60
gtggagcagc tgcgcagtga gcagctgcc aagaaggaca ttatcaagtt tctgcaggaa      120
cacggttcag attcggtagc agaggcgtag ggcgcggccg gctggtgcgg ctgagggagc      180
cctcaacccc ctggag atg ccc ata cat tcc gta ttc ctc tgt gcc ccc gcc      232
    Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala
          -15                -10                -5
ctc gtc ttc ccg cgg ccg gtg gcc tgg aag gcg gag agg ccc agc ttg      280
Leu Val Phe Pro Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu
          1                5                10
tgc ttt ggt gcc tcg ctc ccg cct ctc ggg cgt tct cta ctg ggg cag      328
Cys Phe Gly Ala Ser Leu Pro Pro Leu Gly Arg Ser Leu Leu Gly Gln
          15                20                25
ggg agc agc ttt att tct tgg ggc aca cag gct gca att gta gag tta      376
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Gly Ser Ser Phe Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu
 30 35 40

kaa cct cat t
 Xaa Pro His
 45

386

<210> 351
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..307

<221> sig_peptide
 <222> 68..253
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LACVFFLSHPLFX/XP

<221> misc_feature
 <222> 279
 <223> n=a, g, c or t
 Oligonucleotide

<400> 351
 ttttactctg taattgttac taattgattt ttgmataggg agcacattcc catggttcaa 60
 aattcaa atg gta tac gat gaa aaa tct ctc tcc tgt tcc cat acc cca 109
 Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro
 -60 -55 -50
 gcc acc cag ttc ctc tcc tgg gat gca tcc agt gtt tac agt ttc tta 157
 Ala Thr Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu
 -45 -40 -35
 tat atc ctc tca gca aga gtt aat gta gac gta dgc agm tac att cgt 205
 Tyr Ile Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg
 -30 -25 -20
 gtg tac ata ctt gcc tgt gtg ttt ttc ctc tca cac ccc ctt ttt aad 253
 Val Tyr Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa
 -15 -10 -5
 sra cca aat ggt agt gta tat tgt cnm cgt cat tct ccc cct tac ctt 301
 Xaa Pro Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu
 1 5 10 15
 ttt tgc 307
 Phe Cys

<210> 352
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..169

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<221> sig_peptide
<222> 56..163
<223> Von Heijne matrix
      score 5.30000019073486
      seq VCLLIISLVLISG/LG

<400> 352
gttcctttggt gatacaaaca ctgtattttg agtaatcttt tccctatatt tcgaa atg      58
                                                    Met
ctg cct tta tca cct act aaa ttc cta aat gtg ttc ttg ggc ctg ttc      106
Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu Phe
-35                               -30                               -25                               -20
ctc tat tat ctt caa ttg gta tgt ctg ctt att att tct ttg gtt ttg      154
Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val Leu
                               -15                               -10                               -5
ata tct ggg tta ggg g      170
Ile Ser Gly Leu Gly
      1

<210> 353
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..292

<221> sig_peptide
<222> 149..235
<223> Von Heijne matrix
      score 5.30000019073486
      seq LNQTLMLLREVLA/SH

<400> 353
tttctaattct sbtcaaattt tatcaccata caatcagtggt taktgttggg aatagtgcaa      60
ctgcattatt gactaccatt gaagaaatgc atttgctaag caaaaaaata ttcttcaatt      120
agcttgaagt cttcatgcaa gtaaatta atg gac aag gtt gaa ctc cca cca      172
                               Met Asp Lys Val Glu Leu Pro Pro
                               -25
cct gat ctt gga cca agt tct gca cta aat cag aca ctc atg ttg ctg      220
Pro Asp Leu Gly Pro Ser Ser Ala Leu Asn Gln Thr Leu Met Leu Leu
-20                               -15                               -10
cgt gaa gtt tta gca tct cac gat tct tca gtk gta cca tta gat gct      268
Arg Glu Val Leu Ala Ser His Asp Ser Ser Val Val Pro Leu Asp Ala
-5                               1                               5                               10
cgt caa gct gat ttt gtg cag ggg g      293
Arg Gln Ala Asp Phe Val Gln Gly
      15

<210> 354
<211> 331
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 148..330

<221> sig_peptide

<222> 148..243

<223> Von Heijne matrix

score 5.30000019073486

seq LVWLWFVVPQTIT/MI

<221> misc_feature

<222> 124

<223> n=a, g, c or t

Oligonucleotide

<400> 354

catttctagc ttttgdktta aagtgcacaga cttgccactc ttcttttccc ttgaacactt 60

acaggetgtg ggaggggttat tagttggtct aatttcaata mtgttccttt cyccagggaa 120

ttgnraggcc caaggagagg gagagag atg ggg gga aca gct ggt tgg agc agt 174

Met Gly Gly Thr Ala Gly Trp Ser Ser

-30 -25

cag aac aca cac aac att kga gta cac cat ctt gtg tgg ctg tgg ttc 222

Gln Asn Thr His Asn Ile Xaa Val His His Leu Val Trp Leu Trp Phe

-20 -15 -10

gtg gtc ccc caa aca att aca atg ata aca cca aag atc act gaa cac 270

Val Val Pro Gln Thr Ile Thr Met Ile Thr Pro Lys Ile Thr Glu His

-5 1 5

aga cca sta ata aca gat atr dtr ata atg aya aca ttt gaa awa ttg 318

Arg Pro Xaa Ile Thr Asp Xaa Xaa Ile Met Xaa Thr Phe Glu Xaa Leu

10 15 20 25

gga gaa tta ccc a 331

Gly Glu Leu Pro

<210> 355

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 2..91

<221> sig_peptide

<222> 2..55

<223> Von Heijne matrix

score 5.30000019073486

seq ALYLCVCVCVCLI/AR

<400> 355

t atg tgt ctv agt gta gct ttg tat tta tgt gtg tgt gtg tgt gta tgt 49

Met Cys Leu Ser Val Ala Leu Tyr Leu Cys Val Cys Val Cys Val Cys

-15 -10 -5

ctg att gca cgg gtg tac ttt tgt att tat gtg tgt gtg tgg tt	93
Leu Ile Ala Arg Val Tyr Phe Cys Ile Tyr Val Cys Val Trp	
1 5 10	

<210> 356
 <211> 178
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..178

<221> sig_peptide
 <222> 92..133
 <223> Von Heijne matrix
 score 5.30000019073486
 seq LHLLFGLFPVLWM/FL

<400> 356	
tgacccttgt ccagtctttt ccaggaaaaa catgccctca agatgttttt ctatcttgag	60
gaaatgatgg aaatgagata gttccaaggg t atg ctt cac ctt ctt ttt ggc	112
Met Leu His Leu Leu Phe Gly	
-10	

tta ttt cct gtt ctt tgg atg ttt cta gtg tat ttc ttt ctt tct tct	160
Leu Phe Pro Val Leu Trp Met Phe Leu Val Tyr Phe Phe Leu Ser Ser	
-5 1 5	
ttt ttt ttt ttt ttt ttt	178
Phe Phe Phe Phe Phe Phe	
10 15	

<210> 357
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..105

<221> sig_peptide
 <222> 40..93
 <223> Von Heijne matrix
 score 5.30000019073486
 seq CVYLFCACMCVCA/FF

<221> misc_feature
 <222> 54
 <223> n=a, g, c or t
 Oligonucleotide

<400> 357	
tatatttata taaatatata taaatacaca catatatat atg tat gtg tgt atn	54
Met Tyr Val Cys Xaa	

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                                -15
tgt gtg tat ctt ttt tgt gca tgt atg tgt gta tgt gct ttt ttt ttt      102
Cys Val Tyr Leu Phe Cys Ala Cys Met Cys Val Cys Ala Phe Phe Phe
                   -10                   -5                   1

ttt tt      107
Phe

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<210> 358
<211> 209
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 44..208

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<221> sig_peptide
<222> 44..151
<223> Von Heijne matrix
      score 5.30000019073486
      seq FLFTLIGASLLQS/AS

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<400> 358
ggggggcgac gtaagggcgc tccgcgagcc cgtctctcct cga atg aaa sga aac      55
                                Met Lys Xaa Asn
                                -35
aac ctc cgg cga cag agc ccc gct ctc agg cac tgc tgg aga mcc gag      103
Asn Leu Arg Arg Gln Ser Pro Ala Leu Arg His Cys Trp Arg Xaa Glu
                   -30                   -25                   -20
acc gac ttc ttt ctc ttt acc ctc att ggc gct tct ctc ctg cag tcc      151
Thr Asp Phe Phe Leu Phe Thr Leu Ile Gly Ala Ser Leu Leu Gln Ser
                   -15                   -10                   -5
gcc tct ggg ccc tgc cgc att tct tsa smc tta aag tgg cat tct aaa      199
Ala Ser Gly Pro Cys Arg Ile Ser Xaa Xaa Leu Lys Trp His Ser Lys
1                   5                   10                   15
ggc act tta a      209
Gly Thr Leu

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<210> 359
<211> 298
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 135..296

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<221> sig_peptide
<222> 135..194
<223> Von Heijne matrix
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      seq LGLGLPLLPPNHP/SV

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<400> 359

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agcatttgcm ttcggagggc cagargggca ggcagagctt aattccttgg gcaaggctgg      60
ggctgttgga atggggtctg gagggccagga gccacctgt ctgggccaga aaggggcctk    120
ggtgcagggc aggc atg tgg ccc aag arg ggg cta ctg gga ttg ggg ctc      170
                Met Trp Pro Lys Xaa Gly Leu Leu Gly Leu Gly Leu
                -20                -15                -10
cca ctg ctg ccc cct aac cat ccc tcg gta gcc caa ggg aca ctc gtt      218
Pro Leu Leu Pro Pro Asn His Pro Ser Val Ala Gln Gly Thr Leu Val
                -5                1                5
tcc tcc cac tct ggt tct ggc tct gag ggt agg gtg gcg ctc agg agt      266
Ser Ser His Ser Gly Ser Gly Ser Glu Gly Arg Val Ala Leu Arg Ser
                10                15                20
gat gtc cac agc ccc aag aca acc csc caa cg      298
Asp Val His Ser Pro Lys Thr Thr Xaa Gln
25                30

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<210> 360
<211> 460
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..458

<221> sig_peptide
<222> 54..179
<223> Von Heijne matrix
score 5.30000019073486
seq AMAXLFLSAPPQA/EV

<221> misc_feature
<222> 150,285,328
<223> n=a, g, c or t
Oligonucleotide

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<400> 360
gagggtgggc tgccgtgctg ctggcgggcg ctgaggccaa atagttgcat cac atg      56
                                   Met
tat cta atc cga gag tct cat gct tct ggt agc tcc tca gtg acc agc      104
Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr Ser
-40                -35                -30
tcc tgc tca ctg mcc tca gra agc ccc aac cct cag gca atg gck ncc      152
Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala Xaa
-25                -20                -15                -10
ttg ttc ctg tct gcc cca ccc cag gcc gag gtg acc ttc gag gac gtg      200
Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp Val
                -5                1                5
gct gtg tac ctc tcc cgg gag gaa tgg ggc cgc ctg ggc cct gct cag      248
Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala Gln
                10                15                20
agg ggc bkc tac agg gac gtg atg ctg gag acc tac ngg aac bta gtc      296
Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa Val
                25                30                35
tca ctg gga gta gga cct gca ggc ccc aag cnt gga gtg atc tcg cag      344

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Ser	Leu	Gly	Val	Gly	Pro	Ala	Gly	Pro	Lys	Xaa	Gly	Val	Ile	Ser	Gln	
40					45				50						55	
ttg	gag	cga	ggg	gat	gag	ccc	tgg	gtc	ctg	gat	ggt	cag	ggc	acc	tct	392
Leu	Glu	Arg	Gly	Asp	Glu	Pro	Trp	Val	Leu	Asp	Val	Gln	Gly	Thr	Ser	
			60				65					70				
ggg	aaa	gag	cac	ctg	aag	aag	tca	aca	gcc	cag	ctc	ttg	gga	cca	gaa	440
Gly	Lys	Glu	His	Leu	Lys	Lys	Ser	Thr	Ala	Gln	Leu	Leu	Gly	Pro	Glu	
			75				80					85				
ctg	aag	tac	aag	gag	ttg	ay										460
Leu	Lys	Tyr	Lys	Glu	Leu											
			90													

<210> 361
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 153..317
 <221> sig_peptide
 <222> 153..263
 <223> Von Heijne matrix
 score 5.30000019073486
 seq ALSSLCVSWGTS/TV

<400> 361																
ctctttttccg	gttaacgcgg	cgtgagaagc	catgagcagc	aaagtctctc	gcgacaccct											60
gtacgaggcg	gtgcgggaag	tctgcacgg	gaaccagcgc	aasgccgcaa	gttcctggag											120
acggtggagt	tgcaggatca	gcttgaagaa	ct atg atc	ccc aga agg	aca agc											173
			Met Ile	Pro Arg	Arg Thr	Ser										
				-35												
gct tct cgg	gca ccg tca	gtc ccc caa	aac gca	ggc tta	agt cca	ctc										221
Ala Ser Arg	Ala Pro Ser	Val Pro Gln	Asn Ala	Gly Leu	Ser Pro	Leu										
-30		-25		-20		-15										
ccc gcc cta	agt tct ctg	tgt gtg tcc	tgg ggg	acc agc	agc act	gtg										269
Pro Ala Leu	Ser Ser Leu	Cys Val Ser	Trp Gly	Thr Ser	Ser Thr	Val										
		-10		-5		1										
acg agg cta	agg ccg tgg	ata tcc ccc	aca tgg	aca tcg	agg gcg	cg g										318
Thr Arg Leu	Arg Pro Trp	Ile Ser Pro	Thr Trp	Thr Ser	Arg Ala	Arg										
	5		10			15										

<210> 362
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 192..359

<221> sig_peptide
 <222> 192..233

<223> Von Heijne matrix
 score 5.30000019073486
 seq VCIFCFLTSKAFP/NP

<221> misc_feature

<222> 277

<223> n=a, g, c or t
 Oligonucleotide

<400> 362

tattgggttg	ttttcttatt	atcaaattgt	gaaagttctt	tacatattot	gggtagaact	60
cctttatcag	atacatgttt	tgcaaattgt	ttctaccatt	ctctgtctdh	tctttctctt	120
aatactttca	cagtttttca	tagcagaaat	ttataaatta	atgaagccca	ctttatactt	180
ttattttctt	t atg gtt tgc atc ttt	tgt ttc tta act tcg aaa gct ttt	230			
	Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe					
	-10	-5				
cct aac cct aga tca cag gat ttt ctc tta gat ttc tct agg cat tnt	278					
Pro Asn Pro Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa						
1 5 10 15						
ata ggt tta ggt ttc aca ttt agg tcc gca atg cat ttt gaa aac ttc	326					
Ile Gly Leu Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe						
20 25 30						
cgt ctg waa ggt ttg ggt caa gat tcc ctt tgt c	360					
Arg Leu Xaa Gly Leu Gly Gln Asp Ser Leu Cys						
35 40						

<210> 363

<211> 212

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 138..212

<221> sig_peptide

<222> 138..197

<223> Von Heijne matrix
 score 5.30000019073486
 seq GFCSVTSSPLASA/GR

<221> misc_feature

<222> 152

<223> n=a, g, c or t
 Oligonucleotide

<400> 363

cacaaaatca	aaaackkagt	tgacgtatgc	cactttccag	ttactattga	gatatatatg	60
cgtgtgtgta	tatattacat	atatatgta	tatatcatat	tkatatattt	akaaawttat	120
atmgavcata	catatat atg taw atr tat ktn kkt ava ggg ttt tgc tct	170				
	Met Xaa Xaa Tyr Xaa Xaa Xaa Gly Phe Cys Ser					
	-20	-15	-10			
gtc aca agc agt cct ctt gcc tca gca ggt agg act aca cgc	212					
Val Thr Ser Ser Pro Leu Ala Ser Ala Gly Arg Thr Thr Arg						

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<210> 364
<211> 242
<212> DNA
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<222> 127..240

<221> sig_peptide
<222> 127..195
<223> Von Heijne matrix
score 5.30000019073486
seq LVPCPLLISVALS/VK

<221> misc_feature
<222> 71,73
<223> n=a, g, c or t
Oligonucleotide

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actttaactt cctggagctc taatttctcc ttctcaggta gaagaatgcc attcactccc 60
aagtggtag nmncagcag ccagtgtag gaagggtcat caagtcagtt gtcagaaacc 120
tcaatk atg tca ctg twt ahg cta tgt gac cct gac cta gtt cct tgc 168
Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys
-20 -15 -10
cct ctc ttg atc tca gtt gct tta tct gta aaa ttt cac att tkt cag 216
Pro Leu Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln
-5 1 5
caa gtc aac ctt cca tgt tcc tct ca 242
Gln Val Asn Leu Pro Cys Ser Ser
10 15

<210> 365
<211> 248
<212> DNA
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<222> 7..246

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<223> Von Heijne matrix
score 5.30000019073486
seq LXPCLTSFSCXGA/SF

<400> 365
tgtaca atg atg atc ctt atc cta att ctt gag cat atc gtc acc kcc 48
Met Met Ile Leu Ile Leu Ile Leu Glu His Ile Val Thr Xaa
-35 -30

aaa aga aac ccc aaa cct gtt aca gtc cct got ttt ctg csc cct tgc	96
Lys Arg Asn Pro Lys Pro Val Thr Val Pro Ala Phe Leu Xaa Pro Cys	
-25 -20 -15 -10	
ttg act tct ttc tct tgt kct gga gca tct ttc tct ctk ttw ggt gdg	144
Leu Thr Ser Phe Ser Cys Xaa Gly Ala Ser Phe Ser Leu Xaa Gly Xaa	
-5 1 5	
aga agg ggt tgg caa cat ggc agc tgc tgc toc acc att ccc tta ttt	192
Arg Arg Gly Trp Gln His Gly Ser Cys Cys Ser Thr Ile Pro Leu Phe	
10 15 20	
csa act cta aat tcc ctt ggg cag gga ctc att ggc cca gcc tac ata	240
Xaa Thr Leu Asn Ser Leu Gly Gln Gly Leu Ile Gly Pro Ala Tyr Ile	
25 30 35	
ggg ggc gg	248
Gly Ala	
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<210> 366
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 seq HAISILLICIGASS/QG

<221> misc_feature
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 <223> n=a, g, c or t
 Oligonucleotide

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aaaacatata tccacacaaa aacttgcaca cataknttca tagcagcatt attcatccaa	60
aaagtagagg tactcaaagt actttcaact gataaacaca gatgaacaaa atgtatgtcc	120
aaacagtaga atattatttca gctataaaaa agaacagagt acacttagca aactaagaat	180
agaaggaact tcttcaatct gataaaggac atccatgaaa aaccaccac taatgtcata	240
cttaatcatg aaaaaccgaa tgcttttctc ctaagatagg aaaaagacaa gt atg tct	298
Met Ser	
-15	

act cat gcc atc tct att cta ctt tgt att ggt gct tct agc cag ggc	346
Thr His Ala Ile Ser Ile Leu Leu Cys Ile Gly Ala Ser Ser Gln Gly	
-10 -5 1	
agg gg	351
Arg	

<210> 367
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 score 5.19999980926514
 seq ATVNAASLPPCFG/VK

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 Met Glu Glu Gln Glu Thr Glu Val Gly Gly Arg Ser Ser
 -30 -25 -20
 cgg aaa aat gca gcc acc gtc aac gcc gcc tcc ctg cca ccg tgc ttc 96
 Arg Lys Asn Ala Ala Thr Val Asn Ala Ala Ser Leu Pro Pro Cys Phe
 -15 -10 -5
 ggg gta aaa agc tgc cgt tgc cgt cgg tgc agt tgc cgt cgc tgc ctc 144
 Gly Val Lys Ser Cys Arg Cys Arg Arg Cys Ser Cys Arg Arg Cys Leu
 1 5 10 15
 cta tac ttc tct tgg cct cgg gga agg att tcc cca ccg gtg gga caa 192
 Leu Tyr Phe Ser Trp Pro Arg Gly Arg Ile Ser Pro Pro Val Gly Gln
 20 25 30
 tgt gcg ggg agg gga t 208
 Cys Ala Gly Arg Gly
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<210> 368
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 <212> DNA
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<220>
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 <222> 11..445

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 <223> Von Heijne matrix
 score 5.19999980926514
 seq CCCHAGASSGATA/WE

<400> 368
 agaatccaag atg cgc ggg atc car gca aar ggg tct ccg ggc cag agt 49
 Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser
 -30 -25
 tcg gcc gst gtt ctg wcg cct tgc tgc tgt cac gcg ggc gct tcg tcc 97
 Ser Ala Xaa Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser
 -20 -15 -10 -5
 ggg gcg acg gcg tgg gag gag acc ccg cgg tcg cgt tgc cac atc gcc 145
 Gly Ala Thr Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala
 1 5 10
 gtt kcg agt aca aat aca gct tca agg ggc cgc acc tgg tgc aga gcg 193

Val	Xaa	Ser	Thr	Asn	Thr	Ala	Ser	Arg	Gly	Arg	Thr	Trp	Cys	Arg	Ala		
		15					20				25						
acg	gga	ccg	tgc	cct	tct	ggg	ccc	acg	cgg	gga	gta	agc	cgg	agc	aga	241	
Thr	Gly	Pro	Cys	Pro	Ser	Gly	Pro	Thr	Arg	Gly	Val	Ser	Arg	Ser	Arg		
		30					35				40						
ggg	ctg	ggg	gcc	ggg	ttc	ctc	tcc	ccc	ttc	tgc	tgc	ctc	ttc	gcc	ttt	289	
Gly	Leu	Gly	Ala	Gly	Phe	Leu	Ser	Pro	Phe	Cys	Cys	Leu	Phe	Ala	Phe		
45					50					55					60		
cat	ccg	cgg	cta	ccc	tgg	tgt	gct	gag	gtt	ccc	gtt	cca	gca	gct	gca	337	
His	Pro	Arg	Leu	Pro	Trp	Cys	Ala	Glu	Val	Pro	Val	Pro	Ala	Ala	Ala		
				65					70						75		
cac	cat	atg	cgc	tgt	gga	ggg	gac	ctc	ctg	gca	gcc	cct	ccg	ccg	ggg	385	
His	His	Met	Arg	Cys	Gly	Gly	Asp	Leu	Leu	Ala	Ala	Pro	Pro	Pro	Gly		
			80					85					90				
ccc	tcc	tgg	ttc	gca	cgg	ttc	cct	ccg	ctt	gtc	ccc	gag	tct	ttc	cct	433	
Pro	Ser	Trp	Phe	Ala	Arg	Phe	Pro	Pro	Leu	Val	Pro	Glu	Ser	Phe	Pro		
		95					100					105					
cac	cat	tct	gtt	c												446	
His	His	Ser	Val														
			110														

<210> 369
 <211> 125
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..123
 <221> sig_peptide
 <222> 22..93
 <223> Von Heijne matrix
 score 5.19999980926514
 seq LIWVFGGLVSVLSX/FL

<400> 369																
ctatcaagag	gcttttcccc	t	atg	ttt	tct	tct	agg	agt	ttt	atg	gtt	tca				51
			Met	Phe	Ser	Ser	Arg	Ser	Phe	Met	Val	Ser				
							-20					-15				
ggg	ctt	att	tgg	gtc	ttt	ggg	ctt	gta	tct	gtt	ttg	agt	bga	ttt	ttg	99
Gly	Leu	Ile	Trp	Val	Phe	Gly	Leu	Val	Ser	Val	Leu	Ser	Xaa	Phe	Leu	
			-10					-5					1			
tgt	atg	gtg	tat	gat	cag	ggg	cag	gg								125
Cys	Met	Val	Tyr	Asp	Gln	Gly	Gln									
		5				10										

<210> 370
 <211> 132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 39..131

<221> sig_peptide

<222> 39..77

<223> Von Heijne matrix

score 5.19999980926514

seq MLLAVSLSLVSNC/NF

<400> 370

atcttagagg aaagtctttc agtttttccc cattcagt atg tta tta gct gtg agc 56
Met Leu Leu Ala Val Ser

-10

ctg tcc ctt gtc tct aat tgt aac ttt gta ctc act gac caa ctt ttc 104
Leu Ser Leu Val Ser Asn Cys Asn Phe Val Leu Thr Asp Gln Leu Phe

-5

1

5

cct gcc cct gcc tcc ctc atc ccc gaa g 132
Pro Ala Pro Ala Ser Leu Ile Pro Glu
10 15

<210> 371

<211> 127

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..126

<221> sig_peptide

<222> 4..90

<223> Von Heijne matrix

score 5.19999980926514

seq TGVFLFSIIGSFG/FP

<400> 371

tga atg aac caa gat ttc aac cca gaa att gag gct tca cca caa gtg 48
Met Asn Gln Asp Phe Asn Pro Glu Ile Glu Ala Ser Pro Gln Val
-25 -20 -15

aag act ggg gtt ttc ttg ttt tca att att ggg agt ttt gga ttt cca 96
Lys Thr Gly Val Phe Leu Phe Ser Ile Ile Gly Ser Phe Gly Phe Pro
-10 -5 1

gga atg tgc aat tgt aaa aac cca gcc cgg g 127
Gly Met Cys Asn Cys Lys Asn Pro Ala Arg
5 10

<210> 372

<211> 196

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 125..196

<221> sig_peptide
 <222> 125..184
 <223> Von Heijne matrix
 score 5.19999980926514
 seq IVSSLFSWLLSLT/SV

<221> misc_feature
 <222> 119
 <223> n=a, g, c or t
 Oligonucleotide

<400> 372
 taaaaatctt ttatgttcta cccactcctt cctcgttccc tctcccccact cctccctccc 60
 cccatcttaa gcccatggca acccctgac tttttactgt ctccatcgtt ttgccttbnc 120
 caga atg cca tgt agt tgg agt cat ata gta agt agc ctt ttc agt tgg 169
 Met Pro Cys Ser Trp Ser His Ile Val Ser Ser Leu Phe Ser Trp
 -20 -15 -10
 ctt ctt tca ctt acc agt gtg ccc ggg 196
 Leu Leu Ser Leu Thr Ser Val Pro Gly
 -5 1

<210> 373
 <211> 148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..148

<221> sig_peptide
 <222> 56..139
 <223> Von Heijne matrix
 score 5.19999980926514
 seq PVLSCCLTAGRA/RL

<400> 373
 actttcttca caccaggac gcagggtgcc gctgccggcc acagaaaccc caaga atg 58
 Met
 ttt ttc ttt ggc tat tca gag gac atc tat tgt gtg tca ggc cct gtg 106
 Phe Phe Phe Gly Tyr Ser Glu Asp Ile Tyr Cys Val Ser Gly Pro Val
 -25 -20 -15
 ctg agc tgt tgt tgc ctg aca gca gga aga gcg cgg ctc tgg 148
 Leu Ser Cys Cys Cys Leu Thr Ala Gly Arg Ala Arg Leu Trp
 -10 -5 1

<210> 374
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..199

<221> sig_peptide

<222> 26..73

<223> Von Heijne matrix

score 5.19999980926514

seq AALICPWSSQVPS/SP

<400> 374

```
ctagggagga ctcaatgctc tttgt atg cct tat gca gcg ctg atc tgt ccc      52
                               Met Pro Tyr Ala Ala Leu Ile Cys Pro
                               -15                               -10
```

```
tgg agt tcc cag gtt ccc agc tcc ccc cct gca agc ctt gaa gcc tcc      100
Trp Ser Ser Gln Val Pro Ser Ser Pro Pro Ala Ser Leu Glu Ala Ser
      -5                               1                               5
```

```
agc aac gtc tat ctc cag gag agc agg gca gcc tat gca agt gtt ccg      148
Ser Asn Val Tyr Leu Gln Glu Ser Arg Ala Ala Tyr Ala Ser Val Pro
10                               15                               20                               25
```

```
gca gga cca gaa gtg gcc act caa cac acg tcc tca cca gtc acc cct      196
Ala Gly Pro Glu Val Ala Thr Gln His Thr Ser Ser Pro Val Thr Pro
      30                               35                               40
```

```
atg g      200
Met
```

<210> 375

<211> 112

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..111

<221> sig_peptide

<222> 52..105

<223> Von Heijne matrix

score 5.19999980926514

seq LTYSLAFLFIKA/GT

<400> 375

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aataaccctt tcacagcact tgcctgtttt taatgaatct aattattcac a atg caa      57
                               Met Gln
```

```
ctt tta tat tta aca tac tct tta gct ttc ctg cta ttt atc aag gct      105
Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile Lys Ala
      -15                               -10                               -5
```

```
ggc acc g      112
Gly Thr
1
```

<210> 376

<211> 146

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> 74..145

<221> sig_peptide
<222> 74..133
<223> Von Heijne matrix
score 5.19999980926514
seq AAAVTSSAAPSRA/RQ

<400> 376
ggctggagcg cgcgccctcct agcggascgg ggcaattgga aggccgcgcc tcaggaaaac 60
aggatggtag tga atg gca ccg agc cgc ccc agg gct gcc gcc gtc acc 109
Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr
-20 -15 -10
tcc tcg gcg gct ccg agt cgt gcg agg cag ggg gcc c 146
Ser Ser Ala Ala Pro Ser Arg Ala Arg Gln Gly Ala
-5 1

<210> 377
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 218..388

<221> sig_peptide
<222> 218..343
<223> Von Heijne matrix
score 5.19999980926514
seq QHLLSWAXQXGRX/QV

<221> misc_feature
<222> 139
<223> n=a, g, c or t
Oligonucleotide

<400> 377
cattttgtcg gtagaggcag aaggwgaagg tcgggttgta gaagctgggg tggccggcag 60
ctcgtcctc ggtgttcgtg ggctttgtcg gtccgtgcct cgtctctccc tggaaagggg 120
gggaggcttc gacgtcgrnr aggragmmgc tgccgcgtta gttccgagct tgaagtcact 180
aggacttctc tcaaacttgt gtgctgagga gactcag atg ttg gcc tca gct cct 235
Met Leu Ala Ser Ala Pro
-40
agg ctg aac tca gca gat cgg ccc atg aaa act tct gta ttg aga caa 283
Arg Leu Asn Ser Ala Asp Arg Pro Met Lys Thr Ser Val Leu Arg Gln
-35 -30 -25
agg aag gga tct gtc aga aag caa cac ttg tta tct tgg gct tdc cag 331
Arg Lys Gly Ser Val Arg Lys Gln His Leu Leu Ser Trp Ala Xaa Gln
-20 -15 -10 -5
yaa ggh aga kga cag gta gtg gag atc ctg caa tct gaa aag cag act 379
Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu Gln Ser Glu Lys Gln Thr
1 5 10

daa rgt gac g
Xaa Xaa Asp
15

389

<210> 378
<211> 143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..142

<221> sig_peptide
<222> 2..115
<223> Von Heijne matrix
score 5.19999980926514
seq LHGSLDAVSQAQG/RP

<400> 378
a atg tac ccc cta ggc agg gga gag cag ggc cct gct gca ccc aag tcc 49
Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser
-35 -30 -25
tgg ttg ctc ctc ccc acc aca ctg gcc ctc cat gga agc ctt gat gca 97
Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala
-20 -15 -10
gtg agc cag gcc caa gga cgc ccc gcc cac cct gac gca ccc ccc a 143
Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro
-5 1 5

<210> 379
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..260

<221> sig_peptide
<222> 198..245
<223> Von Heijne matrix
score 5.19999980926514
seq FIAALFTIAETWN/QP

<400> 379
cagatggtgg tgaggttgta gagaaaaagg aacgcttata cactgttggt gcgagtgtaa 60
attagtttaa ccattgtgga agatgatatg gcaattccac aaagacctaa agtcagraat 120
tmcattcaa cccagtaatc ccattactgg gtatatactc aaaggaatat aaattgttgt 180
gttacaaaga cacatgc atg cgt gtg ttc att gca gca ctg ttc aca ata 230
Met Arg Val Phe Ile Ala Leu Phe Thr Ile
-15 -10
gca gag aca tgg aat caa ccc aaa tgc cca g 261
Ala Glu Thr Trp Asn Gln Pro Lys Cys Pro

-5

1

5

<210> 380
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..227

<221> sig_peptide
<222> 63..152
<223> Von Heijne matrix
score 5.19999980926514
seq LCFLSVHFRLRWG/DS

<400> 380
gggacgtggg aaaatgacta cgcgtcactc gtgatgtcgc gcatccgata ggcccttttc 60
ag atg gca aaa ggc ctg agg gtg aat ctg ggc gag ctg gtt gag tcc 107
Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser
-30 -25 -20
atg cgt ttg tgc ttc ctc tca gtc cac ttt cgc tta cga tgg ggc gac 155
Met Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp
-15 -10 -5 1
tct tgt cca tcg tca cct cac cgg gaa act ttt cct gcc ggg cca gtt 203
Ser Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val
5 10 15
aat ggt ccc ctg tac cac ccc cgg g 228
Asn Gly Pro Leu Tyr His Pro Arg
20 25

<210> 381
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..299

<221> sig_peptide
<222> 39..89
<223> Von Heijne matrix
score 5.09999990463257
seq QLLVLFSGQTGTA/QD

<400> 381
agtttttagt ctcagaccag accaccgggc gcgccccg atg ccg agc ccg cag ctt 56
Met Pro Ser Pro Gln Leu
-15
ctg gtg ctc ttc ggc agc cag aca ggc acg gct cag gat gtg tcg gag 104
Leu Val Leu Phe Gly Ser Gln Thr Gly Thr Ala Gln Asp Val Ser Glu
-10 -5 1 5

aga ctg ggt cgc gag gcc cgg ggc cgg cgg ctt ggc tgc cgg gtg cag	152
Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg Leu Gly Cys Arg Val Gln	
10 15 20	
gcc ctg gac tcc tac ccg gtg gtg aat ctg att aac gag ccc ctg gtg	200
Ala Leu Asp Ser Tyr Pro Val Val Asn Leu Ile Asn Glu Pro Leu Val	
25 30 35	
ata ttt gtt tgt gca act ayw ggc caa gga gac ccc cct gac aac atg	248
Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly Asp Pro Pro Asp Asn Met	
40 45 50	
aag aac ttc tgg agg ttt ata ttc cgg aag aac ctg ccc tcc acc gcc	296
Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys Asn Leu Pro Ser Thr Ala	
55 60 65	
cgg g	300
Arg	
70	

<210> 382
 <211> 151
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..151

<221> sig_peptide
 <222> 8..130
 <223> Von Heijne matrix
 score 5.09999990463257
 seq SFLFLACIFQXGS/XX

<400> 382	
atacata atg tct tcc att ttg ggt gtc tca tcc tca tgg tgg tat tta	49
Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu	
-40 -35 -30	
tat tat ggc tat tgt ata ttt gtt aaa aag tgc tct ttt tgc agt ttc	97
Tyr Tyr Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe	
-25 -20 -15	
ctg ttc ctt gcc tgt att ttt caa ggc tkt tck ckt kat wca aac aca	145
Leu Phe Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr	
-10 -5 1 5	
caa agc	151
Gln Ser	

<210> 383
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..253

<221> sig_peptide

<222> 101..184

<223> Von Heijne matrix

score 5.09999990463257

seq CLCGSAPCLLCRC/CP

<400> 383

gcgtccggaa gtgtctcgca gatagtaaat aatctcggaa aggcgagaaa gaagctgtct 60

ccatcttgct tgtatccgct gcwcttgtaga cgttgtaggag atg ggg agc gtc ctg 115

Met Gly Ser Val Leu

-25

ggg ctg tgc tcc atg gcg agc tgg ata cca tgt ttg tgt gga agt gcc 163

Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala

-20

-15

-10

ccg tgt ttg cta tgc cga tgc tgt cct agt gga aac aac tcc act gta 211

Pro Cys Leu Cys Arg Cys Cys Pro Ser Gly Asn Asn Ser Thr Val

-5

1

5

act aga ttg atc tat gca ctt ttc ttg ctt gtt gga gta tgg gg 255

Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val Gly Val Trp

10

15

20

<210> 384

<211> 456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..454

<221> sig_peptide

<222> 128..265

<223> Von Heijne matrix

score 5.09999990463257

seq IGSCSVMSGALC/VP

<400> 384

tacaactttg aaaagccctt cctctggctt gctagacagc tcattggaga cgttaacttg 60

gaatttggtg ccatgcctgc tcttgccctca ccagagattg tcatggaccc aaatttgcca 120

gtgtagt atg agc wkr wtt agm agg ttg stt aga caa ctg ctc tcc cag 169

Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln

-45

-40

-35

rtg agg rwg atg acc tgt gag aat gaa gct gga gcc cag tgt car aag 217

Xaa Arg Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys

-30

-25

-20

tct agt ttt ata ggc agc tgt tct gtg atg tca agt ggt gca ctg tgt 265

Ser Ser Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys

-15

-10

-5

gtg cca ctt tat tat cta gct aag ggc aac atg tgc tcc atc tgt ggg 313

Val Pro Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly

1

5

10

15

atg ctg aag gag atg aat ggg ctt tgg agt gaa tgt gac agt tta aaa 361

Met Leu Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys

20

25

30

aat acc ttc att gtt tgg rcc tgc ata ttt agc tgt ttg gga atg caa 409

Asn	Thr	Phe	Ile	Val	Trp	Xaa	Cys	Ile	Phe	Ser	Cys	Leu	Gly	Met	Gln	
		35					40					45				
ttg	awt	tct	tct	kgr	gtt	tca	aat	gta	aga	ctg	cta	ctg	tca	cat	ca	456
Leu	Xaa	Ser	Ser	Xaa	Val	Ser	Asn	Val	Arg	Leu	Leu	Leu	Ser	His		
		50				55					60					

<210> 385
 <211> 193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..192

<221> sig_peptide
 <222> 1..78
 <223> Von Heijne matrix
 score 5.09999990463257
 seq AFPFVCLTFCVGG/GP

<400> 385																	
atg	cct	cat	cca	ctg	gct	acc	tct	gcg	ttt	ctg	cgt	tcc	gcc	ttt	cct		48
Met	Pro	His	Pro	Leu	Ala	Thr	Ser	Ala	Phe	Leu	Arg	Ser	Ala	Phe	Pro		
	-25					-20					-15						
ttt	gtt	tgt	ctc	acg	ttt	tgc	gtg	gga	ggc	ggt	ccc	ggg	att	tca	ggg		96
Phe	Val	Cys	Leu	Thr	Phe	Cys	Val	Gly	Gly	Gly	Pro	Gly	Ile	Ser	Gly		
-10					-5				1				5				
gtc	tac	cgg	ctc	ctt	atg	gcg	aat	gca	acc	cga	aga	gag	agt	gag	gta		144
Val	Tyr	Arg	Leu	Leu	Met	Ala	Asn	Ala	Thr	Arg	Arg	Glu	Ser	Glu	Val		
			10					15					20				
agc	ctc	cgc	ggg	ttg	ggc	agg	gac	gga	gag	ggg	gcc	cgc	gcg	act	cca	g	193
Ser	Leu	Arg	Gly	Leu	Gly	Arg	Asp	Gly	Glu	Gly	Ala	Arg	Ala	Thr	Pro		
			25				30					35					

<210> 386
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..279

<221> sig_peptide
 <222> 199..267
 <223> Von Heijne matrix
 score 5.09999990463257
 seq SLMVFLNLFFLNC/DP

<400> 386																	
tgtttatagg	ttttaactct	tatgggttaga	atgggttgta	gtcatagwg	tgtagacac												60
ctgctaattt	cctcaggaca	cattcccaga	agtgaatta	ccaagtcaaa	gagcataaat												120
acttttagaga	tacatgataa	attgtgccag	ctacctttcc	aaaagagttg	tactagttga												180


```

ggtttctgcc agcagtat atg aca gtt ggg ctc cat att tta aga gat tca      231
                Met Thr Val Gly Leu His Ile Leu Arg Asp Ser
                -20                                -15
cta atg gtg ttt ctc aac ctt ttt ttt tta aac tgt gac cca cac agg      279
Leu Met Val Phe Leu Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg
        -10                                -5                                1

```

```

gg                                                                 281

```

```

<210> 387
<211> 111
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 5..109

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<221> sig_peptide
<222> 5..67
<223> Von Heijne matrix
      score 5.09999990463257
      seq MFCVSLLLHHAYP/LP

```

```

<400> 387
cacc atg gta aga tgg gga cat ccc cct atg ttc tgt gtc tct ctc ctg      49
      Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu
      -20                                -15                                -10
ctc cac cat gct tat cct ttg cct tcc acc atg att gta agt ttc cca      97
Leu His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro
      -5                                1                                5                                10
agg cct ccc ctg gg                                                                 111
Arg Pro Pro Leu

```

```

<210> 388
<211> 374
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 96..374

```

```

<221> sig_peptide
<222> 96..173
<223> Von Heijne matrix
      score 5.09999990463257
      seq AMVCFGCPGGASS/RC

```

```

<221> misc_feature
<222> 344
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 388

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ttttggccgc catgttttcg tcgcagtaac tgcottggtg tcagtagtca ttgccagttt 60
 cgggcgttct ggacaattgg gatgctgcag agttc atg gct ggg gct gct cgt 113
 Met Ala Gly Ala Ala Arg
 -25

tgg gtg gga caa kaa tcc tct gca atg gtt tgt ttt ggc tgc cca gga 161
 Trp Val Gly Gln Xaa Ser Ser Ala Met Val Cys Phe Gly Cys Pro Gly
 -20 -15 -10 -5

ggg ggc tca agt cgc tgc cgc tcc cct cgt ggg cgt cag gcc tca aga 209
 Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg Gly Arg Gln Ala Ser Arg
 1 5 10

gtt ccc cgc cta gaa aat gga gct cag cga gtc gtg cgt acc atg gtg 257
 Val Pro Arg Leu Glu Asn Gly Ala Gln Arg Val Val Arg Thr Met Val
 15 20 25

cac ctg gtt ttg cag cct aag cgg gtc act tta gtg cat cct cct cgc 305
 His Leu Val Leu Gln Pro Lys Arg Val Thr Leu Val His Pro Pro Arg
 30 35 40

gga ttg gag cct gtt tgc acc cct ata gcm vga atg arn ccc aag tca 353
 Gly Leu Glu Pro Val Cys Thr Pro Ile Ala Xaa Met Xaa Pro Lys Ser
 45 50 55 60

cac ggg ctc aga agt tct ttg 374
 His Gly Leu Arg Ser Ser Leu
 65

<210> 389
 <211> 192
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..192

<221> sig_peptide
 <222> 52..153
 <223> Von Heijne matrix
 score 5.09999990463257
 seq PXLLSXLHGLLYG/SP

<400> 389
 ggcagacttc aaccaggctg tgggaggaga gctcagtggg gcacagagaa g atg ggt 57
 Met Gly

gtt gtc agt ggg ggt gtt ggt gac ttg acc aca aaa acc caa gag aat 105
 Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln Glu Asn
 -30 -25 -20

ggg ctc tta cca gvc cty ctc tcc wkc ctk cac gga ctg ctc tat ggc 153
 Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu Tyr Gly
 -15 -10 -5

agc cct gat gca gar ctc acg ggc ccg gat ccc tgg gat 192
 Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp
 1 5 10

<210> 390
 <211> 371
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 321..371

<221> sig_peptide

<222> 321..365

<223> Von Heijne matrix

score 5.09999990463257

seq FLSXTCVLSCXRS/LS

<400> 390

```
tctgttcagg ttttgtatgt gttcatagta taatcttggg ttgtagggtg tgtgtatctg      60
ggaagaaact ttacaatctc taacaggcct ggaaggtcta atctataaaa gtatttcatt      120
gaccttgaag aaggtcaatt atttatataa gaaaataaac tcaacatttt atccataaaa      180
aatgtaattc cggaatttat gttagtataa ttataacact gataacataa aaagtgcctat      240
taatccttaa gaaagagtta ccttttcttt tctatcttca tcacagctag cccagtctta      300
gtctatttca ttagcttcct atg ggc ttc ctc tca ckt aca tgc gtg ctc tct      353
                               Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser
                               -15                -10                -5
```

```
tgc dtg cgc tcg ctc tct      371
Cys Xaa Arg Ser Leu Ser
                        1
```

<210> 391

<211> 328

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 184..327

<221> sig_peptide

<222> 184..300

<223> Von Heijne matrix

score 5

seq LVCFFNSVSFLFG/VS

<400> 391

```
cogttatgtg ttcagctcaa ttagattaat taccttcctc accaggagtc acaatgcttt      60
gcagtttatc tgcggttaact aaatgttagt tttgtaagta aaagggtactg ttattgacct      120
cgaaagggct atagttcctt tgaacttaca gagaagagtt ccaaacaact atttctaacc      180
aag atg gaa tat ggg tca gca aaa ttg tct tca ggt aga gtt ttc tac      228
    Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr
                -35                -30                -25
```

```
ttg cca aga gac ttt ggc att gag agg aga gtt ctt gtt tgt ttt ttt      276
Leu Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe
                -20                -15                -10
```

```
aac tct gta tca ttt ctg ttt ggt gtc tct ara aaa aaa tcc gra caa      324
Asn Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln
                -5                1                5
```

```
tgg g      328
```

Trp

<210> 392
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 252..302

<221> sig_peptide
<222> 252..290
<223> Von Heijne matrix
score 5
seq MLSGLVLNSWALA/YQ

<400> 392
tgaccttgta gcagttatct ttgttaaact ccttcatttc ttattttaaa taattaatta 60
attaatttag agacagggtc tcaactatgtc acccaggctg tagtgcagtg gtgcaatcat 120
ggctcactgt agccttgacc tcccaggctc aagcaatctt cctacctcag cctctcaggc 180
agctgggact acagaccac agcactacgc ctgacttatg attttatttt ttgtggagac 240
agggtcttac t atg ttg tct ggg ctt gtc tta aac tct tgg gcc tta gcc 290
Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala
-10 -5
tac caa cta gct g 303
Tyr Gln Leu Ala
1

<210> 393
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 298..366

<221> sig_peptide
<222> 298..345
<223> Von Heijne matrix
score 5
seq VFFXGXSIIILVLG/ST

<221> misc_feature
<222> 265
<223> n=a, g, c or t
Oligonucleotide

<400> 393
tttttccccg cccctgagac cctgcagcac catctgtcat ggcggctggg ctgtttggtt 60
tgagcgctcg ccgtcttttg gcggcagcgg cgacgcgagg gctcccggcc gcccgcgctc 120
gctgggaatc tagcttctcc argamytgtg gtcgccccgt ccgctgtggc gggaaagcgg 180
tccccagaac cgaccacacc gtggcaagag gaccagaac ccgaggacga aaacttgtat 240

gagaagaasc cagactccca tggknatgac aaggaccccg ttttggacgt ctggaac	297
atg cga ctt gtc ttc ttc ktw ggc gks tcc atc atc ctg gtc ctt ggc	345
Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly	
-15 -10 -5	
agc acc ttt gkg gcc tat ctg	366
Ser Thr Phe Xaa Ala Tyr Leu	
1 5	

<210> 394
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..125

<221> sig_peptide
 <222> 21..68
 <223> Von Heijne matrix
 score 5
 seq SDFLLFVSLSL/PS

<400> 394	
agcttggcat ataggctcaa atg tta tca tca gat ttt ttt ctc ctc ttt gtc	53
Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val	
-15 -10	
tct tta tct tta tct cca ttt cct ttt ttt ctt ttt cct ccc ctc ttt	101
Ser Leu Ser Leu Ser Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe	
-5 1 5 10	
tcc tgc ttt ctc tta ccc acc cgg g	126
Ser Cys Phe Leu Leu Pro Thr Arg	
15	

<210> 395
 <211> 329
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..327

<221> sig_peptide
 <222> 154..195
 <223> Von Heijne matrix
 score 5
 seq FIAALFTVAKIWN/QP

<400> 395	
tgaaaatgta aattagtgca gttattatgg magtcagtat ggaacttcct caaaaaacta	60
acaataaaac tcccatatga tccagcaatc ctaccactgr atatttatcc aaaggaaagg	120
aagtcggat atttaacagg catctgcacc ccc atg ttt att gca gca cta ttc	174
Met Phe Ile Ala Ala Leu Phe	

score 5
seq LSLFVFFWLVGFS/FF

<221> misc_feature
<222> 284..285
<223> n=a, g, c or t
Oligonucleotide

<400> 397
ttgtgaactc ttctattatt attaagtgtt gtcaattgtc agcatccata ttctattccg 60
atgatgaata gaagcattat atttcagcat caaaatgcag ttgggggtcgt aatgagcatc 120
attagggacc tta atg gga gtc aga act gta tgt cat ttt att cag gtt 169
Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val
-25 -20 -15
ttt cta agt tta ttt gtg ttt ttt tgg tta gtt ggt ttt tct ttt ttc 217
Phe Leu Ser Leu Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe
-10 -5 1
ttt ttt tta cdb ttt tct acc aag cag gtg aga gtw gaa cag cat tgt 265
Phe Phe Leu Xaa Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys
5 10 15
gat ttt aaa agt aca cca nnd gta gag tct tcc agt acc gtt ggc cat 313
Asp Phe Lys Ser Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His
20 25 30
gcc 316
Ala
35

<210> 398
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..251

<221> sig_peptide
<222> 63..143
<223> Von Heijne matrix
score 5
seq LSCFYLLAIVSNA/VM

<400> 398
atgttgtagc ttctgtcata atttccttcc cttttaaggc tgaataattt tccattgtgt 60
at atg tac cat att ttg ttc atc cat tca ttc att gat aga tac ttg 107
Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu
-25 -20 -15
agt tgc ttc tac ctt ttg gca att gtg agt aat gct gtt atg aac atg 155
Ser Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met
-10 -5 1
ggg gta caa atg tct gtt ttg agt cct tgt ttt gct ttc gtg cat tct 203
Gly Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser
5 10 15 20
att aaa aat gtt aag gtt ctt tgc ttt tta ctt ttt ttt ctc ttt ggg 251

Ile Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly
25 30 35

<210> 399
<211> 120
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..120

<221> sig_peptide
<222> 10..75
<223> Von Heijne matrix
score 5
seq VQWLLVYSPSCAA/TI

<400> 399
tcatttacc atg cag ttc acc gtt tta atg tgt cca gtt cag tgg ttg tta 51
Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu
-20 -15 -10
gtg tat tca ccc agt tgt gca gcc acc atc aca gtc aat ttt aaa aca 99
Val Tyr Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr
-5 1 5
ttt tca tca ccc caa acc ggg 120
Phe Ser Ser Pro Gln Thr Gly
10 15

<210> 400
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 342..461

<221> sig_peptide
<222> 342..452
<223> Von Heijne matrix
score 5
seq VSCLSAGLRVCCS/QR

<221> misc_feature
<222> 246,260
<223> n=a, g, c or t
Oligonucleotide

<400> 400
ctctgtcccc ggggctgggt ctctgtctgct ccggttcctg ggctcctaatt tcttggtcca 60
gcttcttcca ggcacatcct cttctctgcc ctccgtccat ttgggagccg gagatgggtg 120
gctkggggcc gcccagtag tgagacagt gaagtaaacc ccatctgccg ttcccgtgcg 180
tagagaaaaa cgttgaccgc gaggctgggg aggagagttg cctctgagga agaagggcac 240

agaganccaa aattagtttn gaaagcatcc tgatttggtg cccgaggcct ggaaagaaat 300
 ggccggctggg gtgcggcgga ggtaggggag gaaaacgttg g atg aga agg gcc tgg 356
 Met Arg Arg Ala Trp
 -35
 act cag gaa agg gaa ccg cgt ccg tgt gag ccc gct gag cgc gca gac 404
 Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro Ala Glu Arg Ala Asp
 -30 -25 -20
 cct gcc cct gtc tcc tgt ctg tct gca ggt ctg cgc gtc tgt tgt tcc 452
 Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu Arg Val Cys Cys Ser
 -15 -10 -5
 cag cgc tct gc 463
 Gln Arg Ser
 1

<210> 401
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..204
 <221> sig_peptide
 <222> 94..168
 <223> Von Heijne matrix
 score 4.90000009536743
 seq DFFICLLAICVSS/FE

<400> 401
 tactgtttat tgattctttg attatggcca ttcttacagg agtaagggtgg tatcacactg 60
 tggttttgat ttgcatttcc ctgacatta gtg atg ttg cat ttg att tgc att 114
 Met Leu His Leu Ile Cys Ile
 -25 -20
 tcc ctg atc gtt aat gat ttt ttc ata tgt ttg ttg gcc att tgc gta 162
 Ser Leu Ile Val Asn Asp Phe Phe Ile Cys Leu Leu Ala Ile Cys Val
 -15 -10 -5
 tct tct ttt gag aat tgt cta ttt atg tcc tta gcc cac agt gg 206
 Ser Ser Phe Glu Asn Cys Leu Phe Met Ser Leu Ala His Ser
 1 5 10

<210> 402
 <211> 330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..329

<221> sig_peptide
 <222> 42..230
 <223> Von Heijne matrix
 score 4.90000009536743

seq VTSLANLIPPVKA/XP

<400> 402

```

acagggctcc actgcagtta ggagccggtg agtccgggtg g atg agg tca gag cgc      56
                                   Met Arg Ser Glu Arg
                                   -60
ccc atg gtg tgg tgc tgc ctc ttt gtc cgt tcg cag cga aaa cgg aaa      104
Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser Gln Arg Lys Arg Lys
                                   -55                                   -50                                   -45
cag agc acc caa gat gaa gat gct gtt agc ctt tgc agt ctc gac ata      152
Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu Cys Ser Leu Asp Ile
                                   -40                                   -35                                   -30
agt gag cct agt aat aaa cgg gtc aaa ccc ctt tcc cga gtc acg tcg      200
Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser
                                   -25                                   -20                                   -15
cta gca aac ctc atc ccg ccc gtg aag gcc ayg cca tta aag cgc ttc      248
Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa Pro Leu Lys Arg Phe
                                   -10                                   -5                                   1                                   5
agt caa acc ctg cag cgc tcc att agc ttc cgc agt gag agt cgc cct      296
Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro
                                   10                                   15                                   20
gac atc ctc gcc ccc cga ccc tgg tcc aga aat g      330
Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn
                                   25                                   30

```

<210> 403

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 168..311

<221> sig_peptide

<222> 168..227

<223> Von Heijne matrix

score 4.90000009536743

seq CILISTAFPSLLT/QI

<400> 403

```

tgagcagatg gtgccaggat ttaaacctat gtttatcaga tgcagatgac ccaaacagtg      60
gcttatctgt tggtaatatt tatttagatc aagttaaaca taaatgactt tgcattactc      120
tttggtcact ttttcctagt catttcaaat agtctgtctt atttctc atg gtt ttt      176
                                   Met Val Phe
                                   -20
tgg aca aaa ttt tgt att tta att agt aca gca ttt cct tct tta ttg      224
Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro Ser Leu Leu
                                   -15                                   -10                                   -5
aca cag att att ttc cct aaa tct att aca ttt gct ttc cag ttt ttc      272
Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe Gln Phe Phe
                                   1                                   5                                   10                                   15
tgg aac agg gaa aaa caa aaa aca aaa aca cca act ggg      311
Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly

```

<210> 404
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..274

<221> sig_peptide
 <222> 80..190
 <223> Von Heijne matrix
 score 4.90000009536743
 seq MLIMLGIFNVHS/AV

<400> 404
 cccgtgcgagg gcatacctggg cttctcccca ccgctttccg agcccgtttg cacctcggcg 60
 atccccgact cctttcttt atg gcg tcg ctc ctg tgc tgt ggg ccg aag ctg 112
 Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu
 -35 -30
 gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc atg ttg ata 160
 Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile
 -25 -20 -15
 atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg att gag gac 208
 Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp
 -10 -5 1 5
 gtt ccc ttc acg gag aaa gat ttt gag aat ggc ccc cag aac ata tac 256
 Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr
 10 15 20
 aac ctt tac gag cat ggg 274
 Asn Leu Tyr Glu His Gly
 25

<210> 405
 <211> 153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..152

<221> sig_peptide
 <222> 69..116
 <223> Von Heijne matrix
 score 4.90000009536743
 seq SALLLEXLQXAIP/RX

<400> 405
 tttccctgc cctgtcctct cattccctt cttctggagc atttcatcca cagaccctt 60
 gcccaaga atg tct gtc tca gct ctg ctt cta gag mtc ctc caa gmt gcc 110
 Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala

	-15		-10		-5	
atc cct cgy mam acc tca ggc ttm caa gac ctg ccc aac tgg g						153
Ile Pro Arg Xaa Thr Ser Gly Xaa Gln Asp Leu Pro Asn Trp						
1		5		10		

<210> 406
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..206

<221> sig_peptide
 <222> 57..173
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VIAIVSFTTLCSS/LY

<400> 406	
aaataaaaaa tattaaaaaa taatctcatc ttgatttta gatttagggg gtgtgc atg	59
	Met
cag gct tgt tat atg ggt atg tgg tat act gcc gag gct tgg ggt acg	107
Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly Thr	
-35	-30
att gag tcc ctc acc cag gta gtg agc gta atc gca ata gtt agt ttt	155
Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser Phe	
-20	-15
aca acc ctg tgc tcc tct ctg tat tcc ccc caa gta gtc ccc agt gtt	203
Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser Val	
-5	1
ggg	206
Gly	

<210> 407
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 277..477

<221> sig_peptide
 <222> 277..462
 <223> Von Heijne matrix
 score 4.90000009536743
 seq PLACPLLLPIFS/HA

<221> misc_feature
 <222> 22
 <223> n=a, g, c or t
 Oligonucleotide

<400> 407

```
aatggattga gatggggaag anaaaaagcc ccaaattcat gaaatgtagc tgckacagtc      60
cccacctcct tagctgtccc caaacctaa gcaggtaatc ataacttcca ttctgtgctc      120
accttacctc tgctggcacc tttttggaca gggttctcta cttggcgagg tgacccaaat      180
cttcattcct gcagggtctg agtcctmrgc cgctgcgata gtttgaacat tgtttgtccc      240
cacmraaact catcttgagg cttggtcccc actgta atg atg ttg aga ggt ggc      294
                               Met Met Leu Arg Gly Gly
```

-60

```
ggg aca ttt aag grg tgt ttg agt cat gag gga tcc agc ttc acg aag      342
Gly Thr Phe Lys Xaa Cys Leu Ser His Glu Gly Ser Ser Phe Thr Lys
-55                               -50                               -45
```

```
gga tta gcg cag gag tgc gtg agt rct tct tgt ggg act cga ttg att      390
Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser Cys Gly Thr Arg Leu Ile
-40                               -35                               -30                               -25
```

```
act gca gtw gcc agt kgt tac aaa gca agg ctg cct ctg gcc gcg tgc      438
Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg Leu Pro Leu Ala Ala Cys
-20                               -15                               -10
```

```
ccd ctt ctg ctt cct att ttc tcc cat gct aga agc agc ac      479
Pro Leu Leu Leu Pro Ile Phe Ser His Ala Arg Ser Ser
-5                               1                               5
```

<210> 408

<211> 289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 84..287

<221> sig_peptide

<222> 84..203

<223> Von Heijne matrix

score 4.90000009536743

seq SLKICGLVFGILA/LT

<400> 408

```
agccgactca cttgcaactc cacctcagca gtggtctctc agtcctctca aagcaaggaa      60
agagtactgt gtgctgagag acc atg gca aag aat cct cca gag aat tgt gaa      113
                               Met Ala Lys Asn Pro Pro Glu Asn Cys Glu
                               -40                               -35
```

```
gac tgt cac att cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt      161
Asp Cys His Ile Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys
-30                               -25                               -20                               -15
```

```
aaa tca ctt aag att tgt gga ctg gtg ttt ggt atc ctg gcc cta act      209
Lys Ser Leu Lys Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr
-10                               -5                               1
```

```
cta att gtc ctg ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc      257
Leu Ile Val Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro
5                               10                               15
```

```
aaa aaa gcc tat gac atg gag cac act acg gg      289
Lys Lys Ala Tyr Asp Met Glu His Thr Thr
20                               25
```

<210> 409
 <211> 341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..339

<221> sig_peptide
 <222> 94..216
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LSLVSHAPGEALA/RA

<400> 409
 gtgtttgcaga aatccggcaa tcgacctgag gaattgcgag ccgctcagct cccgggacgt 60
 ttggagctgc tgctaaataa tttctgtctca gcc atg tcg ccg gct cca gat gca 114
 Met Ser Pro Ala Pro Asp Ala
 -40 -35
 gcc ccg gct cct gcg tcg atc tcc ctg ttt gac ctc agc gcg gat gct 162
 Ala Pro Ala Pro Ala Ser Ile Ser Leu Phe Asp Leu Ser Ala Asp Ala
 -30 -25 -20
 ccg gtc ttt cag ggc ctg agc ctg gtg agc cac gcg cct ggg gag gct 210
 Pro Val Phe Gln Gly Leu Ser Leu Val Ser His Ala Pro Gly Glu Ala
 -15 -10 -5
 ctg gcc cgg gct ccg cgt act tcc tgt tca ggc tca ggg gag aga gaa 258
 Leu Ala Arg Ala Pro Arg Thr Ser Cys Ser Gly Ser Gly Glu Arg Glu
 1 5 10
 agc cca gaa aga aag cta ctc cag ggt cct atg gat att tca gag aag 306
 Ser Pro Glu Arg Lys Leu Gln Gly Pro Met Asp Ile Ser Glu Lys
 15 20 25 30
 tta ttt tgt tca act tgt gac cag acc ttc cag aa 341
 Leu Phe Cys Ser Thr Cys Asp Gln Thr Phe Gln
 35 40

<210> 410
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 153..320

<221> sig_peptide
 <222> 153..257
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LFIFIGSLQPVPT/RF

<400> 410
 cacacacaaa ctctcaagtg gcctaattcc ctctcaccaa accaatcaca atacagataa 60

```

aagagaataa cttgtgttca tttttgtaca aacaaaaaag atataaattg tgaatgrtgc 120
atgrtttttta awtwmccaag taaactgggc aa atg ctt ctg cat tat tta aag 173
                               Met Leu Leu His Tyr Leu Lys
                               -35                               -30

cta aaa ggt gat cag tgg aaa ctt tcc tct gtt agt act cta ata ctt 221
Leu Lys Gly Asp Gln Trp Lys Leu Ser Ser Val Ser Thr Leu Ile Leu
                               -25                               -20                               -15

ttt ata ttt atc ggc tca cta caa cct gtg cct acc agg ttc aag cga 269
Phe Ile Phe Ile Gly Ser Leu Gln Pro Val Pro Thr Arg Phe Lys Arg
                               -10                               -5                               1

ttc tcc tgt ctc gdc cac ctg agt agc cga gac cac agg caa gca cta 317
Phe Ser Cys Leu Xaa His Leu Ser Ser Arg Asp His Arg Gln Ala Leu
5                               10                               15                               20

cgg g 321
Arg

```

```

<210> 411
<211> 635
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 84..635

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<221> sig_peptide
<222> 84..542
<223> Von Heijne matrix
      score 4.90000009536743
      seq MIVSLAAVAWVGQ/QV

```

```

<400> 411
gggttggtggt tgggtgtgctg gtttcggttg gaggactcgt tggggaggtg gcctgcgctt 60
gtagagactg catccccgag acg atg gcg gag gga gat aat cgc agc acc aac 113
                               Met Ala Glu Gly Asp Asn Arg Ser Thr Asn
                               -150                               -145

ctg ctg gct gca gag act gca agt ctg gaa gaa cag ctg caa gga tgg 161
Leu Leu Ala Ala Glu Thr Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp
                               -140                               -135                               -130

gga gaa gtg atg ctg atg gct gat aaa gtc ctc cga tgg gaa aga gcc 209
Gly Glu Val Met Leu Met Ala Asp Lys Val Leu Arg Trp Glu Arg Ala
                               -125                               -120                               -115

tgg ttt cca cct gcc atc atg ggt gtg gtt tct ttg gtg ttt ctg att 257
Trp Phe Pro Pro Ala Ile Met Gly Val Val Ser Leu Val Phe Leu Ile
                               -110                               -105                               -100

atc tac tat cta gat cca tct gtt ctg tcc ggc gtt tcc tgt ttt gtt 305
Ile Tyr Tyr Leu Asp Pro Ser Val Leu Ser Gly Val Ser Cys Phe Val
-95                               -90                               -85                               -80

atg ttt ttg tgc ttg gct gac tac ctt gtt ccc att cta gcg cct aga 353
Met Phe Leu Cys Leu Ala Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg
                               -75                               -70                               -65

att ttt ggc tcc aat aaa tgg acc act gaa caa cag caa aga ttc cat 401
Ile Phe Gly Ser Asn Lys Trp Thr Thr Glu Gln Gln Gln Arg Phe His
                               -60                               -55                               -50

```

gaa att tgc agc aat cta gta aaa act cga cgc aga gct gtg ggt tgg	449
Glu Ile Cys Ser Asn Leu Val Lys Thr Arg Arg Arg Ala Val Gly Trp	
-45 -40 -35	
tgg aaa cgc ctc ttc aca cta aag gaa gaa aaa cct aag atg tac ttc	497
Trp Lys Arg Leu Phe Thr Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe	
-30 -25 -20	
atg acc atg atc gtt tcc ctt gct gcg gtt gct tgg gtg gga caa caa	545
Met Thr Met Ile Val Ser Leu Ala Ala Val Ala Trp Val Gly Gln Gln	
-15 -10 -5 1	
gtc cac aac ctg ctt ctc acc tac ctg ata gtg act tcc tta cta ttg	593
Val His Asn Leu Leu Leu Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu	
5 10 15	
ctt cct gga cta aac caa cat gga atc att ttg aag tac att	635
Leu Pro Gly Leu Asn Gln His Gly Ile Ile Leu Lys Tyr Ile	
20 25 30	

<210> 412
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..335

<221> sig_peptide
 <222> 33..110
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LLRGLLAGPAATS/WS

<400> 412	
aatggacgag aggtcaggggt aggttttttga ag atg gcg gcc ctc aag gct ctg	53
Met Ala Ala Leu Lys Ala Leu	
-25 -20	
gtg tcc ggc tgt ggg cgg ctt ctc cgt ggg cta cta gcg ggc ccg gca	101
Val Ser Gly Cys Gly Arg Leu Leu Arg Gly Leu Leu Ala Gly Pro Ala	
-15 -10 -5	
gcg acc agc tgg tct cgg ctt cca gct cgc ggg ttc agg gaa gtg gtg	149
Ala Thr Ser Trp Ser Arg Leu Pro Ala Arg Gly Phe Arg Glu Val Val	
1 5 10	
gag acc caa gaa ggg aag aca act ata att gaa ggc cgt atc aca gcg	197
Glu Thr Gln Glu Gly Lys Thr Thr Ile Ile Glu Gly Arg Ile Thr Ala	
15 20 25	
act ccc aag gag agt cca aat cct cct aac ccc tct ggc cag tgc ccc	245
Thr Pro Lys Glu Ser Pro Asn Pro Pro Asn Pro Ser Gly Gln Cys Pro	
30 35 40 45	
atc tgc cgt tgg aac ctg aag cac aag tat aac tat gac gat gtt ctg	293
Ile Cys Arg Trp Asn Leu Lys His Lys Tyr Asn Tyr Asp Asp Val Leu	
50 55 60	
ctg ctt agc cag ttc atc cgg cct cat gga ggc atg ctg ccc	335
Leu Leu Ser Gln Phe Ile Arg Pro His Gly Gly Met Leu Pro	
65 70 75	

<210> 413
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..156

<221> sig_peptide
 <222> 25..93
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LVGFKQVVAWTFA/SD

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 413
 agaaactgac atttgbntgt tttta atg ggg tcc ctg ctg ttc atc agg cag 51
 Met Gly Ser Leu Leu Phe Ile Arg Gln
 -20 -15
 aca ctt gtg ggc ttt aaa cag gtc gtt gct tgg acc ttt gct tct gat 99
 Thr Leu Val Gly Phe Lys Gln Val Val Ala Trp Thr Phe Ala Ser Asp
 -10 -5 1
 tca cat tgt gsa aaw gtg gww atg gtd wtc tws agt cag ttg arw aat 147
 Ser His Cys Xaa Xaa Val Xaa Met Val Xaa Xaa Ser Gln Leu Xaa Asn
 5 10 15
 ccc cca ctg gg 158
 Pro Pro Leu
 20

<210> 414
 <211> 202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..202

<221> sig_peptide
 <222> 59..130
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LLLRGSLLASXRA/XX

<221> misc_feature
 <222> 160
 <223> n=a, g, c or t
 Oligonucleotide

<400> 414
 ctgggagcga ccgctccgct cgtctcgttg gttccggagg tcgctgcggc ggtgggaa 58
 atg ctg gcg cgc gcg gcg gag grc act ggg gcc ctt ttg ctg agg ggc 106
 Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly
 -20 -15 -10
 tct cta ctg gct tct grc cgc gck ycg sys vcg cct cct ctg gga ttg 154
 Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu
 -5 1 5
 scc cgn aac acc gwt ggt act gtt cgt gcc gca gca gga ggc ctg ggt 202
 Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly
 10 15 20

<210> 415
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..229
 <221> sig_peptide
 <222> 146..196
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LLSFCLCSDFISQ/DA

<400> 415
 gtmaaactcc cgcagacttc tctgtagatc gctgagcgat actttcggca gcacctcctt 60
 gattctcagt ttgtctggag gccgcaacca ggcctactc aaccctcctt cccaggaggc 120
 ccaggccccc aagctcagat caccc atg aat gcc tcc ctc ttg tct ttc tgc 172
 Met Asn Ala Ser Leu Leu Ser Phe Cys
 -15 -10
 ctt tgt tca gat ttc atc tct caa gat gcc ctc ctt ctc act gtc ata 220
 Leu Cys Ser Asp Phe Ile Ser Gln Asp Ala Leu Leu Leu Thr Val Ile
 -5 1 5
 ttt cct ccc 229
 Phe Pro Pro
 10

<210> 416
 <211> 265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..263
 <221> sig_peptide
 <222> 27..206
 <223> Von Heijne matrix
 score 4.90000009536743
 seq LVGVIVHSGQAHA/GH

<400> 416
atgatgaaca aataaggttt ccctgg atg cta aac atg gag cct tac aca gtt 53
Met Leu Asn Met Glu Pro Tyr Thr Val
-60 -55
tca gga atg gct cgc caa gat tct tct tct gaa gtt ggg gaa aat ggg 101
Ser Gly Met Ala Arg Gln Asp Ser Ser Ser Glu Val Gly Glu Asn Gly
-50 -45 -40
cga agt gtg gat cag ggc ggt gga gga tcc cca cga aaa aag gtt gcc 149
Arg Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys Val Ala
-35 -30 -25 -20
ctc aca gaa aac tat gaa ctt gtc ggt gtc atc gta cac agt ggg cag 197
Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser Gly Gln
-15 -10 -5
gca cac gca ggc cac tac tat tcc ttc att aag gac agg cga ggg tgt 245
Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg Gly Cys
1 5 10
gga aaa gga aag tgg ctg gg 265
Gly Lys Gly Lys Trp Leu
15

<210> 417
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..228
<221> sig_peptide
<222> 160..219
<223> Von Heijne matrix
score 4.90000009536743
seq LHLXSSRXPPILA/SP

<221> misc_feature
<222> 166..167,190
<223> n=a, g, c or t
Oligonucleotide

<400> 417
ttgtctgtct taggcctgga cactgttggt gacttatttc cagattttta tttctctttg 60
gttgaagact gccaaactgtc tcatagagtg tttgatttat ttatttatty athtwgacat 120
gaggwykctc tctgcmaacc caggctggak tgcagtgc atg atv nng gct cac 174
Met Xaa Xaa Ala His
-20
ttc agc ctc cac ctc nkg agc tca agg art cck ccc atc tta gcc tcc 222
Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro Pro Ile Leu Ala Ser
-15 -10 -5 1
cca gta 228
Pro Val

<210> 418

<211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..223

<221> sig_peptide
 <222> 125..175
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VCELSIFFTYVLA/IY

<400> 418
 aaaagtttgt aataagttgc actttcatca agactgtatt agggagtcca gtctcccccac 60
 atccttgtca gcacgggatg acatcagtct tttaaattctt accaacttat tgggaaaaaaa 120
 aaaa atg ata cgt cct gtt tgt gaa ttg agc att ttt ttc acc tat gta 169
 Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val
 -15 -10 -5
 cta gcc att tac ata tct cct tct gtg aat tgt ctg ttt ata tcc ttt 217
 Leu Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe
 1 5 10
 cct gcg gg 225
 Pro Ala
 15

<210> 419
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..293

<221> sig_peptide
 <222> 42..128
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LLSARLLSQEKRA/AE

<400> 419
 gtgctctatg gagctattgc ggccgtgggt ggtcgcgggc r atg cgg ggc tgc cag 56
 Met Arg Gly Cys Gln
 -25
 ctc ctc ggg ctt cgt agc tct tgg ccc ggg gac cta cta agt gct cgg 104
 Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg
 -20 -15 -10
 ctc ttg tcc caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag 152
 Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu
 -5 1 5
 act gtg tcg gaa gag gag aag agg ggg gac tta aca tca gtt gta agt 200
 Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu Thr Ser Val Val Ser

10	15	20	
cta gag tac cct gaa gtg caa tta cag ggt caa agg gtc tat gcm ttc	248		
Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln Arg Val Tyr Ala Phe			
25 30 35 40			
ctg tca ccc att tgt acc tat ggc tct gag gga tgc agc ctc aag	293		
Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly Cys Ser Leu Lys			
45 50 55			

<210> 420
 <211> 194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..194

<221> sig_peptide
 <222> 30..134
 <223> Von Heijne matrix
 score 4.80000019073486
 seq PWVLDIFLTLVFA/LG

<400> 420	
agttgctaga aagcaatgcg cctattcac atg gag aat ctt ccc ttt cct cta	53
Met Glu Asn Leu Pro Phe Pro Leu	
-35 -30	
aaa tta ctt agt gcc tca tca cta aac acc ccc agc tcc aca cca tgg	101
Lys Leu Leu Ser Ala Ser Ser Leu Asn Thr Pro Ser Ser Thr Pro Trp	
-25 -20 -15	
gtg ttg gat atc ttc ctc acc ttg gtg ttt gcc ctg ggg ttc ttc ttc	149
Val Leu Asp Ile Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe Phe	
-10 -5 1 5	
cta tta ctc ccc tac ttc tct tac ctc cgt tgt gac aac cca cca	194
Leu Leu Leu Pro Tyr Phe Ser Tyr Leu Arg Cys Asp Asn Pro Pro	
10 15 20	

<210> 421
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..88

<221> sig_peptide
 <222> 29..67
 <223> Von Heijne matrix
 score 4.80000019073486
 seq MCVCFVFAIFGVRC/CV

<221> misc_feature
 <222> 61

<223> n=a, g, c or t
Oligonucleotide

<400> 421
tatttgggat ttgttgctct gtgtgtat atg tgc gtg tgt gtg ttt gct ata 52
Met Cys Val Cys Val Phe Ala Ile
-10
ttt ggg gtn cgt tgc tgt gtg tgt gtc cgc tgt att tg 90
Phe Gly Val Arg Cys Cys Val Cys Val Arg Cys Ile
-5 1 5

<210> 422
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..159
<221> sig_peptide
<222> 22..153
<223> Von Heijne matrix
score 4.80000019073486
seq XPCPLLFPGACFP/CP

<400> 422
tcatttggtt ttttatttaa t atg att tgc ata ttt tac tct aag att tcc 51
Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser
-40 -35
atc tct gtc ggc tgt ggg agg aca gca gcc gag caa gtt gga tgt aaa 99
Ile Ser Val Gly Cys Gly Arg Thr Ala Ala Glu Gln Val Gly Cys Lys
-30 -25 -20
cag agg tca ttt cac ckc ccy tgc cct ctg ctg ttt cct ggt gct tgc 147
Gln Arg Ser Phe His Xaa Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys
-15 -10 -5
ttt ccc tgc cca ac 161
Phe Pro Cys Pro
1

<210> 423
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 333..419

<221> sig_peptide
<222> 333..380
<223> Von Heijne matrix
score 4.80000019073486
seq ICSVSLMASDGASS/PV

<221> misc_feature
 <222> 323..324,328
 <223> n=a, g, c or t
 Oligonucleotide

<400> 423
 ctgccgcygg acacgggttc ttccagcttt tggctattgt gaataacgct gctatggaca 60
 tgaatgtaca aacatccctt cagatccctc ttccagttct tgtgggtaca taccgccgagt 120
 ggaactgtgg catcatatgg taactctgtg tttaacattt tgaggaacca ccctactgct 180
 tcccacagag gctgtaccag ttacttccc accaacagtg caaggattcc aatttctcca 240
 catccgtgcc aacactattt tctttttgtc gctgttgta ttgtttgtct ggaaaatagc 300
 catgctgagg ggtgagaggt grnnghanrg tt atg aat ttg att tgc gtt tcc 353

Met Asn Leu Ile Cys Val Ser
 -15 -10

ctg atg gcc agt gat ggg gca tct tcc cct gtg ctt ggt ggc tct tca 401
 Leu Met Ala Ser Asp Gly Ala Ser Ser Pro Val Leu Gly Gly Ser Ser

-5 1 5

cac tct tcc tcc cwt rgg g 420
 His Ser Ser Ser Xaa Xaa
 10

<210> 424
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 256..432

<221> sig_peptide
 <222> 256..396
 <223> Von Heijne matrix
 score 4.80000019073486
 seq LVSLPQASFSSS/SE

<400> 424
 agtgaggagt carggaggtg tgtgtgagag agagagagaa aagagagaga cagagacggg 60
 gagagagaga gggagagaga agagagggag gagggagaa gaaaagacgg agggaggtga 120
 ggaggaaggg agggggagag acagagacct agaggggctg aagaccaga cagagctggc 180
 agagctactg agaagaggac tggagcgctc tgagagcctc tcaagatctt ttgggggagc 240
 ccaataaatg tgaac atg gga tct gtc acr gga gct gtc ctc aag acg cta 291

Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu
 -45 -40

ctt ctg tta tct act caa aat tgg aac aga gtc gaa gct ggg aat tcc 339
 Leu Leu Leu Ser Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser

-35 -30 -25 -20
 tat gac tgt gat gat cct ctt gtg tct gcc ttg cct cag gca tcc ttc 387
 Tyr Asp Cys Asp Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe

-15 -10 -5

agc agt tct tcc gag ctc tcc agc agt cat agt cct gga ttt gca 432
 Ser Ser Ser Ser Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala

1 5 10

<210> 425
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 278..418

<221> sig_peptide
 <222> 278..370
 <223> Von Heijne matrix
 score 4.80000019073486
 seq FLLFLFSSCDVP/VP

<400> 425
 ccgaattatt ttagtggttac ttatctttga ataaaatgta tttttcttgg atcaattagt 60
 tgcagcacgt tcttaggaat ggaatagaga agcatcctaa gccagaagga tttttttttt 120
 tctagatcac agtgaagctt taatatggkk ggatatttgt cccagcccaa atcccatgct 180
 gaattgaaac ccctagtgtt ggaggtgggg cctggtggaa ggtgtttgga tcatgaggac 240
 acatctctga tgaatggcct agctcatcct cttagtgt atg atg agt gag tyc tca 295
 Met Met Ser Glu Xaa Ser
 -30
 caa gat ctg gtt gta aag tgt gcc cca cca csg cca ttc ttt ctc ttg 343
 Gln Asp Leu Val Val Lys Cys Ala Pro Pro Xaa Pro Phe Phe Leu Leu
 -25 -20 -15 -10
 ttc ctg ttt tct tca tgt gat gtg cct gtt ccc ctt cac ctt ctg caa 391
 Phe Leu Phe Ser Ser Cys Asp Val Pro Val Pro Leu His Leu Leu Gln
 -5 1 5
 tgg ctg caa agc ttc ctg agg cct agg g 419
 Trp Leu Gln Ser Phe Leu Arg Pro Arg
 10 15

<210> 426
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..230

<221> sig_peptide
 <222> 54..134
 <223> Von Heijne matrix
 score 4.80000019073486
 seq VLLTSGVKPQTFA/VS

<400> 426
 gcagtgagtg ttacagttct taaagatggt gtgtccggag tttgttcctt cca atg 56
 Met
 ttc aga tgt gtc cgg ttt ctt cct tct ggc ggg ttc gtg gtc ttg ctg 104
 Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu Leu

-25	-20	-15	
act tca gga gtg aag cca caa acc ttc gca gtg agt gtt aca gct ctt			152
Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala Leu			
-10	-5	1	5
aaa ggt ggc atg ccc gga gtt gtt cat tcc tcc ggt ggg ttc gtg gtt			200
Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val Val			
10	15	20	
ttg cta act tca gga gcg aas tgc aga cct tc			232
Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro			
25	30		

<210> 427
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 226..381
 <221> sig_peptide
 <222> 226..315
 <223> Von Heijne matrix
 score 4.80000019073486
 seq CLFLNARLAGTLC/QL

<400> 427	
acagacatca gctcgggtca accgcgggcc tcgagccoga gtggctgagg gctgttacct	60
tcaaacccttt gaatcccacg ttttcccctt gacttcctgt caccgttaga gaaaagtgga	120
cagcgtctcg gtcacagagt tggagaaata gtgcagggac tcttcaggga gacggttttc	180
ctcatcaaag caaactgcaa aatcgcttct gccggcgtgg acctg atg aga gtc ggt	237
Met Arg Val Gly	
-30	
cgt cgt gag gga cac cct ctg ttc cct aac gtc ccc cgc tgc tta ttt	285
Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro Arg Cys Leu Phe	
-25	-20
-15	
tta aac gct cgg ttg gcg gga acc ctg tgc cag ctg aaa ctc ctt cag	333
Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu Lys Leu Leu Gln	
-10	-5
1	5
ttt ggc cgc cta gga aac acc gag agt cac cta cat ggg ctg gct ggg	381
Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His Gly Leu Ala Gly	
10	15
20	
gg	383

<210> 428
 <211> 132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..130
 <221> sig_peptide

<222> 32..124

<223> Von Heijne matrix

score 4.80000019073486

seq LLCPLTCPHHSLS/TV

<400> 428

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ttcaacaaat gagtcatagt gttttcgtat t atg tat ttt gat atc cag att      52
                                   Met Tyr Phe Asp Ile Gln Ile
                                   -30 -25
gtc tca gat gtg gtc agc ggg att ccc ttc aaa ctt ctg tgc cct tta      100
Val Ser Asp Val Val Ser Gly Ile Pro Phe Lys Leu Leu Cys Pro Leu
                                   -20 -15 -10
aca tgt ccc cat cat tct ctg agc acc gtg gg      132
Thr Cys Pro His His Ser Leu Ser Thr Val
                                   -5 1
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<210> 429

<211> 165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..165

<221> sig_peptide

<222> 25..117

<223> Von Heijne matrix

score 4.80000019073486

seq FSPFLPSLPLEA/ER

<400> 429

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caaactgttg aaaagttaac tctt atg tta ttt ata ttt tca gac ata gat      51
                                   Met Leu Phe Ile Phe Ser Asp Ile Asp
                                   -30 -25
tgg aag atg gac tta tgc ttt ttc tct ttc tct cct ttc ctt occ tcc      99
Trp Lys Met Asp Leu Cys Phe Phe Ser Phe Ser Pro Phe Leu Pro Ser
                                   -20 -15 -10
ctt cct ttg ttg gag gct gaa aga atg agg gtc agt gat caa ctt cag      147
Leu Pro Leu Leu Glu Ala Glu Arg Met Arg Val Ser Asp Gln Leu Gln
                                   -5 1 5 10
tat acc act gga kac ggg      165
Tyr Thr Thr Gly Xaa Gly
                                   15
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<210> 430

<211> 236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 52..234

<221> sig_peptide
 <222> 52..159
 <223> Von Heijne matrix
 score 4.80000019073486
 seq VLLAIGMFFTAWF/FV

<400> 430
 gccgacgtgt tcttccggtg gcggasggcg gattagcctt cgcggggcaa a atg gag 57
 Met Glu
 -35
 ctc gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc ttc 105
 Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
 -30 -25 -20
 ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc gcc 153
 Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
 -15 -10 -5
 tgg ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat atc 201
 Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
 1 5 10
 tat aaa gag ctc ctc atc tcc tta gtg gcc cga gg 236
 Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
 15 20 25

<210> 431
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 <212> DNA
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 score 4.80000019073486
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 agccccctgc cctgcctccc ctttcacat gtttctctg acaagatttt aagtacagca 120
 attcaagaag atttctctc ctaaacgaca tttatctgaa gtctattgcc tcttgattgc 180
 tggaaaagad tcttaaaatc atttcaaaag taacttataa acaaacttat taaaagtg 238
 atg aaa gga gca ttg aaa tta att agc act aat ttt tca ctg tgc caa 286
 Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
 -15 -10 -5
 agt gtg cag tgt cct tca gag gaa aca ata aca gat ctg gtg agt gtg 334
 Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
 1 5 10 15

cca tgc cag tng gga ctg gg
 Pro Cys Gln Xaa Gly Leu
 20

354

<210> 432
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 <222> 153..359
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 accgttgatg ggactgagaa accagagtta aaacctcttt ggagcttctg aggactcagc 120
 tggaaccaac gggcacagtt ggcaacacca tc atg aca tca caa cct gtt ccc 173
 Met Thr Ser Gln Pro Val Pro
 -65
 aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa 221
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
 -60 -55 -50
 gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa 269
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
 -45 -40 -35
 cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt 317
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
 -30 -25 -20 -15
 ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc 365
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
 -10 -5 1
 tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac 413
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 5 10 15
 cca ttc ata gga ccc ggg 431
 Pro Phe Ile Gly Pro Gly
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seq IVSAACKCGSSQA/AI

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                                         Met Val Asp Glu Cys Leu
                                         -40                               -35
aca gag cct gtg tgg gga agc aaa agg caa ggg tgt agt tca cag gca      102
Thr Glu Pro Val Trp Gly Ser Lys Arg Gln Gly Cys Ser Ser Gln Ala
          -30                               -25                               -20
gaa gcg agc tgt gac att gtc agt gca gcg tgt aag tgt ggc tcc tca      150
Glu Ala Ser Cys Asp Ile Val Ser Ala Ala Cys Lys Cys Gly Ser Ser
          -15                               -10                               -5
cag gcg gcc att gat tgt gag acc tca tct tgc tct gaa gat ttc ccg      198
Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser Cys Ser Glu Asp Phe Pro
          1                               5                               10
gtg
Val
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<210> 434

<211> 334

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<222> 242..283

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<400> 434

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caagactttc cccctcttgc tgccacagat gcagtgaagc ctgccatata taaggtacaa      120
tgtgtggcaa ctctgcaggt ggggtctatg caagctacag acccctctga gtgtggtcag      180
tgccttagcc tggcctggat gcctaccagg cccacccaac acctagctgc tggatattat      240
a atg gca tgg tgg ttt tct gga acc ttc cca cta act cac ccc tgc agc      289
  Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
          -10                               -5                               1
gga tac ggc tct ctg atg gct cct tct agc cct acc cct tct ggg      334
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
          5                               10                               15
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score 4.80000019073486

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catcgtggag ctggggcccc cttttgcctg ggagttttgt agtcgcctag ggtcagcggg 120
gacatcccaa agggcaggcc cggcagccgc c atg gtg gcc aag gat tac ccc 172
Met Val Ala Lys Asp Tyr Pro
-55
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```
ttc tac ctc acg gtc aag aga gcg aac tgc agc ctg gag cta cct ccg 220
Phe Tyr Leu Thr Val Lys Arg Ala Asn Cys Ser Leu Glu Leu Pro Pro
-50 -45 -40 -35
gcc agc ggt ccg gcc aag gac gct gag gag cct agt aat aaa cgg gtc 268
Ala Ser Gly Pro Ala Lys Asp Ala Glu Glu Pro Ser Asn Lys Arg Val
-30 -25 -20
aaa ccc ctt tcc cga gtc acg tcg cta gca aac ctc atc ccg ccc gtg 316
Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val
-15 -10 -5
aag gcc acg cca tta aag cgc ttc agt caa acc ctg cag cgc tcc att 364
Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile
1 5 10
agc ttc cgc agt gag agc gcc t 386
Ser Phe Arg Ser Glu Ser Ala
15 20
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<210> 436

<211> 472

<212> DNA

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<221> CDS

<222> 191..472

<221> sig_peptide

<222> 191..274

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score 4.80000019073486

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<400> 436

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gcgagcatcc tggccagaac aagccaagga gccaagacga gagggacaca cggacaaaca 120
acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg 180
cgcccgaggg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc 229
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
-25 -20
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```

gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac      277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His
-15          -10          -5          1
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc      325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
          5          10          15
cca agg gaa cat cag ttc tac gag acc ctc cct gct gag atg cgc aaa      373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys
          20          25          30
ttc act ccc cag tac aaa gga caa agc caa agg ccc ctt gtt agc tgg      421
Phe Thr Pro Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp
          35          40          45
cca tcc ctg ccc cat ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag      469
Pro Ser Leu Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln
50          55          60          65
gga
Gly

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<210> 437
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<212> DNA
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<220>
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tacatccatg aagctaggag agcgacactc aaagactgca ctattgagag aagctaacgt      120
taaaggcagt gaatatattc gggagtccag ctccggaacc cgggagctct tttagtggga      180
ggggcgggcg tgatggcgct tctggcctcc ga atg cta ggg ggc gct gtg atc      233
                               Met Leu Gly Gly Ala Val Ile
                               -30
gcc ggg cgg cct ctt ggg cgc tgg gag tcc acc gcg caa ssc atc ctg      281
Ala Gly Arg Pro Leu Gly Arg Trp Glu Ser Thr Ala Gln Xaa Ile Leu
          -25          -20          -15
gcc ttt ctt cag tcc cca cgt gcg atc ctt ccc ggc aac ttt ttc gag      329
Ala Phe Leu Gln Ser Pro Arg Ala Ile Leu Pro Gly Asn Phe Phe Glu
          -10          -5          1          5
aaa aat gcc caa att caa ggc ggc ccg tgg ggt ggg ggg tca gga aaa      377
Lys Asn Ala Gln Ile Gln Gly Gly Pro Trp Gly Gly Gly Ser Gly Lys
          10          15          20

```

```

aca tgc gcc cct ggc cga tsa gat cct ggc tgg gaa tgc ggt gcg ggc      425
Thr Cys Ala Pro Gly Arg Xaa Asp Pro Gly Trp Glu Cys Gly Ala Gly
          25                      30                      35
ggg ggt nng gga gaa gcg gcg ggg tcg cgg gam agg ara agc gg      469
Gly Gly Xaa Gly Glu Ala Ala Gly Ser Arg Xaa Arg Xaa Ser
          40                      45                      50

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<210> 438
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<212> DNA
<213> Homo sapiens

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ttgattcttc ctatcc atg agc atg gca tgt ttt ttc cat ttg ttt gtg tca      112
          Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser
          -15                      -10                      -5
tct ctg att tcc ttt gag cag tgt ttt gka atg cta aga aaa ttg ctt      160
Ser Leu Ile Ser Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu
          1                      5                      10
aaa att ata      169
Lys Ile Ile
          15

```

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<210> 439
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<220>
<221> CDS
<222> 211..447

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<221> sig_peptide
<222> 211..345
<223> Von Heijne matrix
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      seq PWLEVGLFFWLHA/AP

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cttttgccct gcaggattct ttttcattct tgcagggact tctggggccg gagtatgtaa      120
aactcctggg tctctgtgtg tgccctgagt gctgctctac tgagactctg catacacagc      180
tctgtatatc ggacccawgg ccctggtggc atg ggc tca cga gga gat ccc ctg      234

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                                -45                                -40
atc tgt ggg ttg caa aga tct gtg gga gaa gtg tgg ttt cct gga tgg      282
Ile Cys Gly Leu Gln Arg Ser Val Gly Glu Val Trp Phe Pro Gly Trp
      -35                                -30                                -25
ggg cac aca atc act cac tgc ttc cct tgg ctg gag gtg ggg ctt ttt      330
Gly His Thr Ile Thr His Cys Phe Pro Trp Leu Glu Val Gly Leu Phe
      -20                                -15                                -10
ttt tgg ctc cat gct gct cct ggg cgg gcg att gcc cta ccc cat ttt      378
Phe Trp Leu His Ala Ala Pro Gly Arg Ala Ile Ala Leu Pro His Phe
      -5                                1                                5                                10
tct tca ttc tct gtg ggt caa gdb gtt cac ttg gtc agt cca ttg tgr      426
Ser Ser Phe Ser Val Gly Gln Xaa Val His Leu Val Ser Pro Leu Xaa
      15                                20                                25
gam ctg gat att tca gtt gaa      447
Xaa Leu Asp Ile Ser Val Glu
      30

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gcaccactgg tgtctccwrc gcctgcaccg gctcctgcac gtgcaaagag tgcaa atg      178
                                                Met
cac ctc ctg caa gaa gag ctg ctg ctc ctg ctg ccc cgt ggg ctg tgc      226
His Leu Leu Gln Glu Glu Leu Leu Leu Leu Leu Pro Arg Gly Leu Cys
      -15                                -10                                -5
caa gtg tgc cca cgg ctg tgt ctg caa agg gmc gtt gga gaa ctg cag      274
Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu Gln
      1                                5                                10
mtg cnn nky cct gat gtg gga aca gct ctt ctc cca gat gtt aat aga      322
Xaa Xaa Xaa Pro Asp Val Gly Thr Ala Leu Leu Pro Asp Val Asn Arg
      15                                20                                25                                30
aca agc tgc aca acc tgg      340
Thr Ser Cys Thr Thr Trp

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 <222> 292..408

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 <222> 292..375
 <223> Von Heijne matrix
 score 4.69999980926514
 seq QLVTRLLLSPSQS/TQ

<400> 441
 agaagatggg gaaagaggaa ggaaaggatg cccagatata gggagcttta gcgatgtagt 60
 gaacggacag aagatcagga acaagttgag ttcattgtgt ggagatggca rraagatgga 120
 gattggtgag ctgagtggag aagtgccata gacgggtgtt ttgccagagt gtctgcggat 180
 tgctcatacc tgggaaggat tctttgtatg gttcccttag gctgagggag ggtatcagct 240
 ttacagacct tgtgggatta caaaagggcc accacacact cttcaaccaa t atg tgt 297
 Met Cys
 cta tct tgc att caa ggc tca ttc ttt gtt gaa att ttg cag ttg gtc 345
 Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln Leu Val
 -25 -20 -15
 act agg cta ttg tta tct cca tct caa agt aca cag aca cac aca cac 393
 Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His Thr His
 -10 -5 1 5
 aca cac aca cac aca a 409
 Thr His Thr His Thr
 10

<210> 442
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 203..319

<221> sig_peptide
 <222> 203..298
 <223> Von Heijne matrix
 score 4.69999980926514
 seq AILLLVXVSDKNE/QQ

<221> misc_feature
 <222> 225..227,279
 <223> n=a, g, c or t
 Oligonucleotide

<400> 442
cacactagaa tagactggaa caacttggat ttagtgattc cgatgcttat caggaaggtc 60
tctgttcttt tataggaaga aaaaacatag ttatTTTTtct tttatgatac aaaggatatgc 120
tttctatgca agctggatac cagaccaaga ataataaatc acaatttcat aaggtttcta 180
agacttgata ttatatgggg at atg acc att ttg agg gaa atg tnn nca tca 232
Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser
-30 -25
ctt tat gta ctt gaa gct aag gat act gct atc tta ttg ctt gtt tna 280
Leu Tyr Val Leu Glu Ala Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa
-20 -15 -10
gtg agc gat aag aat gaa cag cag ctt ggg agg ggc gtg g 320
Val Ser Asp Lys Asn Glu Gln Gln Leu Gly Arg Gly Val
-5 1 5

<210> 443
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 102..254
<221> sig_peptide
<222> 102..188
<223> Von Heijne matrix
score 4.69999980926514
seq ICCNLYFLLFCRS/SF

<400> 443
cttcttttcta actcctgcat atacctttgc atttatgtag cttctggagg gcacatggag 60
gtagctcacc atggtttttaa tttgcatttc tctgataatg a atg aga ctt agt tct 116
Met Arg Leu Ser Ser
-25
tcc tgt ggg ttg cct gtt aag act ttg cca ttt atc tgt tgc aat ctt 164
Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe Ile Cys Cys Asn Leu
-20 -15 -10
tat ttc ttg ctg ttt tgt agg agt tct ttt tta tat ttt gga tat gat 212
Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu Tyr Phe Gly Tyr Asp
-5 1 5
ccc att aat act tac atg tat tac aat gtt ttc tcc cac tcg gg 256
Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe Ser His Ser
10 15 20

<210> 444
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..283
<221> sig_peptide

<222> 17..220

<223> Von Heijne matrix

score 4.69999980926514

seq GCLLXPLLVSCLG/SL

<400> 444

tagatggcga ctcctt atg tta ctg acg aga ccg gcg gtg agt gcg gga ggc 52
Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly

-65 -60

gcg gas cgc ttc tct ccg ggc tct cgg ggc agg ggt tcg gac ttg gaa 100
Ala Xaa Arg Phe Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu

-55 -50 -45

agg ggt ctg tgc ccc gcc cat ccc ggg gcc cct cct ttg ccc cgc ccc 148
Arg Gly Leu Cys Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro

-40 -35 -30 -25
ccg gac cgc ctt ccc cat tca ttc tct cct acg ggg tgt ctc ctg hgc 196
Pro Asp Arg Leu Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa

-20 -15 -10

ccc ctt ctg gtc tcg tgt ttg ggg tct ctg ctt ccg gtc acc caa acc 244
Pro Leu Leu Val Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr

-5 1 5

ctg ggg tcc ttc agt gct ggt ccc tgc ttc agg acc ctc a 284
Leu Gly Ser Phe Ser Ala Gly Pro Cys Phe Arg Thr Leu

10 15 20

<210> 445

<211> 240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 103..240

<221> sig_peptide

<222> 103..177

<223> Von Heijne matrix

score 4.69999980926514

seq ILXSLSSSVPSRA/GS

<400> 445

tcttttgtaa tgaagcatgg cagccaggcc tagcacactt ccctctgcac accatcctgc 60
tcaggcctct gtgcctcggc tgtgctgttc cttctgcttg ga atg cat tca ctg 114

Met His Ser Leu

-25

tgt cca ctt agc caa ttc cta cct att ctt tma agc ctc agt tcc agt 162
Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser Leu Ser Ser Ser

-20 -15 -10

gtc ccc tcg agg gca ggc agt gct ttc cca tct gcc cta ggt cca ctc 210
Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala Leu Gly Pro Leu

-5 1 5 10

tac cag cct cta ctt ggg ccc cca gca tgg 240
Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp

15 20

<210> 446
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..184

<221> sig_peptide
 <222> 8..139
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LVFLSVXLLFLLF/LV

<400> 446
 tcctttt atg cga aca caa gta tat gag ggg ttg tgt aaa aat tat ttt 49
 Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe
 -40 -35
 tct ctt gct gta cta caa aga gat aga atc aaa ctg ctt ttt ttc gac 97
 Ser Leu Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp
 -30 -25 -20 -15
 ata ctg gtt ttt ctt tct gtt tww ctt ctc ttt ctt cta ttt ctt gtg 145
 Ile Leu Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val
 -10 -5 1
 gat atw atg gct aat adc aca aca agt tta ggg agg ccc 184
 Asp Ile Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
 5 10 15

<210> 447
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..360

<221> sig_peptide
 <222> 34..168
 <223> Von Heijne matrix
 score 4.69999980926514
 seq LLSLAQTTKTTA/TT

<221> misc_feature
 <222> 280
 <223> n=a, g, c or t
 Oligonucleotide

<400> 447
 aaaaactctt ttcttttatcc tctttocaga aaa atg ggc caa ttc aca gct gca 54
 Met Gly Gln Phe Thr Ala Ala
 -45 -40

atg gtt ggg aga att tcc tgt ctg gga gtc tgg aaa ctg cca aga gtg	102
Met Val Gly Arg Ile Ser Cys Leu Gly Val Trp Lys Leu Pro Arg Val	
-35 -30 -25	
gaa agc tgc agc cag cca gcg agg cct ctg ttg tca ctg gcc caa aca	150
Glu Ser Cys Ser Gln Pro Ala Arg Pro Leu Leu Ser Leu Ala Gln Thr	
-20 -15 -10	
aca aca aaa aca acc gca aca aca aca aca aca aaa cat gcc acg	198
Thr Thr Lys Thr Thr Ala Thr Thr Thr Thr Thr Thr Lys His Ala Thr	
-5 1 5 10	
tgt gca ctg gca tat aca aac acg ccc aca gaa cca vrc caa gcg gac	246
Cys Ala Leu Ala Tyr Thr Asn Thr Pro Thr Glu Pro Xaa Gln Ala Asp	
15 20 25	
aag gct tca agg aga gct tct ggg ahv ctc rwv ncc gcg gcg agg cat	294
Lys Ala Ser Arg Arg Ala Ser Gly Xaa Leu Xaa Xaa Ala Ala Arg His	
30 35 40	
atc cct tgg cat ggt gcc act gca gcc cag ctc cca gcc ccc ccg cca	342
Ile Pro Trp His Gly Ala Thr Ala Ala Gln Leu Pro Ala Pro Pro Pro	
45 50 55	
tct gtc atc agc gct ctg	360
Ser Val Ile Ser Ala Leu	
60	

<210> 448
 <211> 123
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..122

<221> sig_peptide
 <222> 39..92
 <223> Von Heijne matrix
 score 4.69999980926514
 seq IAILFPNSGSCFA/FS

<400> 448	
cttatctgat tcacagcccg tattcagatt tgccaatt atg ttg att ttc att att	56
Met Leu Ile Phe Ile Ile	
-15	

gct att tta ttt ccc aat tca gga tca tgc ttt gca ttt agt tgt cat	104
Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys Phe Ala Phe Ser Cys His	
-10 -5 1	

gtc tcc ttt ttt ttt ttt t	123
Val Ser Phe Phe Phe Phe	
5 10	

<210> 449
 <211> 193
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 18..191

<221> sig_peptide
<222> 18..62
<223> Von Heijne matrix
score 4.69999980926514
seq RCACFPFFPFAFC/HD

<400> 449
ctctctctctg ttcgggtc atg gtg aga tgt gct tgc ttc ccc ttc ttc ccc 50
Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro
-15 -10 -5
ttc gcc ttc tgc cat gac tgt aag ttt ctt ggg gcc tcc cag tca tgc 98
Phe Ala Phe Cys His Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys
1 5 10
ttc ttg tta agc cgg caa aac tgt gta agc aca gga kga cct tca tcc 146
Phe Leu Leu Ser Arg Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser
15 20 25
aaa tct gat atc aac tca agg tct gga tct tgt tca ctg gca agg gg 193
Lys Ser Asp Ile Asn Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg
30 35 40

<210> 450
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..301

<221> sig_peptide
<222> 8..88
<223> Von Heijne matrix
score 4.69999980926514
seq LAPLXLVFISLLP/AP

<221> misc_feature
<222> 292
<223> n=a, g, c or t
Oligonucleotide

<400> 450
ccagcaa atg gtg agt ttg agg gta ggg gcc tct cca ttt cgg ttc cca 49
Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro
-25 -20 -15
ctg gcc ccc ctc tbt ttg gtt ttc atc tct ctt ctc cca gcc cca ttt 97
Leu Ala Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe
-10 -5 1
ttt cct act ctt tcg ttt cct tgt tgc tgt gtg tcc tgg ctc ttt tct 145
Phe Pro Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser
5 10 15
ctt tct gtg vtt gtc tct ctg cgt ctc agt ctt tbt gtg tcc tgt tta 193

Leu Ser Val Xaa Val Ser Leu Arg Leu Ser Leu Xaa Val Ser Cys Leu	
20 25 30 35	
tct ctc tgg tgt ctc ttg gta ttg ttt ctc tct ccc act ctg tat gtc	241
Ser Leu Trp Cys Leu Leu Val Leu Phe Leu Ser Pro Thr Leu Tyr Val	
40 45 50	
tct gac tca ttc tgc tca ttc tgt gtc ctc cct att gct ctc tgt ccc	289
Ser Asp Ser Phe Cys Ser Phe Cys Val Leu Pro Ile Ala Leu Cys Pro	
55 60 65	
can gct cgt tct t	302
Xaa Ala Arg Ser	
70	

<210> 451
 <211> 367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 150..365
 <221> sig_peptide
 <222> 150..311
 <223> Von Heijne matrix
 score 4.69999980926514
 seq PGLAFLAILTVLA/KP

<400> 451	
aaaatgatcc atgcacacag cctctatagg aaagaaaaaa aatatccaat tgattttctt	60
ccctttttctg cttctaaagt ataccaaatt tcaactgtgat cttaatatcc cccagaacag	120
acacctctga gcagagagca ggccttaga atg gcc cac ccc tgt tta gct cca	173
Met Ala His Pro Cys Leu Ala Pro	
-50	
gca gaa cct tct act ctt tca caa acc kcc cat cca att caa aga acc	221
Ala Glu Pro Ser Thr Leu Ser Gln Thr Xaa His Pro Ile Gln Arg Thr	
-45 -40 -35	
ctg aca act ttc cct cag gct tgg gtt cta acc agc agc ttt tcc ata	269
Leu Thr Thr Phe Pro Gln Ala Trp Val Leu Thr Ser Ser Phe Ser Ile	
-30 -25 -20 -15	
cag cca ggc ctt gca ttc cta gcc att ctc acc gtg tta gcc aaa ccc	317
Gln Pro Gly Leu Ala Phe Leu Ala Ile Leu Thr Val Leu Ala Lys Pro	
-10 -5 1	
ggs tcc tct amc tgg agt cct ggt cag ttc aca cca cac tcc ctg ctg	365
Gly Ser Ser Xaa Trp Ser Pro Gly Gln Phe Thr Pro His Ser Leu Leu	
5 10 15	
gg	367

<210> 452
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 244..348

<221> sig_peptide

<222> 244..336

<223> Von Heijne matrix

score 4.69999980926514

seq HLYXSLFSSFLCS/TP

<400> 452

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ttctttcark tcttactact catccttcat ttatctcctg gatcattgcc cagagaatga      60
aagaaattgc cagtcaagcc agccaggtag gttaaactta tcctggcagt cctggagact      120
gctgcagaact gactgcctga tgtccgtgcc cactgggggt tttccctttt cagaaaggat      180
ttctccctga tctctcccca caaactctgg ctttgctttt tcatttccta agagcaactc      240
aat atg cat ttc ccc atc caa gct acc ttc sac tat tcc cct act gat      288
  Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp
    -30                -25                -20

tct ctc tgt cat tta tat ttk tca ctc ttc tct tcc ttt ctc tgc tct      336
Ser Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser
  -15                -10                -5

acc cct gcc cgg g      349
Thr Pro Ala Arg
1
```

<210> 453

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 87..269

<221> sig_peptide

<222> 87..194

<223> Von Heijne matrix

score 4.69999980926514

seq SCFVPSLVTGALQ/QS

<400> 453

```
agcagtccag agaagtgaat tgacttgcct gaagccacag agcctgcaag tgcgagggct      60
gggattccaa tccaagctct gggcca atg gct ttg cat atc cta gaa tgc gag      113
                Met Ala Leu His Ile Leu Glu Cys Glu
                  -35                -30

agg aac gtt tgt ttt gta gca gtt aga cag cct gct cat gaa agc tgc      161
Arg Asn Val Cys Phe Val Ala Val Arg Gln Pro Ala His Glu Ser Cys
  -25                -20                -15

ttt gtg ccc agc ctt gtg aca ggt gct tta caa caa tcc cag aca cag      209
Phe Val Pro Ser Leu Val Thr Gly Ala Leu Gln Gln Ser Gln Thr Gln
  -10                -5                1                5

cac cca cct tgg gtt tgc cct cag gta cag ggc tcc tat cca tcc tgg      257
His Pro Pro Trp Val Cys Pro Gln Val Gln Gly Ser Tyr Pro Ser Trp
          10                15                20

aag aac aga ggg a      270
Lys Asn Arg Gly
```

<210> 454
 <211> 492
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 317..490

<221> sig_peptide
 <222> 317..412
 <223> Von Heijne matrix
 score 4.69999980926514
 seq RVLXLCNSRVST/RX

<221> misc_feature
 <222> 415..416
 <223> n=a, g, c or t
 Oligonucleotide

<400> 454
 taaggatatt acaaaacatt ttataaacac gtgggtctct tatgaagtac aatccaaagt 60
 ttgcatacaa tttaaaacaa aagcaagaaa tgtcacgctt tgggaacact gtttktctca 120
 cactaaaatg ttctatctga agcaagggga agtgtccaaa ttatagttca caaaatacct 180
 ttatttttctc acaacaaaat catccctagt cagcggccca acattactca tttctgtcat 240
 caaaaaacacc ctttctgtgg gttggtatga aatatccgca ggcatacaca gtactataag 300
 aaagggtttt ttcaaa atg tcc tgt act cac tcc tct tct aac ctg ggt aag 352
 Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys
 -30 -25
 ttt tct gta cac aga gag tac cgt gtc ctc mta ctg tgt aac agt agg 400
 Phe Ser Val His Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg
 -20 -15 -10 -5
 gtc tct ttc act cgn ntc cat gtg aag aga cca cca wac agg cta tgt 448
 Val Ser Phe Thr Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys
 1 5 10
 gtg agc agc aaa ggc tgt tta ttt cac ctg ggt gca ggc agg ct 492
 Val Ser Ser Lys Gly Cys Leu Phe His Leu Gly Ala Gly Arg
 15 20 25

<210> 455
 <211> 177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..175

<221> sig_peptide
 <222> 56..112
 <223> Von Heijne matrix
 score 4.69999980926514

seq AFPLLLVIILLFQ/KQ

```
<400> 455
cacattcata agtatgagct taggctgagg atatatatcc agtgggggat gaaac atg      58
                                         Met
ctt aag aaa ttg agt gca ttt cct tta tta ttg gtt att att ttg cta      106
Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu Leu
      -15                      -10                      -5
ttt caa aaa caa wtt gga ctt tta aaa aat tat amt tca cca cag aga      154
Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln Arg
      1                      5                      10
cag gtg ttg ttt tgt aat cga ag      177
Gln Val Leu Phe Cys Asn Arg
15                      20
```

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<210> 456
<211> 102
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 14..100

<221> sig_peptide
<222> 14..67
<223> Von Heijne matrix
      score 4.69999980926514
      seq CIFLAVLSKISWA/VN
```

```
<400> 456
ctaattgaaa agg atg tcc tat ttc cga tgt ata ttt ttg gca gtt ttg      49
      Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu
      -15                      -10
tca aaa atc agt tgg gct gta aat atg tgc agt ctt att tct ggg tcc      97
Ser Lys Ile Ser Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser
      -5                      1                      5                      10
tcg gg      102
Ser
```

```
<210> 457
<211> 151
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 35..151
```

```
<221> sig_peptide
<222> 35..136
<223> Von Heijne matrix
      score 4.59999990463257
      seq LFLSISLITLYYS/SE
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..311

<221> sig_peptide
<222> 15..86
<223> Von Heijne matrix
score 4.59999990463257
seq QGMLLAILEXCGA/IP

<400> 459
tcctcaagtt cttc atg gtc aag tcc gtc atc ttt ctt tcc ttc tgg caa 50
Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln
-20 -15
ggc atg ctc ctg gcc atc ctg gag rag tgt ggg gcc atc ccc aaa atc 98
Gly Met Leu Leu Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile
-10 -5 1
cac tcg gcc cgc gtg tcg gtg ggc gag ggc acc gtg gct gcc ggc tac 146
His Ser Ala Arg Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr
5 10 15 20
cag gac ttc atc atc tgt gtg gag atg ttc ttt gca gcc ctg gcc ctg 194
Gln Asp Phe Ile Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu
25 30 35
cgg cac gcc ttc acc tac aag gtc tat gct gac aag agg ctg gac gca 242
Arg His Ala Phe Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala
40 45 50
caa gtg cca aca tac ggc cct tac ggc cgc tgt gcc ccc atg aag agc 290
Gln Val Pro Thr Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser
55 60 65
atc tcc agc agc ctc aag gag 311
Ile Ser Ser Ser Leu Lys Glu
70 75

<210> 460
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..424

<221> sig_peptide
<222> 161..418
<223> Von Heijne matrix
score 4.59999990463257
seq AAAALCILILLXA/MY

<400> 460
aggccgggct gatgcgcagg caatttatca tcttgatctc ccaactgagtc agggagctct 60
cctgtcacca gtattgattt cagaggatgg actaaatttc ctaggatttc cattaagaat 120

```

taagaaaaaa gctctaagca cgcagggtag ccagacagac atg gat atg aga tgg      175
                                         Met Asp Met Arg Trp
                                         -85
cac tgt gaa aac tcg cag acc aca gat gac atc ctt gtg gcc tca gca      223
His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile Leu Val Ala Ser Ala
-80                               -75                               -70
gag tgt ccc agc gat gat gag gac att gac ccc tgt gag ccg agc tca      271
Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro Cys Glu Pro Ser Ser
-65                               -60                               -55                               -50
ggg ggg tta gcc aac cca acc cga gca ggc ggc aga gag ccg tat cca      319
Gly Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly Arg Glu Pro Tyr Pro
-45                               -40                               -35
ggc tca gca gaa gtg atc cgg gag tcc agc agc acc acg ggt atg gtc      367
Gly Ser Ala Glu Val Ile Arg Glu Ser Ser Thr Thr Gly Met Val
-30                               -25                               -20
gtt ggg ata gta gcc gct gcc gcc ctg tgc atc ctt atc ctc ctc wat      415
Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Xaa
-15                               -10                               -5
gcc atg tac a                                                              425
Ala Met Tyr
1

<210> 461
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..419

<221> sig_peptide
<222> 45..104
<223> Von Heijne matrix
      score 4.59999990463257
      seq PTLTLTCIGSVVS/SD

<400> 461
aaaaagctgt gggctcagaa gcagagttct ggggtgtctc cacc atg gcc tgg acy      56
                                         Met Ala Trp Thr
                                         -20
cct ctc tgg ccc act ctc ctc act ctt tgc ata ggt tct gtg gtt tct      104
Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly Ser Val Val Ser
-15                               -10                               -5
tct gac ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag aga      152
Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Arg
1                               5                               10                               15
gtc agg atc aca tgc cag gga gac aac ctc gaa gag tat ttt gca agc      200
Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu Tyr Phe Ala Ser
20                               25                               30
tgg tac cga cag agg ccc gga cag gcc cct gtc ctt gtc atc tat ggt      248
Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
35                               40                               45
aaa aac aac cgg ccc tca ggg att cca gsc cgr ktc tct ggc tcc aag      296

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Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Xaa	Arg	Xaa	Ser	Gly	Ser	Lys	
50						55					60					
tca	ggc	aat	aca	gct	tta	ttg	acc	atc	gyc	ggg	gct	cag	gcg	gag	gat	344
Ser	Gly	Asn	Thr	Ala	Leu	Leu	Thr	Ile	Xaa	Gly	Ala	Gln	Ala	Glu	Asp	
65					70				75					80		
gab	gct	gac	tat	tac	tgt	agt	kat	cgc	gac	cat	act	gat	aat	cgg	tgg	392
Xaa	Ala	Asp	Tyr	Tyr	Cys	Ser	Xaa	Arg	Asp	His	Thr	Asp	Asn	Arg	Trp	
			85					90					95			
gtg	ttc	ggc	ggg	ggg	acc	agg	ctg	aca	g							420
Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr								
			100				105									

<210> 462
 <211> 257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..255

<221> sig_peptide
 <222> 46..105
 <223> Von Heijne matrix
 score 4.59999990463257
 seq XILTCLIFRNSEG/FQ

<400> 462	
tttttttttt tccccaagcg aaswtgaaca gttgctaagt ggaaa atg gag gct gaa	57
	Met Glu Ala Glu
	-20
ttt tac atg gkg att ctt acc tgc ttg atc ttc agg aac tca gaa ggg	105
Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg Asn Ser Glu Gly	
-15	-10
	-5
ttt cag att gyc cat gtc cag aaa caa cag tgt ctt ttc aaa aat gag	153
Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu Phe Lys Asn Glu	
1	5
	10
	15
aaa gtg gtc gtg ggc tca tgc aac agg acc atc cag aac cag cag tgg	201
Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln Asn Gln Gln Trp	
20	25
	30
atg tgg act gag gat gaa aag ctc ctt cat gtt aaa tct gca ctg tgc	249
Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys Ser Ala Leu Cys	
35	40
	45
ttg gcc at	257
Leu Ala	
50	

<210> 463
 <211> 117
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 61..117

<221> sig_peptide

<222> 61..111

<223> Von Heijne matrix

score 4.59999990463257

seq ACALCVWLCKVSC/SI

<400> 463

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aataggaaga caaaagacaa aaaaaaatcc accaccacca aaatatccct ttgtacatgt      60
atg tgc gtg tgc gcg tgt gct ttg tgt gtg tgg ttg tgt gtt aaa tca      108
Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
      -15                -10                -5
tgc agt att                                117
Cys Ser Ile
      1
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<210> 464

<211> 142

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..140

<221> sig_peptide

<222> 39..101

<223> Von Heijne matrix

score 4.59999990463257

seq FIYLLAFCMPSE/KC

<400> 464

```
cttattgtgg attgtggttt taattttgta tttccctg atg att agt gat gtt cag      56
                                Met Ile Ser Asp Val Gln
                                -20
cac ctt ttc ata tac ttg tta gcc ttt tgt atg cct tcc ttg gag aaa      104
His Leu Phe Ile Tyr Leu Leu Ala Phe Cys Met Pro Ser Leu Glu Lys
-15                -10                -5                1
tgt cta tac ggg tct ttg gcc cac ttt ttt ttt ttt tt      142
Cys Leu Tyr Gly Ser Leu Ala His Phe Phe Phe Phe
      5                10
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<210> 465

<211> 300

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 216..299

<221> sig_peptide

<222> 216..260

<223> Von Heijne matrix
 score 4.59999990463257
 seq LFRVLFSXTCALX/QD

<400> 465
 agttacttct ttgctagggt gaggaagggt tggaagcgcc tctgcagcc acgaatatcc 60
 tccagtgcct gagagaaaac ggcctaactg aaaacgtccg cggcatacat ccattcttaa 120
 aacttgagtg gctgcttttc tgggtggaaa agagcggat cagacagggt gagcagtcgg 180
 ggaacggatg aacaaagact tgcaccgtgg ccctg atg cct ttg ttc cga gtt 233
 Met Pro Leu Phe Arg Val
 -15 -10
 cta ttc agt tgw act tgt gcg ttg twa cag gac ttt aga atg cag ccc 281
 Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln Asp Phe Arg Met Gln Pro
 -5 1 5
 tgc ccc cca acc ccc aag g 300
 Cys Pro Pro Thr Pro Lys
 10

<210> 466
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 146..235

<221> sig_peptide
 <222> 146..217
 <223> Von Heijne matrix
 score 4.59999990463257
 seq LLFYVLLFRNLYT/HT

<400> 466
 tttatatctt taattgcaag gataaaagaa ggggtgcac tcaaaggcca tgataaatat 60
 aaaggataga aaagttacgt tgatgggtgtg cccctcgata tctagaagat agcatagtc 120
 atgcattctc agaaagatcc tatcc atg tgg tat gta gag atg tgg gtt tct 172
 Met Trp Tyr Val Glu Met Trp Val Ser
 -20
 ttt ttt cta ctt ttt tat gtg ctt ctt ttt aga aac tta tac aca cac 220
 Phe Phe Leu Leu Phe Tyr Val Leu Leu Phe Arg Asn Leu Tyr Thr His
 -15 -10 -5 1
 aca cac cac act ggg 235
 Thr His His Thr Gly
 5

<210> 467
 <211> 220
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..219

<221> sig_peptide
 <222> 58..147
 <223> Von Heijne matrix
 score 4.59999990463257
 seq VLVVSFVVGGLGC/NX

<221> misc_feature
 <222> 218
 <223> n=a, g, c or t
 Oligonucleotide

<400> 467
 accacaactc ccagggtgct ccgcgtcctc gccgctgtcg ccgccgcgga gacaaag 57
 atg gct gcg aga gtc ggc gcc ttc ctc aag aat gcc tgg gac aag gag 105
 Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu
 -30 -25 -20 -15
 cca gtg ctg gtc gtg tcc ttc gtc gtc ggg ggc ctc ggc tgt aat dct 153
 Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa
 -10 -5 1
 gcc ccc att gag ccc cta ctt caa gta ctc cgt cat gat caa caa ggc 201
 Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly
 5 10 15
 cac gcc cta caa cta cna c 220
 His Ala Leu Gln Leu Xaa
 20

<210> 468
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 154..462

<221> sig_peptide
 <222> 154..222
 <223> Von Heijne matrix
 score 4.59999990463257
 seq WTCVAPVYPACSG/RR

<400> 468
 gactgcagcc gcgagctcct ggaggcggcg ggatggaggc ggccggccgag cctggaaacc 60
 tggccggcgt caggcacatc atcctgggtc tctcaggaaa ggggggcgtt gggaaaagca 120
 ccattctccac ggagctggcc ctggcactgc gcc atg cag gca aga agg tgg gaa 174
 Met Gln Ala Arg Arg Trp Glu
 -20
 tcc tgg atg tgg acc tgt gtg gcc cca gta tac ccc gca tgc tcg ggg 222
 Ser Trp Met Trp Thr Cys Val Ala Pro Val Tyr Pro Ala Cys Ser Gly
 -15 -10 -5
 cgc agg gca rdr gct gtk sac cag tgs grr ccg cgg ctg ggc amc sgt 270
 Arg Arg Ala Xaa Ala Val Xaa Gln Xaa Xaa Pro Arg Leu Gly Xaa Xaa
 1 5 10 15

ctt cct gga ccg gga bca gag cat ctc gct cat gtc tgt ggg ctt cct	318
Leu Pro Gly Pro Gly Xaa Glu His Leu Ala His Val Cys Gly Leu Pro	
20 25 30	
gct gga gaa gcc gga cga ggc cgt ggt gtg gag agg ccc caa gaa aaa	366
Ala Gly Glu Ala Gly Arg Gly Arg Gly Val Glu Arg Pro Gln Glu Lys	
35 40 45	
cgc gct gat aaa gca gtw kgt gtc cga cgt ggc ctg ggg gga gct gga	414
Arg Ala Asp Lys Ala Val Xaa Val Arg Arg Gly Leu Gly Gly Ala Gly	
50 55 60	
cta cct ggt ggt gac acg ccc cgg gga cct ccg atg agc aca tgg cca	462
Leu Pro Gly Gly Asp Thr Pro Arg Gly Pro Pro Met Ser Thr Trp Pro	
65 70 75 80	

<210> 469
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 391..438

<221> sig_peptide
 <222> 391..432
 <223> Von Heijne matrix
 score 4.59999990463257
 seq FLFFFGNSPCCGA/TG

<400> 469	
tatagtttca gttatgacat gagcacaac atcatgattt ctgttctttt taatgcactc	60
agactggcta agaatatgtt ctgtgttggg gaattattcca tatgtatttg aaaataatat	120
atactctgct cttgttaggt tctagaaatg tcaattacct caaattctct gagagtgcag	180
ctcagttctt ctatattcctt actgggttctt gctacttgc tctgtcagtt actgagcaaa	240
aagtagcaaa gtcgacagct gtaatacatt tgtttatttc tctcattttt gttagtattt	300
gcttcatgta ctttgaagct rtgttgtag catgcataca cataggatga ttatggcttc	360
ttggaaaatt gacccttta gcattatgta atg ttc ctc ttt ttc ttt ggt aac	414
Met Phe Leu Phe Phe Phe Gly Asn	
-10	

agt cca tgt tgt gga gcc aca ggg	438
Ser Pro Cys Cys Gly Ala Thr Gly	
-5 1	

<210> 470
 <211> 131
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..130

<221> sig_peptide
 <222> 11..85
 <223> Von Heijne matrix

score 4.59999990463257
seq SLSLSASLIIS/PS

<400> 470
atcttttcac atg ggc ctc tcc cac cat cgg gtc tca gcc cca tct tct 49
Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser
-25 -20 -15
ctc tct ctc tct ctc tcg gcc tcc ctc att att tct ccc tct ccc tcc 97
Leu Ser Leu Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser
-10 -5 1
gcc tct cca tct ctc ctt sct ccc cct bcc cgg g 131
Ala Ser Pro Ser Leu Leu Xaa Pro Pro Xaa Arg
5 10 15

<210> 471
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..210

<221> sig_peptide
<222> 115..183
<223> Von Heijne matrix
score 4.5
seq LSMLLRVSNRP/PV

<400> 471
tggcgcgac ttggtcacc gcaccttcg cctcccggt tcgagcgctt ctctgcctc 60
agcctcccga ttacgggga tgacaggag tcaccccccac gctggcttg gctg atg 117
Met
ttt gtg ttt tta gta ggc acg ccg tgt ctc tcc atg ttg ctc agg ctg 165
Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg Leu
-20 -15 -10
gtc tcc aac tcc cga cct cct gtg atg cgc cca cct cgg cct ggg g 211
Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
-5 1 5

<210> 472
<211> 150
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..150

<221> sig_peptide
<222> 25..123
<223> Von Heijne matrix
score 4.5
seq VTITILFLIVSMA/LK

<400> 472
ctttattgag ggatacttta ctct atg aaa ttc act cat ttt aag tgt aca 51
Met Lys Phe Thr His Phe Lys Cys Thr
-30 -25
att cgg tta tta tta cta tat tta cag aat cct gta acc atc aca att 99
Ile Arg Leu Leu Leu Leu Tyr Leu Gln Asn Pro Val Thr Ile Thr Ile
-20 -15 -10
tta ttt tta atc gtt tcc atg gcc ctg aaa ata aac cac ata ccc aag 147
Leu Phe Leu Ile Val Ser Met Ala Leu Lys Ile Asn His Ile Pro Lys
-5 1 5
ggg 150
Gly

<210> 473
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 227..352
<221> sig_peptide
<222> 227..268
<223> Von Heijne matrix
score 4.5
seq SCMSLFPCCPAQS/KN

<400> 473
tatttgatta aaaaagactc ttcttgtttt ctgttttgtc tgagttttca ttataccac 60
ttctcaacta ccccatccca mgggtagaag tttttaaaat ttgcataattt aamattcatt 120
ttcgamttat ctgaaattaa tcaatatctc tactgtagtc ttggataatg ccaagagttt 180
aaaatgctat aatccaaaca cctgtttgga ctcaatatgt catttt atg tct tgt 235
Met Ser Cys
atg tca ctt ttc ccc tgt tgc cct gct cag agt aag aat tat atg tta 283
Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn Tyr Met Leu
-10 -5 1 5
tta tta ttc att att tta ctt cca act caa ttt tta tat tca aaa tta 331
Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr Ser Lys Leu
10 15 20
gtt aca att tgc tgt tgt ttt 352
Val Thr Ile Cys Cys Cys Phe
25

<210> 474
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..141

<221> sig_peptide
 <222> 64..105
 <223> Von Heijne matrix
 score 4.5
 seq LVCCTINSSFALG/IS

<221> misc_feature
 <222> 38
 <223> n=a, g, c or t
 Oligonucleotide

<400> 474
 tactttaagt tctagggtac gtctgcacaa cgtsrggntt tgatacatag gtatatatgt 60
 gcc atg ttg gtt tgc tgc acc atc aac tca tca ttt gca tta ggt att 108
 Met Leu Val Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile
 -10 -5 1
 tct cgt aat gct atc cct ctg cca gcc cct ggg 141
 Ser Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
 5 10

<210> 475
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..298

<221> sig_peptide
 <222> 92..250
 <223> Von Heijne matrix
 score 4.5
 seq ALYVICQFILIRS/GV

<400> 475
 cagattaaga gatggagaaa ggtgtagggm tgattctttt tttggtgaga cctcgcataa 60
 ctatcataaa tttgacagtg agtatgagag a atg gga cgt ggt cct ggc ccc 112
 Met Gly Arg Gly Pro Gly Pro
 -50
 tta caa gag aga tct ctc ttt gag ama aag aga ggc gct cct cca agt 160
 Leu Gln Glu Arg Ser Leu Phe Glu Xaa Lys Arg Gly Ala Pro Pro Ser
 -45 -40 -35
 agc aat att gaa gac ttc cat gga ctc tta ccg aag gtt atc ccc atc 208
 Ser Asn Ile Glu Asp Phe His Gly Leu Leu Pro Lys Val Ile Pro Ile
 -30 -25 -20 -15
 tgt gct cta tat gtg att tgc cag ttc att cta ata agg agt gga gtc 256
 Cys Ala Leu Tyr Val Ile Cys Gln Phe Ile Leu Ile Arg Ser Gly Val
 -10 -5 1
 aac ata tca atg gag caa gtc aca gtc gat gcc agt ctg gg 300
 Asn Ile Ser Met Glu Gln Val Thr Val Val Asp Ala Ser Leu
 5 10 15

<210> 476

<211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..231

<221> sig_peptide
 <222> 112..150
 <223> Von Heijne matrix
 score 4.5
 seq MLYCVVVVHSVCC/AV

<400> 476
 ttttaggggg gtttggttcg tttttgaact gtatacagat gaaattatac agaatgcttt 60
 ttttttggtg tatggccttt ttcactctgt agtgtatttg tgagattcat c atg ttg 117
 Met Leu
 tat tgt gta gtt gtg gtt cat tct gtt tgc tgt gca gta tac tat ttt 165
 Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr Tyr Phe
 -10 -5 1 5
 gtg att att cat aca ata gaa cat att aca tat tta tgt atc cat tct 213
 Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile His Ser
 10 15 20
 acc att cta ctg tgt gtg g 232
 Thr Ile Leu Leu Cys Val
 25

<210> 477
 <211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..234

<221> sig_peptide
 <222> 124..201
 <223> Von Heijne matrix
 score 4.5
 seq VFXSLFLIQLLIS/FS

<221> misc_feature
 <222> 171
 <223> n=a, g, c or t
 Oligonucleotide

<400> 477
 aagtggcagc btcagcaccc agggctgtgg taggtcacag tctctgggyk ggtctcagtg 60
 tccaacactg tagctgggtg ctgccagggt cccagtggtt ggggtcacca ggtctgaaga 120
 gag atg tgc tgg ytg cgg gya tgg ggc cag atc ctc ctg cca gtt ttc 168
 Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe
 -25 -20 -15

cbn tcc ctc ttt ctc atc caa ttg ott atc agc ttc tca gag aat ggt	216
Xaa Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly	
-10 -5 1 5	
ttt atc cac agc ccc atg gg	236
Phe Ile His Ser Pro Met	
10	

<210> 478
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..200

<221> sig_peptide
 <222> 138..179
 <223> Von Heijne matrix
 score 4.5
 seq CGLXILCGPWLHA/AP

<400> 478	
tctacatcac aggtkkatca gtgaaatatg tggtaagatg tacaaataag atgtgccccca	60
ccaccagaat gatcagttct gtgaggacac gtcogtgact gtaccctctt tcagaagtgc	120
tatcrattaa tgttggtt atg tgt ggc ctg akk atc ctc tgt ggg cct tgg	170
Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp	
-10 -5	
ctc cat gca gca cct cca tcc ccg ccg cgg g	201
Leu His Ala Ala Pro Pro Ser Pro Pro Arg	
1 5	

<210> 479
 <211> 151
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..150

<221> sig_peptide
 <222> 25..123
 <223> Von Heijne matrix
 score 4.5
 seq SISLLLLMLXXYWS/CW

<400> 479	
acatagcatt ttatgkacta gaaa atg ttc cat gga agg gtt atg gcc atg	51
Met Phe His Gly Arg Val Met Ala Met	
-30 -25	
ggg kat tta acc aaa cat tta aat cta aac att tct atc tca ctg ttg	99
Gly Xaa Leu Thr Lys His Leu Asn Leu Asn Ile Ser Ile Ser Leu Leu	
-20 -15 -10	

aca tct cca
Thr Ser Pro

511

<210> 481
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..427

<221> sig_peptide
<222> 212..382
<223> Von Heijne matrix
score 4.5
seq IWVRFNFLASSQA/CS

<400> 481
aggagagggga atttgtttta aaagagagaa agacattgag actgtgtaaa ggggatgttg 60
caacctttta aaatctgtga tctcagacca aattatacaa tataatctca gtaggtgccca 120
gtagtaggga aaagtgtcag ccctcgtgtc tggcactaag taccacccac cccaacccca 180
gtgatgggag cctctaaatg actgagattt a atg tct act acc tat ttg aat 232
Met Ser Thr Thr Tyr Leu Asn
-55
gag gac ttg aag aag aaa ttc agt gca gtk ata gag cag gtg ctt ttt 280
Glu Asp Leu Lys Lys Lys Phe Ser Ala Val Ile Glu Gln Val Leu Phe
-50 -45 -40 -35
gca cac tta tcc cca cta cat gtg tgg ctc cag ctc agg tct ctc tgt 328
Ala His Leu Ser Pro Leu His Val Trp Leu Gln Leu Arg Ser Leu Cys
-30 -25 -20
gag trt ttg acc tgc atc tgg gtt aga ttc aat ttt tta gcc tca agc 376
Glu Xaa Leu Thr Cys Ile Trp Val Arg Phe Asn Phe Leu Ala Ser Ser
-15 -10 -5
caa gca tgc tcc aaa tgc aac tcc tgc ttt ctc atc atg tca tcc tct 424
Gln Ala Cys Ser Lys Cys Asn Ser Ser Phe Leu Ile Met Ser Ser Ser
1 5 10
tca cc 429
Ser
15

<210> 482
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 145..384

<221> sig_peptide
<222> 145..261
<223> Von Heijne matrix
score 4.5

seq LIILDLLVPVIGL/IT

<400> 482

tacacgtaca gctcagcctt tctgttagct gcaacttcag tgttggtgaa ttattatgct 60
tctttgcaca ttgacttcta tgggtgctac aacacgtcag cttgtggaat tgagctgctt 120
cctcgaaaag gtcctcgcgt gtgg atg gca ctt atc gtt cta cag cta aca 171
Met Ala Leu Ile Val Leu Gln Leu Thr

-35

ttt gga att gga tac gtt aca cta ctc cag att cat tcc atc tat tca 219
Phe Gly Ile Gly Tyr Val Thr Leu Leu Gln Ile His Ser Ile Tyr Ser
-30 -25 -20 -15

caa tta att att ttg gat ctc ttg gtt cct gta ata ggc tta atc aca 267
Gln Leu Ile Ile Leu Asp Leu Leu Val Pro Val Ile Gly Leu Ile Thr
-10 -5 1

gag cta cca tta cac atc aga gag act tta ctg ttt act tct tcc ttg 315
Glu Leu Pro Leu His Ile Arg Glu Thr Leu Leu Phe Thr Ser Ser Leu
5 10 15

att ctc aca tta aat aca gtg ttt gtc ctg gca gtg aaa ctg aar tgg 363
Ile Leu Thr Leu Asn Thr Val Phe Val Leu Ala Val Lys Leu Lys Trp
20 25 30

ttt tat tat tcc aca cga tat g 385
Phe Tyr Tyr Ser Thr Arg Tyr
35 40

<210> 483

<211> 202

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 39..200

<221> sig_peptide

<222> 39..110

<223> Von Heijne matrix

score 4.5

seq XVAXFLLTFYVIS/QV

<400> 483

catattaatg aaaagtgcc aaaactgaaa aaccaaac atg agg gta gca ggt gct 56
Met Arg Val Ala Gly Ala
-20

gca aar ttg gtg gta rct gtg gca rtg ttt tta ctg aca ttt tat gtt 104
Ala Lys Leu Val Val Xaa Val Ala Xaa Phe Leu Leu Thr Phe Tyr Val
-15 -10 -5

att tct caa gta ttt gaa ata aaa atg gat gca agt tta gga aat cta 152
Ile Ser Gln Val Phe Glu Ile Lys Met Asp Ala Ser Leu Gly Asn Leu
1 5 10

ttt gca aga tca gca ttg gac aca gct gca cgt tct aca aag cct ccg 200
Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala Arg Ser Thr Lys Pro Pro
15 20 25 30

gg 202

<210> 484
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 148..309

<221> sig_peptide
 <222> 148..192
 <223> Von Heijne matrix
 score 4.5
 seq TLVFLSTRQVLQC/QP

<400> 484
 gcggggctgg aggcggtggc tgcggttgcg ggacgggcac tatgctgggc cttcctacca 60
 cttatgtgtg gcttggtagt ggcctagggt ctctcctccc tgetgaagtc cctctcctgc 120
 aggtggccgt ctgccggcc cagcacc atg cac acg ctt gtg ttc ttg agc aca 174
 Met His Thr Leu Val Phe Leu Ser Thr
 -15 -10
 cgg cag gtg ctg cag tgc cag cca gct gcc tgc cag gcc ctg ccc ctg 222
 Arg Gln Val Leu Gln Cys Gln Pro Ala Ala Cys Gln Ala Leu Pro Leu
 -5 1 5 10
 ctg cca cgc gaa ctc ttc ccc ctg ctg ttc aag gtg gcc ttc atg ghc 270
 Leu Pro Arg Glu Leu Phe Pro Leu Leu Phe Lys Val Ala Phe Met Xaa
 15 20 25
 aag aag aca gtg gta ctg cgc gak ttg gta cac acg cgg g 310
 Lys Lys Thr Val Val Leu Arg Xaa Leu Val His Thr Arg
 30 35

<210> 485
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 372..419

<221> sig_peptide
 <222> 372..413
 <223> Von Heijne matrix
 score 4.5
 seq TVVISCLVGECGS/WK

<400> 485
 agccggtggc agcacagcca ggacagccat ttcctcagca gccttcggta aaggcaacag 60
 attctgacgg taactgtgta tcagttggaa ttactgcact aactttgagg gccatactca 120
 aggactccaa taataaccaa gtcaatggcc ttagtggaat tacaacaatt ccgttttagca 180
 gctgttgggc caactacaca gaccttactc cccttagaac aggaaaaaat tataagattg 240
 aatttatact ggataatgtt gttggggtag aatccagaac tttcagcctg ctggcagagt 300
 ctgtctctag cagtggcagc agcagcagca gcmacagcaa agcatcaact gtgggtacat 360
 atgccagat a atg act gtm gta att agc tgt ctg gtt gga gaa tgt ggc 410

Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly
-10 -5

tct tgg aaa t 420
Ser Trp Lys
1

<210> 486
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..225

<221> sig_peptide
<222> 10..150
<223> Von Heijne matrix
score 4.5
seq PIFGLLVPSQIFS/SL

<400> 486
caaccatac atg tgc aca ctc aca gac aca cac act cac gtc caa gtg cac 51
Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His
-45 -40 -35
aag tca aaa cct tgc cag ctc ctc tcc cct cct cca cca rsc cat ggt 99
Lys Ser Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Xaa His Gly
-30 -25 -20
cct ctt ctt ctc cct atc ttt ggc ctt ctt gtg ccc tct cag att ttc 147
Pro Leu Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe
-15 -10 -5
agc tct ctt ctc aat tct cta cat ctg ggc ctg cct tcc ttc cca aag 195
Ser Ser Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys
1 5 10 15
atg cca ctc atg att ttc ctc ccc cgc tgg g 226
Met Pro Leu Met Ile Phe Leu Pro Arg Trp
20 25

<210> 487
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..454

<221> sig_peptide
<222> 221..409
<223> Von Heijne matrix
score 4.5
seq QILXSTLAMKIHS/QQ

<400> 487

```

agaaaatgga ggcgaatctg tatttccagt taactgctca gaagagagat gctgaagagc 60
tgtagtcgtg catccttctc accctccgtt agaaagcctc ctctcatcct cagaagacta 120
ctgtcagagg atgtaggvat ggacatcccc tttgaagagg gcgtgctgag tcccagtgtc 180
gcagacatga ggcctgaacc tcctaattct ctggatctta atg aca ctc atc ctc 235
                               Met Thr Leu Ile Leu
                               -60
gga gaa tca agc tca cag ccc caa ata tca atc ttt ctc tgg acc aaa 283
Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile Phe Leu Trp Thr Lys
-55 -50 -45
gtg aag gat cta ttc tct ctg atg ata act tgg aca gtc cag atg aaa 331
Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp Thr Val Gln Met Lys
-40 -35 -30
ttg aca tca atg tgg atg aac ttg ata ccc ccg atg aag cag att ctt 379
Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro Met Lys Gln Ile Leu
-25 -20 -15
tdg agt aca ctg gcc atg aag atc cac agc caa caa aga ttc tgg cca 427
Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln Gln Arg Phe Trp Pro
-10 -5 1 5
aga gtc aga gtc tat tcc aga ata tac 454
Arg Val Arg Val Tyr Ser Arg Ile Tyr
10 15

```

<210> 488

<211> 329

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 253..327

<221> sig_peptide

<222> 253..309

<223> Von Heijne matrix

score 4.5

seq VLFLNLFQKIEE/EE

<400> 488

```

cggctaattg gatgcctcca gctttgttct ttttgcttag gattgctttg gctatttggg 60
ctcctttttg ggtccatatt aatttttaaaa cagttttttc tggttttgtg aaggatgtca 120
ttggtagttt ataggaatag cahtgaatct gtagattgct ttgggcagta tggccatttt 180
aacaatatta attcttccta tctatgaata tggaatgttt ttccatgtgt ttgtgtcatc 240
tctttatacc tg atg tat aaa gaa aag ctg gta tta ttc cta ctc aat ctg 291
                               Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu
                               -15 -10
ttc caa aaa att gag gag gag gaa ctc ttc cct aat ga 329
Phe Gln Lys Ile Glu Glu Glu Glu Leu Phe Pro Asn
-5 1 5

```

<210> 489

<211> 414

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 149..412
 <221> sig_peptide
 <222> 149..292
 <223> Von Heijne matrix
 score 4.5
 seq LELVATLPDDVQP/GP

<221> misc_feature
 <222> 396
 <223> n=a, g, c or t
 Oligonucleotide

<400> 489
 gaaagtgcag gcagctgtgg aaggcgaagt tcaatcccag agtccgcccc ctgaattggg 60
 gcctttccgg aggaggaagc tctgaaaaac agggggggccc agtgccattc cgcagggaat 120
 tgtcgcttgc gttcagctgt tctacaca atg gac tca gta cct gcc act gtg 172
 Met Asp Ser Val Pro Ala Thr Val
 -45
 cct tct atc gcc gct acc ccg ggg gac ccg gaa ctt gtg gga ccc ttg 220
 Pro Ser Ile Ala Ala Thr Pro Gly Asp Pro Glu Leu Val Gly Pro Leu
 -40 -35 -30 -25
 tct gtg ctc tac gca gcc ttc ata gcc aag ctg ctg gag cta gtt gct 268
 Ser Val Leu Tyr Ala Ala Phe Ile Ala Lys Leu Leu Glu Leu Val Ala
 -20 -15 -10
 aca ttg cct gat gat gtt cag cct ggg cct gat ttt tat ggr stg sca 316
 Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Xaa Xaa
 -5 1 5
 tgg aaa ctg tat tta tca ctg cct tct tgg gaa tkg ttc gtt tgc cat 364
 Trp Lys Leu Tyr Leu Ser Leu Pro Ser Trp Glu Xaa Phe Val Cys His
 10 15 20
 ttt ctt atg gag act gtc ctt gtt gtg aag gnt aga gta tat cwa gtc 412
 Phe Leu Met Glu Thr Val Leu Val Val Lys Xaa Arg Val Tyr Xaa Val
 25 30 35 40
 ac 414

<210> 490
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 69..185
 <221> sig_peptide
 <222> 69..122
 <223> Von Heijne matrix
 score 4.5
 seq AVWASVASPASIC/CG

<400> 490

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agttccggcc tccaaggggc gggcagaagt tggaaacatg cggetgtcgg tcgctgcagc      60
gatctccc atg gcc gcg tat ttc gcc gta tgg gcc tcg gtc gcg agt ccc      110
      Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro
            -15                -10                -5
gca tcc atc tgt tgc ggr amy tgg ctc aca ggg ctg gtg cgg cac gaa      158
Ala Ser Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu
            1                5                10
cgc atc gag gca cca tgg gcg cgt ggg      185
Arg Ile Glu Ala Pro Trp Ala Arg Gly
            15                20

```

```

<210> 491
<211> 348
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 247..348

<221> sig_peptide
<222> 247..333
<223> Von Heijne matrix
      score 4.5
      seq ILLILQLLKXSLK/KC

```

```

<221> misc_feature
<222> 323..324
<223> n=a, g, c or t
      Oligonucleotide

```

```

<400> 491
ttatgttttaa aaggtcacaa gtctagaata actgaattgg gaattggaaa taccttaatt      60
ctataatttg tatctaaaat taggttttcc cttttaagtt gttaattttc tatggkttgt      120
gctgcatgct ttcactttta ttagtactta cagccaaaga gatgggcaaa tgtctagaaa      180
aatatgattt ttgattcagg aatttgtgcc tagtgatggc ctccaataga gaattttcca      240
gagaga atg aag act cag ttt cta agt tgg ggc aaa ttt agt ttt tgt      288
      Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys
            -25                -20
ttt ggt att ctt ctt ata tta cag cta tta aaa bnn tct ctt aaa aaa      336
Phe Gly Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys
-15                -10                -5                1
tgc cgg cac ggg      348
Cys Arg His Gly
            5

```

```

<210> 492
<211> 126
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 5..124

```


<221> sig_peptide
 <222> 5..79
 <223> Von Heijne matrix
 score 4.5
 seq LRFILPSSWDCRC/AP

<400> 492
 ctac atg ctt cct gct gtg gct gtc tcg gaa ccc gtg gtc ctc cgc ttc 49
 Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe
 -25 -20 -15
 att ctg ccg agt tcc tgg gat tgc agg tgc gcg ccg cca ctc ctg act 97
 Ile Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr
 -10 -5 1 5
 ggt ttt tgt att ttt tgg ktg gag acg gg 126
 Gly Phe Cys Ile Phe Trp Xaa Glu Thr
 10 15

<210> 493
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..298

<221> sig_peptide
 <222> 119..217
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WLLMVAPRLPAGA/RD

<400> 493
 acaactgactg cctggtgcag cccatgtgac gggtcgagct ccggggccctg ctgtccctgg 60
 ccgggctatc ccagtggctt caggcacctt ctccagacct acccagaaag atgcccg 118
 atg gat cct gca gct ccg tgg ctt ttc tgg gaa gca gcg gcc cct gct 166
 Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
 -30 -25 -20
 ctc aag aga ccc tgg ctc ctg atg gtg gcc cca agg ttg cca gct ggt 214
 Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
 -15 -10 -5
 gct agg gac tca gga cag ttt ccc aga aaa ggc caa gcg ggc agc ccc 262
 Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
 1 5 10 15
 tcc agg ggc cgg gtg agg aag ctg ggg ggt gcg gtg gg 300
 Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
 20 25

<210> 494
 <211> 295
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 182..295

<221> sig_peptide

<222> 182..274

<223> Von Heijne matrix

score 4.40000009536743

seq SRLXALLSPYAFT/LX

<400> 494

```
tttatacaca cacacacaca cacactcata ttcattacat gtgtgtactt tctggttgct      60
tcagtaggac ttttctaggc ttctttggac tatgtgtgat attttacttc agggactgaa      120
tttcacaact gcctactatg caactttgtg attttcttga aagcacaakt actatatata      180
a atg aaa atg tcc acc ccc tcc ccg ctt tct aaa aaa gtg ctc aga aac      229
  Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
    -30                -25                -20
cag gtc tca aga ttg rtt gcg ttg ctt tcc cca tac gct ttc act ctg      277
Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
-15                -10                -5                1
sct cgt ctt gcc tca ggg      295
Xaa Arg Leu Ala Ser Gly
      5
```

<210> 495

<211> 244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..243

<221> sig_peptide

<222> 70..114

<223> Von Heijne matrix

score 4.40000009536743

seq RFLLLYATQQGQA/KA

<400> 495

```
ggaagtcgag ttgtgcaggt tcgtgcccggt ctggcgcggtc gtggtttcac tggtacatgc      60
cttgaagtg atg agg agg ttt ctg tta cta tat gct aca cag cag gga cag      111
  Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln
    -15                -10                -5
gca aag gcc atc gca gaa gaa atg tgt rag caa gct gtg gta cat gga      159
Ala Lys Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly
      1                5                10                15
ttt tct gca gat ctt cac tgt att agt gaa tcc gat aag gtc tgc gtg      207
Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val
      20                25                30
att cag aat aca cct act ttt gca acg ggg ggg cgg g      244
Ile Gln Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg
      35                40
```

<210> 496
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..213

<221> sig_peptide
 <222> 91..171
 <223> Von Heijne matrix
 score 4.40000009536743
 seq FVNLNLCFAYTFA/LY

<400> 496
 atttaagtcc agagagcaag gtgattgcag tttctttggt cggtttgctt attttttact 60
 gcttatttct gtgtgcataa attcagcgac atg cta ata gac ata tgg tca atg 114
 Met Leu Ile Asp Ile Trp Ser Met
 -25 -20
 gtg ctt aga gaa aat ctg ttt gta aac ctg aat ctc tgt ttt gcc tac 162
 Val Leu Arg Glu Asn Leu Phe Val Asn Leu Asn Leu Cys Phe Ala Tyr
 -15 -10 -5
 aca ttt gca ttg tat tcc tgc cct gct cca act cgt tgt cct aga cca 210
 Thr Phe Ala Leu Tyr Ser Cys Pro Ala Pro Thr Arg Cys Pro Arg Pro
 1 5 10
 tcc ag 215
 Ser

<210> 497
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..254

<221> sig_peptide
 <222> 36..89
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WFPLSCSPSLPLS/IP

<400> 497
 cttttgggggt tgcgtgtttc ttccctctct gctgg atg ctg tct tgc ccc tgg 53
 Met Leu Ser Cys Pro Trp
 -15
 ttt ccc cta tcc tgt tct ccc tcc ttg cct ctg agc atc cca gac tgc 101
 Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro Leu Ser Ile Pro Asp Cys
 -10 -5 1
 ctg cct gcc ttc ctc tgg ccg ctg ggg ata ccc tgg cct gat gga gag 149
 Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile Pro Trp Pro Asp Gly Glu
 5 10 15 20

```

ggt cta aga cct tcc cgt ctt ctc cgg aca cgg gaa aac att acc cct      197
Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr Arg Glu Asn Ile Thr Pro
                25                      30                      35
ctc tct tta ttc gct atg ctg agt ggc agg gag ggt gcc ccg ctc ctg      245
Leu Ser Leu Phe Ala Met Leu Ser Gly Arg Glu Gly Ala Pro Leu Leu
                40                      45                      50
gtc ccc ctg g
Val Pro Leu
                55

```

```

<210> 498
<211> 82
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 23..82

```

```

<221> sig_peptide
<222> 23..61
<223> Von Heijne matrix
      score 4.40000009536743
      seq MVVVSFLASSSLP/AE

```

```

<400> 498
ctttttcgtc tgggctgccac ac atg gta gtt gtt tcg ttt ctt gcc tcc tct      52
                        Met Val Val Val Ser Phe Leu Ala Ser Ser
                        -10                      -5
tcc ttg ccg gcg gag acc cct aag caa ggg
Ser Leu Pro Ala Glu Thr Pro Lys Gln Gly      82
                1                      5

```

```

<210> 499
<211> 474
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 39..473

```

```

<221> sig_peptide
<222> 39..359
<223> Von Heijne matrix
      score 4.40000009536743
      seq IIILFVVITSRRG/SP

```

```

<400> 499
ttcctggacc gcgctggaag ccctggcggc ggcggccc atg ggg csc ttg gcg ctg      56
                        Met Gly Xaa Leu Ala Leu
                        -105
cyc gcc tgg ctg cag ccc agg tat agg aag aat gcg tat ctt ttc atc      104
Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys Asn Ala Tyr Leu Phe Ile

```

```

      -100      -95      -90
tat tac tta atc cag ttc tgt ggc cas tct tgg ata ttt gca aat atg      152
Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser Trp Ile Phe Ala Asn Met
-85      -80      -75      -70
aca gtc aga ttc ttt tca ttt gga aaa gat tca atg gtt gac act ttt      200
Thr Val Arg Phe Phe Ser Phe Gly Lys Asp Ser Met Val Asp Thr Phe
      -65      -60      -55
tat gct att gga ctt gtg atg cga ctt tgc caa tcc gta tct ctc ctg      248
Tyr Ala Ile Gly Leu Val Met Arg Leu Cys Gln Ser Val Ser Leu Leu
      -50      -45      -40
gaa ctg ctg cac ata tat gtt ggc att gag tca aac cat ctt ctc cca      296
Glu Leu Leu His Ile Tyr Val Gly Ile Glu Ser Asn His Leu Leu Pro
      -35      -30      -25
agg ttt ttg cag ctc aca gaa aga ata atc atc ctt ttt gtg gtg atc      344
Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile Ile Leu Phe Val Val Ile
      -20      -15      -10
acc agt cga aga gga agt cca acg aga aat atg tgg tgt gtg tgt tat      392
Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn Met Trp Cys Val Cys Tyr
-5      1      5      10
tcg tct ttg gat cta tgg ata tgg tta rgt aca ctt ata gca tgk tda      440
Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa Thr Leu Ile Ala Xaa Xaa
      15      20      25
tca gtc ata gga ata tcc tat gct gtc ttg aca t      474
Ser Val Ile Gly Ile Ser Tyr Ala Val Leu Thr
      30      35

```

<210> 500
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 177..239

<221> sig_peptide
 <222> 177..230
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SLTLTALLVPSRV/QP

```

<400> 500
cttcactcat ggggagagca tttctacctg acaccctccc atttctgttt tocttaccca      60
gatctacctt ctgagatatc atccttcttc agggagataa ggaaaaaaag ccacagggtc      120
ccggagagacc aggggaatgg tgagtgtttc ctgtctccat tactggctgt aacagg atg      179
Met
gac aca ttc cct tct ctt acc ctg act gcc tta ttg gtg cct agt aga      227
Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser Arg
      -15      -10      -5
gtt cag ccc cag gg      241
Val Gln Pro Gln
1

```

<210> 501

<211> 430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..429

<221> sig_peptide
 <222> 178..237
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LRYVASAVFGVIG/SQ

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 501
 gaggtgagtc ctggrntgc gtggttgggg cggagagcat tatctgcggc tccgattttg 60
 cagattctgg ctgagggcgtt cgtgatgtca gcagcagccg agacgggctt gttaaaggcc 120
 ggttgctagg gctgggggaa ctcagattgc ttcacctgtg gtatcagaca tcacaac 177
 atg ggg ctc acc aag cag tac cta cgc tat gtt gct agt gcg gtc ttt 225
 Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
 -20 -15 -10 -5
 ggc gtt atc ggc agc caa aaa ggt aat att gtc ttt gtg aca ctt cgt 273
 Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
 1 5 10
 ggt gag aaa gga cgt tat gtg gca gta cca gct tgt gaa cac gtt ttc 321
 Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
 15 20 25
 atc wgg gac tta agg aaa gga gag aag att ctt atc ctt cag ggg ctt 369
 Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
 30 35 40
 aaa caa gaa gtt act tgc tta tgc ccc tcc cca gat ggg cta cac tta 417
 Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
 45 50 55 60
 gct gtt ggg tat g 430
 Ala Val Gly Tyr

<210> 502
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..413

<221> sig_peptide
 <222> 333..404
 <223> Von Heijne matrix
 score 4.40000009536743

seq VFFSVLYVQQGLS/SQ

<221> misc_feature

<222> 7,359

<223> n=a, g, c or t

Oligonucleotide

<400> 502

agggasnggc agtgatcacg caagccggag cggcgggctg acgttggacg agctgccagg	60
tagctgaaag caggcagcca ggcagccgag acacttccca gcgattccag cctgggctcc	120
gcagaagcct cgctgaatcc cagccagctg gttctaacct tccagaatcg caatcccttc	180
tccccacagc cagccctcgc cgagcaagca gcaggatgtt tgcagtgtcg cgcccagggc	240
tctgagactg agcctgccat ccaactcgcac gcctttcttt cagggctttt cggctgttgg	300
ctacactgat gtgaccccc tccctttttg ga atg atg ggg atc ttt ttg gtg	353
Met Met Gly Ile Phe Leu Val	

-20

tat gtn gga ttt gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt	401
Tyr Val Gly Phe Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu	
-15 -10 -5	

tct tct caa gca	413
Ser Ser Gln Ala	
1	

<210> 503

<211> 167

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 26..166

<221> sig_peptide

<222> 26..91

<223> Von Heijne matrix

score 4.40000009536743

seq WVLDPALLLTCLT/FP

<400> 503

gaatcggaca acttaaagtc tcgat atg agc ctc gga ttg cat tcg aac tcc	52
Met Ser Leu Gly Leu His Ser Asn Ser	
-20 -15	

tgg gtt cta gac cca gct ctg cta cta act tgt ctg acc ttc ccc att	100
Trp Val Leu Asp Pro Ala Leu Leu Leu Thr Cys Leu Thr Phe Pro Ile	
-10 -5 1	

tat aaa ctg ttg tgg gtg aga ggt ggg acw agg wga act ctr wgr gcv	148
Tyr Lys Leu Leu Trp Val Arg Gly Gly Thr Arg Xaa Thr Leu Xaa Ala	
5 10 15	

ctg cac tcg gcg cgg acg g	167
Leu His Ser Ala Arg Thr	
20 25	

<210> 504

<211> 420

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 217..420

<221> sig_peptide
<222> 217..396
<223> Von Heijne matrix
score 4.40000009536743
seq MWVXCXFCFVLF/FE

<221> misc_feature
<222> 47..48,368..369,373
<223> n=a, g, c or t
Oligonucleotide

<400> 504
ggktccgctc cctggggcgc acgtcagtca ggaggcggaa ggcgagnnga ggcggggaagg 60
ttgtagtgcc gcgagttgag ctctctttgc ctaagtggtc gcgccccctt taagagcagc 120
gattgtaagg agaggcggtc ccggtgtcct cgggtcccag gtgattgtga agtgctgacc 180
aattgccact ggacatactt gaaacaaaat aggaaa atg gca gca aac tct tca 234
Met Ala Ala Asn Ser Ser
-60 -55
gga caa ggt ttt caa aac aaa aat aga gtt gca atc ttg gca gaa ctg 282
Gly Gln Gly Phe Gln Asn Lys Asn Arg Val Ala Ile Leu Ala Glu Leu
-50 -45 -40
aca aag aga aaa gaa aac tac tta tgc aga acc agt ctt caa caa atc 330
Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg Thr Ser Leu Gln Gln Ile
-35 -30 -25
atc ctg gar cta ggt att gac act ata atg tgg gtt tnn tgt ntg ttt 378
Ile Leu Glu Leu Gly Ile Asp Thr Ile Met Trp Val Xaa Cys Xaa Phe
-20 -15 -10
tgt ttt gtt ttg ttt tgt ttt gag acg gag tct cgc cct gtc 420
Cys Phe Val Leu Phe Cys Phe Glu Thr Glu Ser Arg Pro Val
-5 1 5

<210> 505
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 43..456

<221> sig_peptide
<222> 43..147
<223> Von Heijne matrix
score 4.40000009536743
seq PAPLLFLPPAAPG/GE

<221> misc_feature

<222> 416..417

<223> n=a, g, c or t
Oligonucleotide

<400> 505

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gtagtcggat agttggcggg tggttgagtg gaagcggctcg cc atg tcc gcg ggg      54
                               Met Ser Ala Gly
                               -35
agc gcg aca cat cct gga gct ggc ggg cgc cgc agc aaa tgg gac caa      102
Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser Lys Trp Asp Gln
-30                               -25                               -20
cca gct cca gcc cca ctt ctc ttc ctc ccg cca gcg gcc cca ggt ggg      150
Pro Ala Pro Ala Pro Leu Leu Phe Leu Pro Pro Ala Ala Pro Gly Gly
-15                               -10                               -5                               1
gag gtc acc agc agt ggg gga agt cct ggg gsc acc aca gct gct cct      198
Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr Thr Ala Ala Pro
5                               10                               15
tca gga gcc ttg gat gct gct gct gct gtg gct gcc aag att aat gcc      246
Ser Gly Ala Leu Asp Ala Ala Ala Ala Val Ala Ala Lys Ile Asn Ala
20                               25                               30
atg ctc atg gca aaa ggg aag ctg aaa cca act cag rat gct tct gag      294
Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln Xaa Ala Ser Glu
35                               40                               45
aag ctt cag gct cct ggc aaa ggc cta act agc aat aaa agc aag gat      342
Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn Lys Ser Lys Asp
50                               55                               60                               65
gac ctg gtg gta gct gaa gta gaa att aat gat gtg cct ctc aca tgt      390
Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val Pro Leu Thr Cys
70                               75                               80
agg aac ttg ctg act cga gga cag ann caa gac gag atc agc cga ctt      438
Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu Ile Ser Arg Leu
85                               90                               95
agt ggg gct gca gta tca a      457
Ser Gly Ala Ala Val Ser
100
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<210> 506

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 141..314

<221> sig_peptide

<222> 141..203

<223> Von Heijne matrix
score 4.40000009536743
seq IRAVCLSGGSCWG/GV

<400> 506

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ctctttctgt cttgattttt ctgtgtgtct ctctgcgtct tgtctatattg ttttctctct      60
ttcttctctg tggccctccc ctttgtctct tcctttctgt tttctctctgt agttctctct      120
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cttctctccc ctgattgctc atg agt ccc ctt gat cag gct gta ata cgt gct 173
                Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala
                -20                -15

gtg tgt ctc agt gga ggt tcc tgc tgg gga gga gtc cgt tgt ctt gtg 221
Val Cys Leu Ser Gly Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val
-10                -5                1                5

cgt ggg ggc ccg aac ata ggc cct gca gcc cag ctg ctt ggg ggc att 269
Arg Gly Gly Pro Asn Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile
                10                15                20

cca ctc tgc tgg cca cca gct gtg act gca ggt gaa gtg aaa ctg c 315
Pro Leu Cys Trp Pro Pro Ala Val Thr Ala Gly Glu Val Lys Leu
                25                30                35

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<210> 507
<211> 208
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 152..208

<221> sig_peptide
<222> 152..196
<223> Von Heijne matrix
      score 4.40000009536743
      seq SFHFIXFLFPWA/EX

<221> misc_feature
<222> 201..202
<223> n=a, g, c or t
      Oligonucleotide

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<400> 507
agaatcgcg aggcgcaatt gtgccctggt tcgccaagat gtcgttccca aagtataagc 60
cgtcgagcct gcgcactctg cctgagaccc tcgacccagc ccggetcctg tctctctgta 120
ttcctgcagt ccttttaagg aagaaaagtg a atg aac tca ttt cat ttt att 172
                Met Asn Ser Phe His Phe Ile
                -15                -10

tss ttc ctc cct ttc ccc tgg gct gaa wnn gcg cag 208
Xaa Phe Leu Pro Phe Pro Trp Ala Glu Xaa Ala Gln
                -5                1

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<210> 508
<211> 169
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 65..169

<221> sig_peptide
<222> 65..151

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<223> Von Heijne matrix
 score 4.40000009536743
 seq LLSTHTWTDALA/FS

<400> 508
 atacagacac ccagrsagga ccotgaacac acagacaggc acagggaccc ctgtgcccac 60
 aggg atg ggc tgg cac tca cat agt tcc caa ggc gtg caw gca atg cct 109
 Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro
 -25 -20 -15
 ctg ctg ctg tcc aca cac acc tgg aca gac aca gcc ctg gca ttc agc 157
 Leu Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser
 -10 -5 1
 aca cac aca cac 169
 Thr His Thr His
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<210> 509
 <211> 118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..116

<221> sig_peptide
 <222> 12..77
 <223> Von Heijne matrix
 score 4.40000009536743
 seq WFLRSWTWPQTAG/RV

<400> 509
 caattcaagt c atg crg gct gtg aga aac gcg ggg tcg tgg ttc ctg cgg 50
 Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg
 -20 -15 -10
 tcc tgg act tgg ccc cag aca gcc ggc agg gtc gtg gcc aga rsg ccg 98
 Ser Trp Thr Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro
 -5 1 5
 gcc ggg acc atc tgc aca gg 118
 Ala Gly Thr Ile Cys Thr
 10

<210> 510
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 334..402

<221> sig_peptide
 <222> 334..378
 <223> Von Heijne matrix

score 4.40000009536743
seq ALFILVSISLFYA/LF

<400> 510
cctcctcagc ctcctcagta ccattctgtt accaccattg gtcctgcatt ctgagtttgc 60
cacctggcac gtgcccttca aatgtctcca ctgcgtcttt gcctttccct tttctgttgc 120
gtgccatcat tccgattccg attttaacag caacctgctg atttccctgcc atagtttcct 180
actttccatt ctgagcccct ttaatccact tataacaatat aactactccc tgaattattt 240
ggtcatacca cttgtatctg ccgaaccctt attcctcccc tgggggtacgt tttccactaa 300
acacacacag ggaaatgcca cccaaatagc tct atg tgt gcc ttg ttc att ctt 354
Met Cys Ala Leu Phe Ile Leu
-15 -10
gtt tcc att tct ttg ttt tat gca ctt ttt atc tct cca tcc ata caa 402
Val Ser Ile Ser Leu Phe Tyr Ala Leu Phe Ile Ser Pro Ser Ile Gln
-5 1 5

<210> 511
<211> 343
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..341

<221> sig_peptide
<222> 159..317
<223> Von Heijne matrix
score 4.40000009536743
seq NLVLYFLVHLLFS/LS

<400> 511
cagaggcttt tatttgcata aatgtcggac cgtcttagct ctcttgtaga aggaactttt 60
tgccatatta tagtggctca cttacctcc tgggaatgcat tctggcctca agtctgtacc 120
tagcattgat agaggaagcc cagcctggtg tgcacagc atg tac ctg gtg tgc aca 176
Met Tyr Leu Val Cys Thr
-50
aca tgc acc tgg tgt gta ttt tct gaa atg ttt gtt cat gga tta aac 224
Thr Cys Thr Trp Cys Val Phe Ser Glu Met Phe Val His Gly Leu Asn
-45 -40 -35
atc act cag ctc gtg ctg agc cag ctg gat tac ttt ttc cat tcc aat 272
Ile Thr Gln Leu Val Leu Ser Gln Leu Asp Tyr Phe Phe His Ser Asn
-30 -25 -20
ctg aca aac ttg gtc ttg tat ttc tta gtc cat tta ctt ttt tcc ctt 320
Leu Thr Asn Leu Val Leu Tyr Phe Leu Val His Leu Leu Phe Ser Leu
-15 -10 -5 1
agc ctg ttt atg ccg ctg acg gg 343
Ser Leu Phe Met Pro Leu Thr
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<210> 512
<211> 420
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 7..420

<221> sig_peptide
 <222> 7..240
 <223> Von Heijne matrix
 score 4.40000009536743
 seq FWWWLGLXVTWL/IH

<221> misc_feature
 <222> 93,100,137..138
 <223> n=a, g, c or t
 Oligonucleotide

<400> 512
 taagtg atg aag ctg aaa tta tac cta tgt ata tta ggt ccc tgg ggc 48
 Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly
 -75 -70 -65
 tgc aak rkc aaa gta cca cta att ggg ttt ctt aaa aga ata aan hta 96
 Cys Xaa Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa
 -60 -55 -50
 tat nwt ctc aca gtt ctg aaa cct agd agt ctg ara tca ann tca gca 144
 Tyr Xaa Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala
 -45 -40 -35
 ggg ttg gtt cct tct gag gac tct aaa aaa gaa tct gtt tca tgc ctc 192
 Gly Leu Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu
 -30 -25 -20
 tct cct agg ttc tgg tgg tgg ctg gga agc ctg akt gtt act tgg ctt 240
 Ser Pro Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu
 -15 -10 -5
 ata cat gca tca ctc cag tct ctg tct cct ttt tct cat gcc att ttc 288
 Ile His Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe
 1 5 10 15
 tca tgt gtc tct gtg ttt tcc ttt gct tat aag gat acc agt cat att 336
 Ser Cys Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile
 20 25 30
 gaa tta ggg cct gct cta ata acc tca tct caa tta cct ctg caa gga 384
 Glu Leu Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly
 35 40 45
 acc aat ttc caa ata atg tca cac tca cat gta gca 420
 Thr Asn Phe Gln Ile Met Ser His Ser His Val Ala
 50 55 60

<210> 513
 <211> 324
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 219..323

<221> sig_peptide
 <222> 219..317
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LKLLFLILILIAG/YR

<400> 513
 aaaacattct gaatagttaa tttgtcttga cggaaagtaa aaagaacaaa cttgttttat 60
 acaaaatcag atgctccaaa tggtcagttg atgatgatac caatcaaaga aaactaagga 120
 ggaagaaaaa gaaaacagga aagagaggag gcaacaggaa aatcggcctt cgtccttcag 180
 tctacgcttg aaattgccag ggatggataa atctgaag atg aat gaa aaa aag aaa 236
 Met Asn Glu Lys Lys Lys
 -30
 cta ctg gga acg gaa cag aaa caa aaa aaa agg atg gga aat ctg aag 284
 Leu Leu Gly Thr Glu Gln Lys Gln Lys Lys Arg Met Gly Asn Leu Lys
 -25 -20 -15
 ctg cta ttt ctt att ctg atc tta ata gca gga tac agg g 324
 Leu Leu Phe Leu Ile Leu Ile Leu Ile Ala Gly Tyr Arg
 -10 -5 1

<210> 514
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 212..301
 <221> sig_peptide
 <222> 212..292
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SALMLPLGCAVRT/RM

<400> 514
 tttccctcac tctctgcctc ccccatcgca cccacagga gggtttccct cactctctgc 60
 ctcccccatc gcaaccaca ggagggtttc cctcactctg cctcctccaw cgcaccccca 120
 kggagggtgtt tttccctcact ggttctgttg gtggcggtgg cagcaatccg agtcacatgg 180
 caccagagta tgtcacgggt ggcggatctg a atg ggg ctg cag agc ctc aca 232
 Met Gly Leu Gln Ser Leu Thr
 -25
 ctt cca gtg tct tgc agc cct tct gcc ctg atg ctt ccc ttg gga tgt 280
 Leu Pro Val Ser Cys Ser Pro Ser Ala Leu Met Leu Pro Leu Gly Cys
 -20 -15 -10 -5
 gct gtc cgc acg cgc atg ctt ga 303
 Ala Val Arg Thr Arg Met Leu
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<210> 515
 <211> 455
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 342..455

<221> sig_peptide
 <222> 342..434
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LTTLESLAGSVXS/EQ

<400> 515
 tcatatctgg waatggcaaa cagggatgaa aatcgattat gttttggaga ctccttttgg 60
 acatgtatca gtgtgttgat ttgcacaaac caataaaagc cctacatttt ttggaaatgg 120
 atccctagat ttcaagcatg tataatcact caaagtggat atgatcacag gcattcttct 180
 cttgagctca gcaaaactat gcctaccaac accgaagaga agtcaaagat ttttatgaaa 240
 aaaaattgca gatgatgttg gtgagataat aggatatgag caatgaaccc ttgggtgggg 300
 ttccagggca cttaaattgc ctcgtgtctt gagtccttaa g atg gac tca aac aaa 356
 Met Asp Ser Asn Lys
 -30
 aaa tta gta tta tca ata aca ggt aat act gtg tgg att cta aca aca 404
 Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val Trp Ile Leu Thr Thr
 -25 -20 -15
 tta gaa tca tta gct ggc agt gtc aam tct gaa caa gat ttg tca gct 452
 Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu Gln Asp Leu Ser Ala
 -10 -5 1 5
 tat 455
 Tyr

<210> 516
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 196..360
 <221> sig_peptide
 <222> 196..336
 <223> Von Heijne matrix
 score 4.40000009536743
 seq SFXXCFLXLXXS/EM

<221> misc_feature
 <222> 330..332
 <223> n=a, g, c or t
 Oligonucleotide

<400> 516
 aagagcgttg ggcagatata gtctgtagat atttttgaaa cgtcttttggg tttgtcccat 60
 ttgggggttg ctcagcttct tgaatctgta ggttttgggg atcccccamc ctgcaaattt 120
 ggtgatattt ttgtctttat ttctkcaagt gaacttgaaa tcccaccctg ttggttttct 180
 ccttctaaga ctctg atg acg tgt atg tta gcc tgt agg tgt agt ctc amg 231
 Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa

<211> 245
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..244

<221> sig_peptide
 <222> 185..229
 <223> Von Heijne matrix
 score 4.40000009536743
 seq VSYLILTLHHVQT/AV

<400> 518
 agttttcttc agaacagagg ctgagctcga agcgccgggc agtacagtga gggagagccg 60
 aggaaccag cgcggtgcct agcggaactc cagggctgga atcccgagac acaagtgcac 120
 ctgctagctg ttagcacttg gcagacggag ttctcctcta gggtagttct aactttgggt 180
 aata atg ttt gtc agc tac ctg ata tta aca ttg ctc cac gtt caa aca 229
 Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr
 -15 -10 -5
 gca gtg tta gca aga c 245
 Ala Val Leu Ala Arg
 1 5

<210> 519
 <211> 275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..275

<221> sig_peptide
 <222> 96..170
 <223> Von Heijne matrix
 score 4.40000009536743
 seq IFLLYFKFWGTCA/ER

<400> 519
 ttgtttttta gaaaaatgaa taatttcttt ttatattatt ctgttacatt ttttccccac 60
 ttaatagaac gtccagaaaa tctttgcatc tcaga atg cct gaa gct gcc ttg 113
 Met Pro Glu Ala Ala Leu
 -25 -20
 ttc ttg ttt ttt tta ttc att ttt tta tta tac ttt aag ttc tgg ggt 161
 Phe Leu Phe Phe Leu Phe Ile Phe Leu Tyr Phe Lys Phe Trp Gly
 -15 -10 -5
 aca tgt gca gaa cgt gca ggt ttg tta cat agg tat act cgt gcc atg 209
 Thr Cys Ala Glu Arg Ala Gly Leu Leu His Arg Tyr Thr Arg Ala Met
 1 5 10
 gag gtt tgc tgc acc cat caa cca tca tct aca tta ggt att tct cct 257
 Glu Val Cys Cys Thr His Gln Pro Ser Ser Thr Leu Gly Ile Ser Pro
 15 20 25

aat gct ctc ctt ccc cta
 Asn Ala Leu Leu Pro Leu
 30 35

275

<210> 520
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..180

<221> sig_peptide
 <222> 91..159
 <223> Von Heijne matrix
 score 4.40000009536743
 seq LCMHLSIHPXXCA/CI

<400> 520
 gtctgagcgg cacagacgag atctcgatcg aaggcgagat ggcggacgtg ctagatcttc 60
 acgaggctgg gggcgaagat ttcgccatgg atg agg atg ggg acg aga gca tcc 114
 Met Arg Met Gly Thr Arg Ala Ser
 -20
 ccg cct ctg tgc atg cat ctg tcc atc cat ccc cky mtc tgt gca tgc 162
 Pro Pro Leu Cys Met His Leu Ser Ile His Pro Xaa Xaa Cys Ala Cys
 -15 -10 -5 1
 atc tgt cca tcc atc cag gg 182
 Ile Cys Pro Ser Ile Gln
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<210> 521
 <211> 218
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..217

<221> sig_peptide
 <222> 104..211
 <223> Von Heijne matrix
 score 4.40000009536743
 seq XVCVCVCVCVCVC/VC

<221> misc_feature
 <222> 145,151,174
 <223> n=a, g, c or t
 Oligonucleotide

<400> 521
 atttatgtag gcagggtggat gccaaactgcc agtgcagggt ggcataagtt agcgttccaa 60
 agttaagcta tgggtgcattc caaatccatt cacacttagg aga atg tac cca aga 115

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Met Tyr Pro Arg
-35
gtg tgg gga tgt ttt caa tta ctg cat ttn ctt can bga aca aga acs 163
Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa Xaa Thr Arg Thr
-30 -25 -20
aca ggt aag tnw gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt 211
Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys
-15 -10 -5
gtg tgt g 218
Val Cys
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<210> 522
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<212> DNA
<213> Homo sapiens

<220>
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<222> 12..311

<221> sig_peptide
<222> 12..53
<223> Von Heijne matrix
score 4.40000009536743
seq AAVVLAATRLLRG/SG

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ggagacgcaa g atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg 50
Met Ala Ala Val Leu Ala Ala Thr Arg Leu Leu Arg
-10 -5
ggc tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg 98
Gly Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala
1 5 10 15
tac aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct 146
Tyr Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser
20 25 30
tct ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga 194
Ser Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly
35 40 45
cag gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc 242
Gln Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg
50 55 60
gtg gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt 290
Val Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu
65 70 75
atc aat tca gga tcg aga tat ga 313
Ile Asn Ser Gly Ser Arg Tyr
80 85

<210> 523
<211> 502
<212> DNA
<213> Homo sapiens

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<220>
 <221> CDS
 <222> 324..500

<221> sig_peptide
 <222> 324..398
 <223> Von Heijne matrix
 score 4.30000019073486
 seq ALYLSLNLYFANS/LY

<221> misc_feature
 <222> 284,469..470,472
 <223> n=a, g, c or t
 Oligonucleotide

<400> 523
 gtctaggctc ttcaagttag gattcatatc tatgacatgt gctgtacagt gcttctactg 60
 tgaggtagtc tcccagacag aaaccacatg ggccttcagg catagatggg cagtaaataa 120
 ttactttaca gtgggtgcat ttcttaggag acmcagagtr agaccttaag tgagatctta 180
 cctacctcct cccatccaat ctatccatc aaggttggac cttaaagcagc cttgagctta 240
 ataatgatgt gtgttagaac aaggatactg agattagact aagntgggtc tttaagtcag 300
 ccgtctctga caaagggcac aca atg tac tgt ctg arg tgt gtg gag aaa ata 353
 Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile
 -25 -20
 gca aaa gct ctt tat ctc agc ctt aat tta tat ttt gca aat tca ctt 401
 Ala Lys Ala Leu Tyr Leu Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu
 -15 -10 -5 1
 tat tat atg tgt gtg tgt tca tac ata tac ttt tat tta tkt att tat 449
 Tyr Tyr Met Cys Val Cys Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr
 5 10 15
 ktk tat kkt tta ata aaa ann dng tct tat tat gtt gcc cag act ggt 497
 Xaa Tyr Xaa Leu Ile Lys Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly
 20 25 30
 ctc aa 502
 Leu

<210> 524
 <211> 118
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 11..118
 <221> sig_peptide
 <222> 11..97
 <223> Von Heijne matrix
 score 4.30000019073486
 seq SAVFLTAVFSSHS/WL

<400> 524
 atctttgttg atg tgt cag ctc cgc agg ggt ttg ggg aaa cgg ccg ctg 49

Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu
-25 -20
agt gag gcg tgc gct gtg ttt ctc acc gcg gtc ttt tcc tcc cac tct 97
Ser Glu Ala Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser
-15 -10 -5
tgg ctg gtt gga ccc cgc tat 118
Trp Leu Val Gly Pro Arg Tyr
1 5

<210> 525
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 176..274

<221> sig_peptide
<222> 176..268
<223> Von Heijne matrix
score 4.30000019073486
seq LTFCLIDLSNVDS/GX

<400> 525
cctgagttct agtttgattg cactgtggtc tgagagacag tttgttataa tttctgttct 60
tttacgtttg ctgaggagag ctttacttcc aactatgtgg tcgatttttg aataggtgtg 120
gtgcggtgct gaaaaaaatg tatattctgt tgatttgggg tggagagttc tgtag atg 178
Met
tct gtt agg tcc act tgg tgc aga gct cag ttc aat tcc tgg gta tcc 226
Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val Ser
-30 -25 -20 -15
ttg tta act ttc tgc ctc att gat ctg tct aat gtt gac agt ggg amg 274
Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly Xaa
-10 -5 1
gg 276

<210> 526
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..366

<221> sig_peptide
<222> 103..261
<223> Von Heijne matrix
score 4.30000019073486
seq LRLTWLVAAGLEG/RV

<400> 526
tcactacttc tccccoggac tccttggttag tctgttagtg ggagatcctt gttgcogtcc 60

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cttcgcctcc ttcaccgccg cagacccctt caagttctag tc atg gtg agt ggg      114
                               Met Val Ser Gly
                               -50
gtt ccc tcg ggg ctg ggg aag agt gcg cgt ccc agg gga cgg cgg gcc      162
Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg Gly Arg Arg Ala
-45 -40 -35
cgg aaa cta ctg cct gca cct cgg gcc gcg ccc agg aca gct cca gac      210
Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg Thr Ala Pro Asp
-30 -25 -20
tac ccc ggg ccc ctc cgg tta acc tgg ctt gtg gcg gcc ggg ctg gaa      258
Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala Ala Gly Leu Glu
-15 -10 -5
ggg cga gtt cac ttg gca gac acc agt tcg ggc cgg aaa acc tgg ccc      306
Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg Lys Thr Trp Pro
1 5 10 15
ggg tgc ggc cat cag tgg aaa tgg aaa gcc ctc ttg atc cta gtg agg      354
Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu Ile Leu Val Arg
20 25 30
gct ttc ccc gca      366
Ala Phe Pro Ala
35

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<210> 527
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 316..426
<221> sig_peptide
<222> 316..408
<223> Von Heijne matrix
score 4.30000019073486
seq VCSSLRSXRPCWC/DG

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<400> 527
catttcctaa tctctgcatt ttccagcaag taagtgggtg tgacttggtg ctttcaagta      60
tgttttgtct aaaattcata gatgctgaac tgtgtatatt tgttgtcaag ttgaaaggt      120
acttgggttt ttgggggtgt taggaggtag ggtggatggt actattaaat acatttagac      180
tttttaaaat aagtgtact gatcatttcc aacaaatatt tactatgtcc atacttgtgc      240
tccaaaagac aattctgtct tcctcttgag atacatgtct cggggccct gtaggtctgg      300
tctgagaggg tcccc atg ggt ggc tgt gtc wgc tgg cgc ttt ctt gga cac      351
                               Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His
                               -30 -25 -20
tcc tct gct ctc agg act gtg tgt agc agt ctg cgc tca gya agg cca      399
Ser Ser Ala Leu Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro
-15 -10 -5
tgt tgg tgt gat ggg ctt cgg ctc aga tg      428
Cys Trp Cys Asp Gly Leu Arg Leu Arg
1 5

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<210> 528

<211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..400

<221> sig_peptide
 <222> 83..235
 <223> Von Heijne matrix
 score 4.30000019073486
 seq STCLLRALSSELC/AP

<400> 528
 gacacggaag tagctccgaa caggaagagg acgaaaaaaaa taaccgtccg cgacgccgag 60
 acaaaccgga cccgcaacca cc atg aac agc aaa ggt caa tat cca aca cag 112
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln
 -50 -45
 cca acc tac cct gtg cag cct cct ggg aat tcc agt ata ccc tca gac 160
 Pro Thr Tyr Pro Val Gln Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp
 -40 -35 -30
 ctt gca tct tcc tca ggc tcc acc cta tac cga tgc tcc acc tgc cta 208
 Leu Ala Ser Ser Ser Gly Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu
 -25 -20 -15 -10
 ctc aga gct cta tcg tcc gag ctt tgt gca ccc agg ggc tgc cac agt 256
 Leu Arg Ala Leu Ser Ser Glu Leu Cys Ala Pro Arg Gly Cys His Ser
 -5 1 5
 ccc cac cat gtc agc cgc att tcc tgg acc ctc tct gta tct tcc cat 304
 Pro His His Val Ser Arg Ile Ser Trp Thr Leu Ser Val Ser Ser His
 10 15 20
 ggc cca gtc tgt ggc tgt tgg gcc ttt agg ttc cac aat ccc cat ggc 352
 Gly Pro Val Cys Gly Cys Trp Ala Phe Arg Phe His Asn Pro His Gly
 25 30 35
 tta tta tcc agt cgg tcc cat cta tcc amc tgg ctc cac agt gct ggt 400
 Leu Leu Ser Ser Arg Ser His Leu Ser Xaa Trp Leu His Ser Ala Gly
 40 45 50 55

<210> 529
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..244

<221> sig_peptide
 <222> 68..133
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LFFETGSPSVAQS/GV

<400> 529

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cttacagagt taataagcat caaagaactt actgaaggac tttataaatt aaataaccatt      60
atgtaga atg gtg gtg gtt agt gcc ttt att tat tta ttt ttt gag aca      109
      Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr
            -20                -15                -10

ggg tct ccc tct gtc gcc cag tct gga gtg cag tgg tgt gat ctc ggc      157
Gly Ser Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly
            -5                1                5

tta ctg cag cct ccg cct cct gga ttc aag cga ttc tct tgc ctc agc      205
Leu Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser
      10                15                20

ctc cta ggt agb drg gat tgc aga cgt gcg cca ccc ggg      244
Leu Leu Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Gly
25                30                35

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<210> 530

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 124..432

<221> sig_peptide

<222> 124..195

<223> Von Heijne matrix

score 4.30000019073486

seq LXFLGMFLSGMVA/QI

<400> 530

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ggscctttgga ttggawagag gagctgggca ggaggcaggg caaggagaaa gctgttcggg      60
ggtcttgtct ggatttttgt tgccctctcc aatgttcttc tacctctact acaaggatgg      120
gtc atg ttt gtg tct gka aca rcg ttt ttc ttt kcg ctc ckc ttt ctg      168
      Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu
            -20                -15                -10

ggc atg ttc ctc tct ggc atg gtg gct caa att gat gct aac tgg aac      216
Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn
            -5                1                5

ttc ctg gat ttt gcc tac cat ttt aca gta ttt gtc ttc tat ttt gga      264
Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly
      10                15                20

gcc ttt tta ttg gaa gca gca gcc aca tcc ctg cat gat ttg cat tgc      312
Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys
      25                30                35

aat aca acc ata acc rgg cag cca ctc ctg agt gat aac cag tat aac      360
Asn Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn
      40                45                50                55

ata aac gta gca gcc tca att ttt gcc ttt atg acg aca gct tgt tat      408
Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr
            60                65                70

ggg tgc agt ttg ggt ctg gct tta cg      434
Gly Cys Ser Leu Gly Leu Ala Leu
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<210> 531
 <211> 406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 284..406

<221> sig_peptide
 <222> 284..361
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 score 4.30000019073486
 seq AXYLLVGLFPLKC/HX

<221> misc_feature
 <222> 384
 <223> n=a, g, c or t
 Oligonucleotide

<400> 531
 taatatatgt magaatagca gggaccatgt cttctgttca atatkgtatc ctgagcacct 60
 agtattttaag taggtatttc agtaaataat gtaacatata taataaataa tattaatatt 120
 tgttgactaa atgaatttag gtctggacct tgatggctta atgtctttct aaaaatctac 180
 ttccatatct aagcctttct tgactacttt cgcctttttc tgtgaactta aaagtcttta 240
 ttcattgttt gccggatgct aaacattttac aaaagtaatc ctt atg tca tct gaa 295
 Met Ser Ser Glu
 -25
 att ttc taw ktt dtk cak att gck tat gct tda tat ttg cta gtt ggt 343
 Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr Leu Leu Val Gly
 -20 -15 -10
 ctt ttc cct cta aaa tgc cac wag agt hat ttt tct aag tna caa atc 391
 Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser Lys Xaa Gln Ile
 -5 1 5 10
 tca tca ttt gtg gaa 406
 Ser Ser Phe Val Glu
 15

<210> 532
 <211> 212
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..211

<221> sig_peptide
 <222> 23..76
 <223> Von Heijne matrix
 score 4.30000019073486
 seq LTVTLGRLASACS/HS

<400> 532

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gtttccggcc gaggtcgagg cc atg gca gca tct tcc ctg acg gtc acc tta      52
                Met Ala Ala Ser Ser Leu Thr Val Thr Leu
                -15                                -10

ggg cgg ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg      100
Gly Arg Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly
                -5                                1                                5

ccc gga gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag      148
Pro Gly Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln
                10                                15                                20

agc act tca tat cta cca gga tat gtt cvt aaa aca tcc ctg agt tca      196
Ser Thr Ser Tyr Leu Pro Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser
                25                                30                                35                                40

cca cct tgg ccg agg g                                              212
Pro Pro Trp Pro Arg
                45

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<210> 533
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 <221> CDS
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<221> sig_peptide
 <222> 76..129
 <223> Von Heijne matrix
 score 4.30000019073486
 seq CICSCCLFFSQYLX/XS

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<400> 533
tatagtgat tataatcaag tgtaggcttc ctgaattttg acatcctttt agaacttggg      60
tctggaattc cagaa atg tta att gct gct tgt att tgt tct tgt ttg ttt      111
                Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe
                -15                                -10

ttt agc cag tat ttg gsy ytt tct aat cca gcc gcg gg                  149
Phe Ser Gln Tyr Leu Xaa Xaa Ser Asn Pro Ala Ala
                -5                                1                                5

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 <212> DNA
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<221> sig_peptide
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 <223> Von Heijne matrix
 score 4.30000019073486
 seq WVLSYMWQSASLG/FS

<220>
 <221> CDS
 <222> 78..206

<221> sig_peptide
 <222> 78..119
 <223> Von Heijne matrix
 score 4.30000019073486
 seq FAFLAGCSGSCLW/SR

<400> 536
 aactttaccc agatatacta tatgccaac aatgtttgtc accagggata ccacaacaga 60
 aaacaaatac actaaaa atg ttc gct ttc ctg gcc ggg tgc agt ggc tca 110
 Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser
 -10 -5
 tgc ctg tgg tcc cgg cac ttc ggg aga ctg cgg cgg gcg gct ccc ttg 158
 Cys Leu Trp Ser Arg His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu
 1 5 10
 agc cca gag ttt gag acc ggc ctg ggt aac atg gtg gaa ccc caa tgg g 207
 Ser Pro Glu Phe Glu Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
 15 20 25

<210> 537
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 268..393
 <221> sig_peptide
 <222> 268..318
 <223> Von Heijne matrix
 score 4.30000019073486
 seq FLFVPHLISCNWC/EP

<400> 537
 ttagcaaadc acagatgaag gtctcattac tatatgcaga ggggtgccata agttacaadc 60
 cctttgtgcc tctggctgct ccaacatcac agatgccatc ctgaatgctc taggtcagaa 120
 ctgcccacgg cttaggtaaa catttcttgt ttagctcaaa aaaatcatag aacaaaagtt 180
 tocttcaccc atatttcttc cttggaactt tggaatttta aggtaggcac tgcagacgct 240
 ttgaaatttt aaggtagtcc ctttttag atg ccc acc tac ttc ctt ttt gta cct 294
 Met Pro Thr Tyr Phe Leu Phe Val Pro
 -15 -10
 cat ttg att tca tgt aat tgg tgt gaa cca agg ggt aac aat ccc caa 342
 His Leu Ile Ser Cys Asn Trp Cys Glu Pro Arg Gly Asn Asn Pro Gln
 -5 1 5
 att cca cta ctt gct atc cat act aga aaa aag aat caa cat ttt att 390
 Ile Pro Leu Leu Ala Ile His Thr Arg Lys Lys Asn Gln His Phe Ile
 10 15 20
 act t 394
 Thr

25

<210> 538
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 237..413

<221> sig_peptide
<222> 237..317
<223> Von Heijne matrix
score 4.30000019073486
seq LTSVSLXXXXXXG/SV

<221> misc_feature
<222> 308..309,375
<223> n=a, g, c or t
Oligonucleotide

<400> 538
gaatcctcgc aaagaattgg caatgtcgtt gcctttctct ggcggaaggc tggcwactac 60
cctttgaatt tggaatgtat gtcacacagt tctagagtag aatgcaaact cagcactgtc 120
ctctttgaac caaaatgtct caaaaacaa gattctaatt tatacttaat atttcccca 180
gaagcccaat cattaaagcc acctttccag gaacagaagt gtttttgaca ctgtga atg 239
Met
ctt tgg acc agt ttc cag aat cct ctt cag gta gtg ctt ctc acc agc 287
Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr Ser
-25 -20 -15
gtt tcc ctt ttd aww wtg gbn ndc mta ggt tca gtc cga atc awk cta 335
Val Ser Leu Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa Leu
-10 -5 1 5
tct cac tgg tca agc tca gcc ttc ttc ttc ctd att cw b nck kyw hwt 383
Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa Xaa
10 15 20
ctt tca cat gtg aca aaa caa atg cat ttg aa 415
Leu Ser His Val Thr Lys Gln Met His Leu
25 30

<210> 539
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..158

<221> sig_peptide
<222> 66..107
<223> Von Heijne matrix
score 4.30000019073486

seq LTCLCGCFIVLLV/CV

<400> 539
 tacattcaag gtttagtattg atatgcatgt atttgatcct gtcattgtgt tgtttagctgt 60
 ttatt atg ctg act tgt ttg tgt ggt tgc ttt ata gtg tta ctt gtc tgt 110
 Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys
 -10 -5 1
 gta ctt aaa tgt gtt ttt gta gtg gct agt aat ggc ctt ttc ttt cct 158
 Val Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
 5 10 15
 tt 160

<210> 540
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 207..326
 <221> sig_peptide
 <222> 207..293
 <223> Von Heijne matrix
 score 4.30000019073486
 seq HLSILAFVAIAFG/VL

<400> 540
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 tgcctctgc ccactttttg atgggggtgt ttgttttttt ctgttaaatt tgtttgagtt 120
 cattgtagat tctggatatt agccctttgt cagatgagta gggtgcgaaa attttctccc 180
 atgttgtagg ttgcctgttc actctg atg gta gtt tct ttt gct gtg cag aag 233
 Met Val Val Ser Phe Ala Val Gln Lys
 -25
 ctc ttt agt tta att aga tcc cat ttg tca att ttg gct ttt gtt gcc 281
 Leu Phe Ser Leu Ile Arg Ser His Leu Ser Ile Leu Ala Phe Val Ala
 -20 -15 -10 -5
 att gct ttt ggt gtt ttg gac atg aag tcc ttg ccc acg cca ggg g 327
 Ile Ala Phe Gly Val Leu Asp Met Lys Ser Leu Pro Thr Pro Gly
 1 5 10

<210> 541
 <211> 396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..395
 <221> sig_peptide
 <222> 84..278
 <223> Von Heijne matrix
 score 4.30000019073486

seq FFSRLGATSVXRA/CT

<221> misc_feature

<222> 271,328,344..345,347

<223> n=a, g, c or t

Oligonucleotide

<400> 541

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gcctgtcacc aggaaaggta agc atg gga gga agg aag atg gcg aca gat gaa      113
                               Met Gly Gly Arg Lys Met Ala Thr Asp Glu
                               -65                               -60
gaa aat gtc tat ggt tta gaa gag aac gct cag tcc cgg cag gag tcc      161
Glu Asn Val Tyr Gly Leu Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser
-55                               -50                               -45                               -40
acg cgg agg ctc atc ctt gtt ggg aga aca ggg gcc ggg aag agc gcc      209
Thr Arg Arg Leu Ile Leu Val Gly Arg Thr Gly Ala Gly Lys Ser Ala
                               -35                               -30                               -25
act ggg aac agc atc ctg ggc cag aga cgg ttc ttc tcc agg ctg ggg      257
Thr Gly Asn Ser Ile Leu Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly
                               -20                               -15                               -10
gcc acg tct gtg anc agg gcc tgc acc acg grh agc cgc agg tgg gac      305
Ala Thr Ser Val Xaa Arg Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp
                               -5                               1                               5
aag tgc cac gtg gaa gtc gtr gnd ctm gga cat vwk can nmh ggg aag      353
Lys Cys His Val Glu Val Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys
10                               15                               20                               25
tgt cca aga cag atc ctg gct gtg agg aga gag gtc act gct a      396
Cys Pro Arg Gln Ile Leu Ala Val Arg Arg Glu Val Thr Ala
                               30                               35
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<210> 542

<211> 247

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..247

<221> sig_peptide

<222> 8..100

<223> Von Heijne matrix

score 4.30000019073486

seq ALALTXTLLPAPG/EH

<221> misc_feature

<222> 78,182,194

<223> n=a, g, c or t

Oligonucleotide

<400> 542

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Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln
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	-30		-25		-20		
ctg gct ccc cag gcc ttg gct cta act bmk acc ctc ctc cca gcc cca							97
Leu Ala Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro							
	-15		-10		-5		
gga gaa cac gat tck ccr atg stc att ggc cag ttt ccc cwa aac cct							145
Gly Glu His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro							
	1		5		10		15
ccc tcc gag cac ccg ggc gcc agt ccc agg cgg wmr ngg acg ggc tgg							193
Pro Ser Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp							
		20		25		30	
nra ccc caa agc tgg gac cgg agg gtg agc ccg gca gag gca gag aca							241
Xaa Pro Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr							
	35		40		45		
cgc agg							247
Arg Arg							

<210> 543
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..221

<221> sig_peptide
 <222> 87..209
 <223> Von Heijne matrix
 score 4.30000019073486
 seq HLFTLGFLCSLCP/HP

<221> misc_feature
 <222> 154
 <223> n=a, g, c or t
 Oligonucleotide

<400> 543	
tgctatgttc aatcttgtac aggtcttttg tggacatatg gtctcactcc tcttaggtat	60
ataccgagta gtgaaactgc caggtc atg gga gta tac acg tgt cca att ttt	113
	Met Gly Val Tyr Thr Cys Pro Ile Phe
	-40 -35

gtg cat tac tac gag aac cat gga cca acc ccw agt ttc cnt gcc ttt	161
Val His Tyr Tyr Glu Asn His Gly Pro Thr Pro Ser Phe Xaa Ala Phe	
	-30 -25 -20

att tcc ttt cat cta ttt act ttg ggc ttt ctt tgt tcc cta tgc ccc	209
Ile Ser Phe His Leu Phe Thr Leu Gly Phe Leu Cys Ser Leu Cys Pro	
	-15 -10 -5

cac ccc cac ggg	221
His Pro His Gly	
1	

<210> 544
 <211> 375
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 307..375

<221> sig_peptide

<222> 307..354

<223> Von Heijne matrix

score 4.30000019073486

seq SVSCSSSLWVSLS/KD

<221> misc_feature

<222> 302

<223> n=a, g, c or t

Oligonucleotide

<400> 544

tcaatggaag aaggagwaaa aagagaagag gaaaatggga ccaatactgc tgatcatgtt 60

cgaaattcca gttgggcaaa aaacggctcc taccaagggtg ctcttcataa cgcctctgaa 120

gaagccacag aacaaaacat acgagctggt acccaggcag ttttgcaggt ggatcacttt 180

atggctatatt ttaaaaaataa aataatcatt aaatatcttct gttcagtatt tcagtataca 240

gtatactttt cacaatataa aaatagaagc ttaatactgg gcattcatac tttttaaaga 300

gnatga atg aag aaa tcg gtt tcc tgc tgt agt tct cta tgg gta agt 348

Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser

-15

-10

-5

ctt agt aaa gac gag aat gct gaa atg 375

Leu Ser Lys Asp Glu Asn Ala Glu Met

1

5

<210> 545

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 260..376

<221> sig_peptide

<222> 260..349

<223> Von Heijne matrix

score 4.30000019073486

seq TVLLSGSPRAVVS/AV

<400> 545

tagtggaacag cccaagctgc ttctcttaga atggctgtgg cttcacaagt gatgagaaga 60

gcattgcgctt gatttcagat cccattaca agctcataat gaatgagtca caggagaaag 120

gtgrgacttg gggccctttc gtgctgatg ggaagctcct gmaccccg gtagccctc 180

cagactgtcc ttgccacac gtgtgcactg gcctctttat gccaacccag tgaggacagg 240

ttctgagggga cctggacag atg ctg ctg ccc cta gcc atg gct gga cga tgt 292

Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys

-30

-25

-20

tat aca gcc aag cac agc acw gtg ctg ctc tca gga agc cca agg gct 340

Tyr Thr Ala Lys His Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala
-15 -10 -5
gtg gtc agt gca gtg gtg atg gtg ggc aca ggg tgc 376
Val Val Ser Ala Val Val Met Val Gly Thr Gly Cys
1 5

<210> 546
<211> 109
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..107

<221> sig_peptide
<222> 30..86
<223> Von Heijne matrix
score 4.30000019073486
seq LRAFLLSVPLGKG/SA

<400> 546
cccacagcct tccctggtgt gcctgcagt atg cca tcc tgc tgc tac ctt agg 53
Met Pro Ser Cys Cys Tyr Leu Arg
-15

gct ttt ctg ctc tct gtc cct ctg ggg aaa ggc tca gcc ctt aag gat 101
Ala Phe Leu Leu Ser Val Pro Leu Gly Lys Gly Ser Ala Leu Lys Asp
-10 -5 1 5

ccc gtg ct 109
Pro Val

<210> 547
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 3..305

<221> sig_peptide
<222> 3..74
<223> Von Heijne matrix
score 4.19999980926514
seq LLLSSLWIVCCLH/LD

<400> 547
at atg gtt gct gac aag gag gtg cag aca agg acc ctc ttg ctt tcc 47
Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser
-20 -15 -10

tca cta tgg ata gtc tgt tgc ctc cat cta gat tct ctt att tca rrr 95
Ser Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa
-5 1 5

aaa tat cct ctc cat gca att agg aga tat tta tcg acg ctg aga aac 143

Lys	Tyr	Pro	Leu	His	Ala	Ile	Arg	Arg	Tyr	Leu	Ser	Thr	Leu	Arg	Asn	
	10						15				20					
caa	aga	gcc	gaa	gaa	cag	gtt	gca	cgt	ttt	caa	aaa	ata	cct	aat	ggt	191
Gln	Arg	Ala	Glu	Glu	Gln	Val	Ala	Arg	Phe	Gln	Lys	Ile	Pro	Asn	Gly	
	25					30				35						
gaa	aat	gag	aca	atg	att	cct	gta	ttg	aca	tca	aaa	aaa	gca	agt	gaa	239
Glu	Asn	Glu	Thr	Met	Ile	Pro	Val	Leu	Thr	Ser	Lys	Lys	Ala	Ser	Glu	
40				45					50				55			
tta	cca	gtc	agt	gaa	gtt	gca	agc	att	ctc	caa	gct	gat	ctt	cag	aat	287
Leu	Pro	Val	Ser	Glu	Val	Ala	Ser	Ile	Leu	Gln	Ala	Asp	Leu	Gln	Asn	
			60					65					70			
ggt	cta	aaa	caa	tgt	gaa	g										306
Gly	Leu	Lys	Gln	Cys	Glu											
			75													

<210> 548
 <211> 148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..148

<221> sig_peptide
 <222> 89..130
 <223> Von Heijne matrix
 score 4.19999980926514
 seq HICLFFSFSXXFX/LF

<400> 548	
aggatagctg aaaggagttc atctaactgg agtcccacta gaagtaagaa acccctattg	60
tttatttttt aataatgtaa tttttatt atg cat att tgt ctt ttt ttt tct	112
Met His Ile Cys Leu Phe Phe Ser	
-10	

ttt tct ttw wct ttt tkt ctt ttc ttt ttt ttt ttt	148
Phe Ser Xaa Xaa Phe Xaa Leu Phe Phe Phe Phe Phe	
-5 1 5	

<210> 549
 <211> 374
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 240..374

<221> sig_peptide
 <222> 240..296
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ILARLCRMQTCWC/LS

<400> 549
 tacattcggc cgggccatgg cagcggcgcc cctgaaagtg tgcattcgtgg gctcggggaa 60
 ctgggggttca gctgttgcaa aarkrattgg taataatgtc aagaaacttc agaaatttgc 120
 ctccacagtc aagatgtggg tctttttraar aaamcrgkkr akkggcagra aactgacaga 180
 catcataaat aatgaccatg aaaatgtaaa atatcttcct ggacacaagc tgccagaaa 239
 atg tgg ttg cca tgt caa atc tta gcg agg ctg tgc agg atg cag acc 287
 Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr
 -15 -10 -5
 tgc tgg tgt ttg tca ttc ccc acc agt tca ttc aca gaa tct gtg atg 335
 Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met
 1 5 10
 aga tca ctg gga gag tgc cca aga aag cgc tgg ggg ggg 374
 Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly
 15 20 25

<210> 550
 <211> 476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 147..476
 <221> sig_peptide
 <222> 147..398
 <223> Von Heijne matrix
 score 4.19999980926514
 seq VTILVSLALAFLA/CI

<400> 550
 agacacacgc gaggcgctgt ccttttcagca ccacaagctc gggctgagga gggaggactc 60
 ctggcogtcc tcctcckctt caaattggct tgaatctgct ctgacccccc acgagtgcag 120
 cacagtctgg gaagaaaggc gtaagg atg gwg aag ctg arc agt aac ccc agc 173
 Met Xaa Lys Leu Xaa Ser Asn Pro Ser
 -80
 gag aag gga acc aag ccg cct tca gtt gag gat ggc ttc cag acc gtc 221
 Glu Lys Gly Thr Lys Pro Pro Ser Val Glu Asp Gly Phe Gln Thr Val
 -75 -70 -65 -60
 cct ctc atc act ccc ttg gag gtt aat cac tta cag ctg cct gct cca 269
 Pro Leu Ile Thr Pro Leu Glu Val Asn His Leu Gln Leu Pro Ala Pro
 -55 -50 -45
 gaa aag gtg att gtg aag aca aga acg gaa tat cag ccg gaa cag aag 317
 Glu Lys Val Ile Val Lys Thr Arg Thr Glu Tyr Gln Pro Glu Gln Lys
 -40 -35 -30
 aac aaa ggg aag ttc cgg gtg cca aaa atc gct gaa ttt acg gtc acc 365
 Asn Lys Gly Lys Phe Arg Val Pro Lys Ile Ala Glu Phe Thr Val Thr
 -25 -20 -15
 atc ctt gtc agc ctg gcc cta gct ttc ctt gcg tgc atc gtg ttc ctg 413
 Ile Leu Val Ser Leu Ala Leu Ala Phe Leu Ala Cys Ile Val Phe Leu
 -10 -5 1 5
 gtg gtt tac aaa gcc ttc acc tat gat cac agc tgc cca gag gat tcg 461
 Val Val Tyr Lys Ala Phe Thr Tyr Asp His Ser Cys Pro Glu Asp Ser
 10 15 20

tct atr agc acc ggg
 Ser Xaa Ser Thr Gly
 25

476

<210> 551
 <211> 231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..229

<221> sig_peptide
 <222> 77..139
 <223> Von Heijne matrix
 score 4.19999980926514
 seq EVLSLLFXCIYWG/QY

<400> 551
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 ccacacaact tataaa atg ttc ats gcc gca gca gga gta gag gtc ctg agc 112
 Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser
 -20 -15 -10
 ctc cta ttt ttc tgc atc tac tgg ggt caa tat gcc acc gat ggc att 160
 Leu Leu Phe Xaa Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile
 -5 1 5
 ggc aac gag agt gtg aag atc ttg gcc aag ctg ctc ttc tcc tcc agc 208
 Gly Asn Glu Ser Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser
 10 15 20
 ttc ctc atc ttc ctg ctg atg gg 231
 Phe Leu Ile Phe Leu Leu Met
 25 30

<210> 552
 <211> 229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..229

<221> sig_peptide
 <222> 125..202
 <223> Von Heijne matrix
 score 4.19999980926514
 seq FLSFLSFFFFSFF/LF

<400> 552
 agtttctactc cgaaagtsct tcttacagag caactccaag gatgggctga aaagcacata 60
 gagaaaatgg aacagtgcga agttggaagg tccgtgcggg tggcagcgcc agtgtgggga 120
 tgag atg ctc aca gga cgg ttt tta ggc ggc tca caa ggg ttt ttt ctt 169
 Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu

	-25		-20		-15		
tct	ttt	ctt	tct	ttc	ttt	ttt	ttt
Ser	Phe	Leu	Ser	Phe	Phe	Phe	Ser
	-10		-5		1		5
ttt	ttt	ttt	ttt				
Phe	Phe	Phe	Phe				

217

229

<210> 553
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..232

<221> sig_peptide
 <222> 110..193
 <223> Von Heijne matrix
 score 4.19999980926514
 seq FVFMSKLLLFSS/FL

<400> 553	
acgatcagat ctgakraaaa ttgagcccc aaaagcagtt atcagactat ttgaaataaa	60
gatttatatt cacctttaat aacaatgtac cattaataac acatattac atg ttt att	118
	Met Phe Ile
tkr taw rak atg aaa cag wcr ttt cat att ata gac ttt gtt ttc atg	166
Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe Val Phe Met	
-25 -20 -15 -10	
agt aaa ctt tta tta ttt tca ttt tca ttt tta ara aaa gcr cgc atg	214
Ser Lys Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys Ala Arg Met	
-5 1 5	
awt aca gca gca cct ggg	232
Xaa Thr Ala Ala Pro Gly	
10	

<210> 554
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..141

<221> sig_peptide
 <222> 31..84
 <223> Von Heijne matrix
 score 4.19999980926514
 seq HILTAVLPLVSHQ/QN

<400> 554	
ttacattcct cacttctagt gggttgatta atg gtc aca cca gta cac atc ctg	54
	Met Val Thr Pro Val His Ile Leu

-15

aca gcc gtg ctt cca ctt gtg tct cac cag	caa aac cat ctg ggt gga	102
Thr Ala Val Leu Pro Leu Val Ser His Gln Gln Asn His Leu Gly Gly		
-10	-5 1 5	
agg ttt gca tct ctg gga tcc tca ggc att agg cac ggg		141
Arg Phe Ala Ser Leu Gly Ser Ser Gly Ile Arg His Gly		
10 15		

<210> 555
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 319..375

<221> sig_peptide
 <222> 319..363
 <223> Von Heijne matrix
 score 4.19999980926514
 seq ILHLATLLNLFIS/SN

<221> misc_feature
 <222> 144..145,202,276..277
 <223> n=a, g, c or t
 Oligonucleotide

<400> 555

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tgcattgggt agcatggaca ttttaacaat attgattctt ccaattcatg aacatgaaat	120
atctttccat tttttgaggt ctanncaatc tcttttatca gtgtktccta attctgatta	180
tagagatctt tcacatcttt gnttcaagtt gattoctacg tatttcactt tatttgtggc	240
tgttgtaaat gggattactt tttgcatttc tttchnnsaa ttgttcagtc agcatacagg	300
aatgatactg atttttgt atg ttg att tta cat ctt gca act tta cta aat	351
Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn	
-15 -10 -5	
ttg ttt atc agt tct aac agt ttt g	376
Leu Phe Ile Ser Ser Asn Ser Phe	
1	

<210> 556
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..279

<221> sig_peptide
 <222> 199..243
 <223> Von Heijne matrix
 score 4.19999980926514

seq LASFGPFRSSCFA/AR

<400> 556

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ttcctctccc tcttaccccc accctgtaca aaatgcataa aggatggaaa aactactgca      120
gccagaagtc tttgaatgag gcatcaatgg atgaatatatt aggcagctta gggctgtttc      180
gaaagctgac tgccaagg atg cct ctt gcc tct ttc ggg cca ttt cgg agc      231
                Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser
                -15                -10                -5
agt tgt ttt gca gcc agg tcc atc att tgg aaa tca gga agg caa ggg      279
Ser Cys Phe Ala Ala Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly
                1                5                10
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<210> 557

<211> 340

<212> DNA

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<222> 233..340

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<222> 233..325

<223> Von Heijne matrix

score 4.19999980926514

seq FLLSFLSFRSPLC/HH

<400> 557

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ctgtgtacta taaagtattt ttattggtat ttagtcttgc tgttattggt gctaattgatt      120
gtattgaata attaccagct gttgttagtt atttgaaatt aggtgcctaa agcaacctct      180
catcttgcag aaagtcatct ttcttgaaac tttttaaaaa cttgcttgaa ac atg gag      238
                Met Glu
                -30
act tgg aat ggg acg tct atc ata gta gca cat ctg ara tcc ttc tca      286
Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser Phe Ser
                -25                -20                -15
ttc ctg ctg tca ttt ctg tcc ttt cgc agt cca ctt tgt cac cac ccc      334
Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His His Pro
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ctc ggg      340
Leu Gly
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<210> 558

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 tgcactgctg caatgggctc tgagctggag acggcgatgg agaccctcat caacgtgttc 120
 cacgcccact cgggcaaaga gggggacaag tacaagctga gcaagaagga gctgaaagag 180
 ctgctgcaga cggagctctc tggcttcctg gatgtgaaag agcttatgct gtaggcaaca 240
 gaagccctca agacttttga ggaggcctag aagagtccca taattca atg cag ttc 296
 Met Gln Phe
 ctc tcg ctc atc ttt gcc tcc tgc tcc tca acc acc ccc tta cct ctg 344
 Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro Leu Pro Leu
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 Xaa Gln Cys Cys Thr Leu Pro
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<210> 559
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 ccotggtatg acccactcta gctgagctgt gcagagactg ag atg gtc acc tca 114
 Met Val Thr Ser
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 aag agc agg gga ccc ckt gtc cag act ctg ggg cat gct ggc aac ctg 162
 Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His Ala Gly Asn Leu
 -45 -40 -35
 agg agt ctg cgg gag tgg cct gat ctg tgc tgc ttg agg ctt ttt gtc 210
 Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu Arg Leu Phe Val
 -30 -25 -20
 cca gat cac act gta ctt gct ctg gtg tgc cac agc gca tcc atc tct 258
 Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser Ala Ser Ile Ser
 -15 -10 -5
 gtc ttc cct tct cag gtc acc tgc aga ctc cca agg aca ggg tca cat 306
 Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg Thr Gly Ser His
 1 5 10 15
 ccc atc tgc gtc atc tct caa ggt gcc ttt cac gat cct cac cca aat 354
 Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp Pro His Pro Asn

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 Oligonucleotide

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 gcgaggggtg gcagcgccgg cgccccagaa tccgggacag aaagggtcbc aagagtcgcg 120
 cttggtgmga gaaatcccag atcctgtgat gggggacacc agtgagg atg cct cga 176
 Met Pro Arg
 -25
 tcc atc gat ksg aag gca ctg atc tgg act gtc agg ttg gtg gtc tta 224
 Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu Val Val Leu
 -20 -15 -10
 ttt gcn agt cca awa gtg cgg cca gcg agc agc atg tct tca agg ctc 272
 Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser Ser Arg Leu
 -5 1 5
 ctg ctc ccc gsc ctt cat tac tcg gac tgg act tgc tgg ctt cct gaa 320
 Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp Leu Pro Glu
 10 15 20
 cgg aga ga 328
 Arg Arg
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<210> 561
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 score 4.19999980926514

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<221> misc_feature

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<223> n=a, g, c or t
Oligonucleotide

<400> 561

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tagtgaca atg acc agc ctc ctg act act cct tct cca aga gaa gaa ctg      110
      Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu
      -50                                -45
atg acc acc cca att tta cag ccc act gag gcc ctg tcc cca gaa gat      158
Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp
-40                                -35                                -30                                -25
gga gcc agc aca gca ctc att gca gtt gtt atc acc gtt gtc ttc ctc      206
Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu
      -20                                -15                                -10
acc ctg ctc tcg gtc gtg atc ttg atc ttc ttt tac ctg tac aag aac      254
Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn
      -5                                1                                5
aaa ggc agc tac gtm nnn tat gaa cct aca gaa ggt gag ccc agt gcc      302
Lys Gly Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala
      10                                15                                20
atc gtc cag atg gag adw nnc ttg gcc aag ggc agc gag      341
Ile Val Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu
25                                30                                35

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score 4.19999980926514
seq LIYLVSSFLALNQ/AS

<400> 562

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cttgttctac agatcctccc agaaatctct gggccagggtg gaacccaggg tcagagaggg      120
atgggagaga ggtttaattt tccatgataa ataaaaatct ataaaaataat aaacaagaga      180
aaagagattg gaaacagcca ggttgagca gtgagtgagt aaggaaacct ggctgccctc      240
tccagattcc ccaggctctc agagaagatc agcagaaagt ctgcaagass ctaagaacca      300
tcagccctca gctgcacctc ctccctcca agg atg aca aag gcg sgv ctc atc      354
      Met Thr Lys Ala Xaa Leu Ile
      -15
tat ttg gtc agc agc ttt ctt gcc cta aat cag gcc agc ctc atc agt      402
Tyr Leu Val Ser Ser Phe Leu Ala Leu Asn Gln Ala Ser Leu Ile Ser

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-10	-5	1	5	
cgc tgt gac ttg gcc cag gtg ctg cag ctg gag gac ttg gat ggg ttt				450
Arg Cys Asp Leu Ala Gln Val Leu Gln Leu Glu Asp Leu Asp Gly Phe				
	10	15	20	
gag ggt tac tcc ctg agt gac tgg ctg tgc tgg c				484
Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Trp				
	25	30		

<210> 563
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agacggctaa gagagaggga ggctgcttca aaatcaaattg aggtggtagc agtgcccaca	120
a atg gca cag tta ata atg tgg ctc aag aac cag tta ata ctc ttg ggg	169
Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly	
	-20 -15 -10
ata ttt cgg gga ata aga cac cag att tat cta atc aga act ctt cag	217
Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln	
	-5 1 5
atc agg caa tgg	229
Ile Arg Gln Trp	
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<210> 564
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tcctgggtggc aggtcccag atg ggt cct gtc cca ggt gca gct gca gga gtm	112

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rgg ccc ayg amt ggc gaa ctt gcg grg acc ctg tcc ctc acc tgc agt      160
Xaa Pro Xaa Xaa Gly Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser
      -15          -10          -5
gtc tct ggt gtc tcc atc act agt tat tac tgg agc tgg atc cgc car      208
Val Ser Gly Val Ser Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln
      1          5          10
gcc cca ggg aag ggg ccg gag tgg atc ggg cdk atc gat cat agc ggg      256
Ala Pro Gly Lys Gly Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly
      15          20          25
gat acc gac tac aat ccc tcc ctc cag agt cga gtc acc ctc tca gtg      304
Asp Thr Asp Tyr Asn Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val
      30          35          40          45
gac acg tcg aag aac cag ttc tca ctg agg ttg ctt tct gtg agc gca      352
Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala
      50          55          60

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<210> 565
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 <222> 85..192
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 score 4.19999980926514
 seq LPLFLCPLGMVET/SF

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ccagttggag gcatctgtcc accc atg tgg ttc cag aca cgt tca tgt ggc      111
      Met Trp Phe Gln Thr Arg Ser Cys Gly
      -35          -30
cac cat gac ccc gtc ggc atc aca ggg gta acc aag gtg atc ctc cct      159
His His Asp Pro Val Gly Ile Thr Gly Val Thr Lys Val Ile Leu Pro
      -25          -20          -15
ctc ttc ctg tgt cca ctg ggg atg gta gag acc agc ttc ggg      201
Leu Phe Leu Cys Pro Leu Gly Met Val Glu Thr Ser Phe Gly
      -10          -5          1

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<210> 566
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<221> sig_peptide

<222> 87..413

<223> Von Heijne matrix
score 4.19999980926514
seq LVFLLMYLFPRQL/LI

<400> 566

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ctccaaaggc agatgtgaag aacttg atg tct tat gtg gta acc aag aca aaa      113
                               Met Ser Tyr Val Val Thr Lys Thr Lys
                               -105
gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat ttc ccc cgc      161
Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro Arg
-100                               -95                               -85
ttc tat gtc ctg tac aca atc ttc atg aaa gga ttg cag atg tta tgg      209
Phe Tyr Val Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu Trp
                               -80                               -75                               -70
gct gat gcc aaa aag gct aga aga ata aag aca aat atg tgg aag cac      257
Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys His
                               -65                               -60                               -55
aat ata aag ttt cat caa ctt cca tac cgg gag atg gag cat ttg aga      305
Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu Arg
                               -50                               -45                               -40
cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt att att tcc      353
Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile Ser
                               -35                               -30                               -25
att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg tac ctg ttt      401
Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu Phe
-20                               -15                               -10                               -5
ccc agg caa cta ctg atc agg      422
Pro Arg Gln Leu Leu Ile Arg
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<210> 567

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 48..218

<221> sig_peptide

<222> 48..104

<223> Von Heijne matrix
score 4.19999980926514
seq LSLPSFLCTCCQF/FP

<400> 567

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tttcctttct gttttgggag ggaagtggag ggagttcttt tttcttt atg tat aat      56
                               Met Tyr Asn
tat tac ttc ctt tca ttg ccg agt ttt ctt tgt acc tgt tgt caa ttc      104
Tyr Tyr Phe Leu Ser Leu Pro Ser Phe Leu Cys Thr Cys Cys Gln Phe
-15                               -10                               -5
```


<222> 78..128

<223> Von Heijne matrix
score 4.19999980926514
seq CFALCIILICVMS/CR

<400> 569

```
cacattagtt ttgaaactag ctctaatttc tcctaccagg aggaatttct tccttcttgg      60
caatactgtg gtatttta atg gta ttt tac tgt ttt gca ctt tgt att ata      110
                Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile
                -15                -10

ctt att tgt gtt atg tct tgt cgc cac ctg gg      142
Leu Ile Cys Val Met Ser Cys Arg His Leu
   -5                1
```

<210> 570

<211> 207

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 12..206

<221> sig_peptide

<222> 12..140

<223> Von Heijne matrix
score 4.09999990463257
seq VLITQLCLGKGQS/EP

<400> 570

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tcaatccttg a atg ctc tgg gag act gat ttg agt acc aat aaa act cca      50
                Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro
                -40                -35

gtc tcc tgc aca gct ggc tct gcg tgt gct ctt tct cta ttg caa ttc      98
Val Ser Cys Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe
-30                -25                -20                -15

cct gtc ttg ata act cag ctc tgt cta ggc aaa ggg caa agt gaa ccc      146
Pro Val Leu Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro
                -10                -5                1

att ggg cca tta caa gat ttt gtg tct ttg gaa agc act tca cat ttt      194
Ile Gly Pro Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe
   5                10                15

tat tct ttt ttt t      207
Tyr Ser Phe Phe
   20
```

<210> 571

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 276..371

<221> sig_peptide
 <222> 276..335
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LWCCSPSSRTSSS/LS

<221> misc_feature
 <222> 251
 <223> n=a, g, c or t
 Oligonucleotide

<400> 571
 attctgcagc caactttgtt caccatctcc gcaatgcctt ggacgtcctg catagagagg 60
 tgcccagagt cctggtcaac ctctgggact tctgaaccc cactatsrtg cggcaggtgt 120
 tcctgggrra ccagacaag tgcccagtgc agcaggccag cgttttgtgt aactgcgttc 180
 tgaccctgcg ggagaactcc caagagctag ccaggctggr ggccttcagc cgagcctacc 240
 ggagcagcat nbcgagctgg tggggtcagg ccgct atg aca cgc agg agg act 293
 Met Thr Arg Arg Arg Thr
 -20 -15
 tct ctg tgg tgc tgc agc cct tct tcc aga aca tcc agc tcc ctg tcc 341
 Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg Thr Ser Ser Ser Leu Ser
 -10 -5 1
 tgg cgg atg ggc tcc cag ata cgt cct tct tt 373
 Trp Arg Met Gly Ser Gln Ile Arg Pro Ser
 5 10

<210> 572
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 134..193

<221> sig_peptide
 <222> 134..187
 <223> Von Heijne matrix
 score 4.09999990463257
 seq WCFHAVFFTVVCVC/VR

<400> 572
 gtgacaaagt accacagact ggggtggtga aacacagaaa tttattttct cacaatttctg 60
 gaggtcttag aagtctgaga tcaaggtgtt ggcaggtttg gtttattcta aggcctttct 120
 ctatggcttg tag atg gcc ttc tat ctc tgg tgt ttt cat gcg gtc ttt 169
 Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe
 -15 -10
 ttc act gtg tgt gtg tgt gtg cgg gg 195
 Phe Thr Val Cys Val Cys Val Arg
 -5 1

<210> 573
 <211> 352

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..352

<221> sig_peptide
<222> 173..271
<223> Von Heijne matrix
score 4.09999990463257
seq PLIHLLTSLGHSTC/FR

<400> 573
tcattcttgg gtgtttctcg cagaggggga tttggcaggg tcataggaca atagtggagg 60
gaagggtcagc agataaacia gtgaacaaag gtttctgggt ttctaggca gargaccctt 120
gcggccttcc gcagtgttg tgcctctggg tacttgagat tagggagtgg tg atg act 178
Met Thr
ctt aac gag cat gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt 226
Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu
-30 -25 -20
gca cca ccc tta atc cat tta acb ctg agt gga cac agc aca tgt ttc 274
Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr Cys Phe
-15 -10 -5 1
aga gag cac agg gtt ggg ggc aag gtc ata gat gaa cag cat ccc aag 322
Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His Pro Lys
5 10 15
gca gaa gaa tct ttc tta gta cag gag ggg 352
Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
20 25

<210> 574
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..121

<221> sig_peptide
<222> 35..112
<223> Von Heijne matrix
score 4.09999990463257
seq SLASFLLLTFLPS/LP

<400> 574
accttctctc tctctctctt tcttccctc cttc atg tct ttc tct tcc tct ctc 55
Met Ser Phe Ser Ser Ser Leu
-25 -20
cct cca tct ctc cct cct tcc ctc gct tcc ttc ctc ctt ttg acc ttc 103
Pro Pro Ser Leu Pro Pro Ser Leu Ala Ser Phe Leu Leu Leu Thr Phe
-15 -10 -5
ctt cct tcc ctc cct cgg 121

Leu Pro Ser Leu Pro Arg
1

<210> 575
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..391

<221> sig_peptide
<222> 77..214
<223> Von Heijne matrix
score 4.09999990463257
seq GCAPLRWVPQIRG/CP

<221> misc_feature
<222> 31..32,314
<223> n=a, g, c or t
Oligonucleotide

<400> 575
aaaaactgts sagacttttg cccgtccatt nncrctatct ctccccactc tgggtgtcct 60
acccaaggcg ctgtct atg cgt gcc cag ggc ctg tcc tgc gga tac cca gct 112
Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala
-45 -40 -35
cgc ccc ttg cag ccc ttt tta gag cat ctc gcg ggc tct ggc atc acc 160
Arg Pro Leu Gln Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr
-30 -25 -20
aag cgc aca gcc ccg ggc tgc gct ccc cta agg tgg gtc cct cag atc 208
Lys Arg Thr Ala Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile
-15 -10 -5
cgg ggc tgt cca tta acc agg ctg gcc caa aga ggc gca gac act cga 256
Arg Gly Cys Pro Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg
1 5 10
acc cgg gaa aac tta ttt tat tct cgg ttc ccg ggg ttg cag ctg cca 304
Thr Arg Glu Asn Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro
15 20 25 30
gcg gct gak nac agt gcg tcc gct ttg tct ctc tgc act ccc cgc agc 352
Ala Ala Xaa Xaa Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser
35 40 45
ccc cct ctc ccg ctt cct ctc ccg att aac tcc ccc ggg 391
Pro Pro Leu Pro Leu Pro Leu Pro Ile Asn Ser Pro Gly
50 55

<210> 576
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 133..288

<221> sig_peptide

<222> 133..243

<223> Von Heijne matrix

score 4.09999990463257

seq SISFLPFQASIFG/KT

<400> 576

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aaaggcacag cgcgggcgca ggcgcccaga ggcgacagga gacctcaggc ccagactcca    60
ctccccagct gtgaaaggac tgctggccag acccccaagc tagcccgcca ggctccata    120
gagctgcccc gc atg gct gca tcc agt acc agt cat ctt aaa aat aaa aca    171
          Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr
          -35                -30                -25
aaa acc ttc ctt gcc ccc atg acc aac tgc cac tca att tcc ttt ctt    219
Lys Thr Phe Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu
          -20                -15                -10
cct ttc caa gca agt att ttt gga aag act cgt ctg cag tca ctg agg    267
Pro Phe Gln Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg
          -5                1                5
cct tcc cac cct tac ccc cac    288
Pro Ser His Pro Tyr Pro His
          10                15
```

<210> 577

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 134..262

<221> sig_peptide

<222> 134..250

<223> Von Heijne matrix

score 4.09999990463257

seq FXSCXCVSTLAYT/KG

<400> 577

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attacacagt agagggagga agctaaagga agtctatgga caggtgaggg agggkgagac    60
tggggaattt tctgattgtt cagaggaatc ttgaagatga tggaaatata agatgtgcta    120
aagtttccta gta atg ccc aag gat gct gac ctg gct ttc agt gct tca    169
          Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser
          -35                -30
ttg ttt gaa aga gca gag tcc ctt tat act ctg att tca aaa ttt ktt    217
Leu Phe Glu Arg Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa
          -25                -20                -15
tct tgt dtk tgt gtg tct acc ttg gca tat act aaa gga agg ggg gg    264
Ser Cys Xaa Cys Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
          -10                -5                1
```

<210> 578

<211> 205

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..204

<221> sig_peptide
<222> 115..198
<223> Von Heijne matrix
score 4.09999990463257
seq MPFLFLTLFHCLG/RR

<221> misc_feature
<222> 94
<223> n=a, g, c or t
Oligonucleotide

<400> 578
tgtagaaata cagwtgatgt ttaatagtga ttttgtatcc tatacccttg caaactccac 60
ttcttagttc cagttacttt attgtasytt tttnhttgty ytttactgtg tgtg atg 117
Met
ttt gtg aat aga acc tgt ttt aat tct tcc ttt cca atc tgg atg cct 165
Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met Pro
-25 -20 -15
ttt ctt ttt ctt aca tta ttc cac tgc tta gga cgt cgg g 205
Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
-10 -5 1

<210> 579
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..213

<221> sig_peptide
<222> 25..135
<223> Von Heijne matrix
score 4.09999990463257
seq HFLXAVSASSXA/CL

<400> 579
gcctcctctw gcgctgtcct gtta atg gyg ggc agt agc cgc tgm vkg gga 51
Met Xaa Gly Ser Ser Arg Xaa Xaa Gly
-35 -30
ttg cag ata acc gct tcc cgc acg ggg aaa gtc tac cct gcc tgc cac 99
Leu Gln Ile Thr Ala Ser Arg Thr Gly Lys Val Tyr Pro Ala Cys His
-25 -20 -15
ttt ctg skc gcc gtc agc gcc agt agc tgc cma gca tgt ctg tgg tac 147
Phe Leu Xaa Ala Val Ser Ala Ser Ser Ser Xaa Ala Cys Leu Trp Tyr
-10 -5 1

```

cgc cca atm gct cgc aga ccg gct ggc ccc ggg ggg tca ctc agt tcg      195
Arg Pro Ile Ala Arg Arg Pro Ala Gly Pro Gly Gly Ser Leu Ser Ser
5                               10                               20
gca caa gta cat cca gca g
Ala Gln Val His Pro Ala
25

```

```

<210> 580
<211> 328
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 28..327

```

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<221> sig_peptide
<222> 28..105
<223> Von Heijne matrix
      score 4.09999990463257
      seq VTFWLLCRICTFG/FH

```

```

<400> 580
tgtttgtgat cagtatccaa aggcaaa atg att ttg ttt gac cat tta cat tgt      54
                               Met Ile Leu Phe Asp His Leu His Cys
                               -25                               -20
tca gca tca gga gtg act ttc tgg ttg ctt tgc agg atc tgt acg ttt      102
Ser Ala Ser Gly Val Thr Phe Trp Leu Leu Cys Arg Ile Cys Thr Phe
-15                               -10                               -5
ggg ttt cat ggt ttt tct aaa tac aca gtt tca cgt gga aca cag cag      150
Gly Phe His Gly Phe Ser Lys Tyr Thr Val Ser Arg Gly Thr Gln Gln
1                               5                               10                               15
ggg gca gga avg tgv dgt gga tta cac cag aac tgg gaa cag tgg agg      198
Gly Ala Gly Xaa Xaa Xaa Gly Leu His Gln Asn Trp Glu Gln Trp Arg
20                               25                               30
ggg ctt gtt ggg aag tct agt tct gcc gca gtt gtt ttc tgc ctt acs      246
Gly Leu Val Gly Lys Ser Ser Ser Ala Ala Val Val Phe Cys Leu Thr
35                               40                               45
ttt gac ttg gtt acc agc ttt caa tta gca agt gca att gaa agt aca      294
Phe Asp Leu Val Thr Ser Phe Gln Leu Ala Ser Ala Ile Glu Ser Thr
50                               55                               60
cat ttc cat gct ggg cgc gat ggc tca cac ctg t
His Phe His Ala Gly Arg Asp Gly Ser His Leu
65                               70

```

```

<210> 581
<211> 356
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 264..356

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<221> sig_peptide
 <222> 264..350
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LLLFPASLRLLCV/HP

<221> misc_feature
 <222> 146
 <223> n=a, g, c or t
 Oligonucleotide

<400> 581
 gtckcatttt gcctttgwaa tggaagtcac ttccaagtgt ctgttctcta ggttttcctt 60
 tttttctctt ttagaaattg gacacttcaa taaaatttgt aattacgtcc atctgwtga 120
 htattwgmatt tyratgksca tatctnstgc cagattgtaa actccgcgag tgcacatatc 180
 agatccatta tggttctcat catatcccta gctcctagcg cagtgcgggg cacgtataag 240
 tgctcgaaag ctcccacgtg gtg atg gag cta agc ttg ccc cct tcc atg tgt 293
 Met Glu Leu Ser Leu Pro Pro Ser Met Cys
 -25 -20
 gac tac cca amt ttc tgt ctc ctc ctc ttc ccg gcc tct ctc aga ctc 341
 Asp Tyr Pro Xaa Phe Cys Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu
 -15 -10 -5
 ctc tgt gtg cat ccc 356
 Leu Cys Val His Pro
 1

<210> 582
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 159..239

<221> sig_peptide
 <222> 159..218
 <223> Von Heijne matrix
 score 4.09999990463257
 seq TVGCAGLAGSCRG/IS

<400> 582
 agttcctggtg ctcccgcgga gsatgagacg ttgtgaatta gatgtgagaa gagggacgct 60
 tgggtctgca ccaccaagac cccacaggat cgtgcacccc acccctgctg atgaccatga 120
 ccatctaaar gggaaacatc atttgagggg cctactc atg gat cag aag ccc ctc 176
 Met Asp Gln Lys Pro Leu
 -20 -15
 ttc act gtg ggg tgt gct ggg ttg gcg ggc agt tgc cgt gga atc agt 224
 Phe Thr Val Gly Cys Ala Gly Leu Ala Gly Ser Cys Arg Gly Ile Ser
 -10 -5 1
 ttc ctc agg acc cgc 239
 Phe Leu Arg Thr Arg
 5

<210> 583
 <211> 144
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..142

<221> sig_peptide
 <222> 8..76
 <223> Von Heijne matrix
 score 4.09999990463257
 seq FILLLLLIQDLTMS/PT

<400> 583
 ttttaaa atg tca gtt aat gmt att ttt att ttc tat ttt atc tta tta 49
 Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu
 -20 -15 -10
 tta ttg ata caa gat ctc act atg tca ccc act gct gga atg cag tgg 97
 Leu Leu Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp
 -5 1 5
 cat aat cat ggc cca cca caa gcc ttg cct tgc cca ctg aga abc cc 144
 His Asn His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
 10 15 20

<210> 584
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..280

<221> sig_peptide
 <222> 47..181
 <223> Von Heijne matrix
 score 4.09999990463257
 seq ICLGSPLAECLLG/XX

<221> misc_feature
 <222> 183,210
 <223> n=a, g, c or t
 Oligonucleotide

<400> 584
 ccttgtttaa gccgtgatcg tgacctcacc atgtgtagac agtgag atg tca ttt 55
 Met Ser Phe
 -45
 ctc aat gtg gac atc aca gat tgc ctg tat aac ccc agt gtg tgt ccc 103
 Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser Val Cys Pro
 -40 -35 -30
 gtg gct cag agc agt ctg acc tgt gac ttc ata gat ggt atc tgc ttg 151

Val	Ala	Gln	Ser	Ser	Leu	Thr	Cys	Asp	Phe	Ile	Asp	Gly	Ile	Cys	Leu	
-25						-20					-15					
ggg	tcg	cct	ttg	gct	gag	tgt	ctg	ctt	ggt	gna	gwa	wkw	ksc	att	ttk	199
Gly	Ser	Pro	Leu	Ala	Glu	Cys	Leu	Leu	Gly	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	
-10					-5				1					5		
ggr	atc	aat	rns	cym	tgc	ttt	ccg	tgt	ggt	gtg	aag	tgc	gca	ggt	gtg	247
Gly	Ile	Asn	Xaa	Xaa	Cys	Phe	Pro	Cys	Gly	Val	Lys	Cys	Ala	Gly	Val	
		10					15						20			
gtc	ttg	ggg	ctg	agc	acc	ctg	tgg	tat	gtt	gta	gc					282
Val	Leu	Gly	Leu	Ser	Thr	Leu	Trp	Tyr	Val	Val						
	25						30									

<210> 585
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 242..388

<221> sig_peptide
 <222> 242..352
 <223> Von Heijne matrix
 score 4.09999990463257
 seq FTFLSPSFHSVHL/SE

<400> 585																
tgcatttttta	aaaatagcta	gaagaaaaga	actttaatat	tocccaaaaca	aataaaaatat											60
aaatgtttga	ggtgagggat	atcccaatta	ccctgatttg	gttattattc	attgtatata											120
gttttcaaaa	tatcacatgt	acccccaaaa	tatgtaaaac	tggtatatac	aaataaataa											180
caaaactaaa	aataacagct	gtgcaaacat	ttttaaaagg	cttgctttta	atgggtttca											240
c atg aaa	gta gga	aag gac	tct ctg	gag tct	tta cca	tct tta	tgt gag									289
Met Lys	Val Gly	Lys Asp	Ser Ser	Leu Glu	Ser Leu	Pro Ser	Leu Cys	Glu								
	-35			-30			-25									
aaa cac	att ggt	ccc agt	ggt ctc	ttt acc	ttt ctt	agt cca	tcc ttt									337
Lys His	Ile Gly	Pro Ser	Gly Leu	Phe Thr	Phe Leu	Ser Pro	Ser Phe									
	-20		-15		-10											
cac tct	gta cat	ctt tct	gaa ctc	aat gaa	tta tac	act att	gct gcc									385
His Ser	Val His	Leu Ser	Glu Leu	Asn Glu	Leu Tyr	Thr Ile	Ala Ala									
-5		1		5		10										
ggg																388
Gly																

<210> 586
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 346..435

<221> sig_peptide

<222> 346..396
 <223> Von Heijne matrix
 score 4.09999990463257
 seq VLISASLLRASQL/KI

<221> misc_feature
 <222> 170
 <223> n=a, g, c or t
 Oligonucleotide

<400> 586
 tgtgctgtgt ggtaggaga aggagggatg ggagagagaa ggggaaggaa tgaggcatgg 60
 agagagatca caaccatcgt ctcaatgaag cagcagcaca cacagggatg tgtggtcgwc 120
 ccaagttcag gggagagagt ttaaaggcgg gatgatcata tgtgaagdhc tggcagcacc 180
 aatatggcac tgtcaaagta aaagagaaat agatctgaac tggattttta tgagaataat 240
 agcaaataat aacatttcct agatagtttg atattttattc tggaagtatc gctaccaaca 300
 tcaacatctg ggaagcdag tgggcatcaa aatcctacct ggcta atg gaa agc aaa 357
 Met Glu Ser Lys
 -15
 gtt tta atc agt gca tca ctc cta cgg gcc tct caa tta aaa ata aaa 405
 Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln Leu Lys Ile Lys
 -10 -5 1
 tgr aac aaa atg aca aac ttc tta att ttg t 436
 Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
 5 10

<210> 587
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..377

<221> sig_peptide
 <222> 24..95
 <223> Von Heijne matrix
 score 4.09999990463257
 seq RLPMLSLFRGSHX/XF

<400> 587
 tcctgtcctg ggcgtacgtc aag atg gcg gcg tct gta tta aac acc gtg ctg 53
 Met Ala Ala Ser Val Leu Asn Thr Val Leu
 -20 -15
 agg cgg ctt cct atg cta tct ctc ttc cga ggt tct cay vvg rbq ttc 101
 Arg Arg Leu Pro Met Leu Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe
 -10 -5 1
 agg ttc ccc tcc aga ctc ttt gca cca aag ctc cct ctg agg aag att 149
 Arg Phe Pro Ser Arg Leu Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile
 5 10 15
 ctt tgt cct cag ttc cca ttt ctc ctt ata agg atg agc cct gga aat 197
 Leu Cys Pro Gln Phe Pro Phe Leu Leu Ile Arg Met Ser Pro Gly Asn
 20 25 30

<211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 138..209

<221> sig_peptide
 <222> 138..179
 <223> Von Heijne matrix
 score 4.09999990463257
 seq LASPCVLVQSGX/SL

<221> misc_feature
 <222> 78,80,118
 <223> n=a, g, c or t
 Oligonucleotide

<400> 589
 gaagataata ataatgatta ttataataat gatgatgatt ccaaggaaaa aacctacagc 60
 gaatgttcca tttctacnsn gcacgcagac actctcccta acactgataa cctgagcncc 120
 cagcactgga cggaaga atg ctg gcg tct ccg tgt gta ctg gtt cag ggt 170
 Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly
 -10 -5
 tct ggs bcc agc ctt gtc agg acc ccc tgg tgt cca gag c 210
 Ser Gly Xaa Ser Leu Val Arg Thr Pro Trp Cys Pro Glu
 1 5 10

<210> 590
 <211> 178
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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 Met Asn Ile Ile Leu
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 gaa atc ctt ctg ctt ctg atc acc atc atc tac tcc tac ttg gag tcg 102
 Glu Ile Leu Leu Leu Ile Thr Ile Ile Tyr Ser Tyr Leu Glu Ser
 -10 -5 1
 ttg gtg aag ttt ttc att cct cag agg aga aaa tct gtg gct ggg gag 150
 Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys Ser Val Ala Gly Glu
 5 10 15

att gtt ctc att act gga gct ggg cat g
 Ile Val Leu Ile Thr Gly Ala Gly His
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178

<210> 591
 <211> 308
 <212> DNA
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<220>
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<221> sig_peptide
 <222> 149..265
 <223> Von Heijne matrix
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<221> misc_feature
 <222> 272
 <223> n=a, g, c or t
 Oligonucleotide

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 gtaccgcgct tggcggcagc tggccccaga cttctgtctt ttcaagmkgc aagtraargc 120
 tcggggctgc rraattgcaa ccttgcca atg gac ctg atc ggt ttt ggt tat 172
 Met Asp Leu Ile Gly Phe Gly Tyr
 -35
 gca gcc ctc gtg aca ttt gga agc att ttt gga tat aag cdg aga ggt 220
 Ala Ala Leu Val Thr Phe Gly Ser Ile Phe Gly Tyr Lys Xaa Arg Gly
 -30 -25 -20
 ggt gtt ccg tct ttg att gct ggt ctt ttt gtd gga tgt ttg gcc ggc 268
 Gly Val Pro Ser Leu Ile Ala Gly Leu Phe Val Gly Cys Leu Ala Gly
 -15 -10 -5 1
 tat nsa gct tac cgt gtc tcc aat gac aaa cga gat gta a 308
 Tyr Xaa Ala Tyr Arg Val Ser Asn Asp Lys Arg Asp Val
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<210> 592
 <211> 219
 <212> DNA
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<221> sig_peptide
 <222> 16..72
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 seq XTFLAAXRRLVTG/QT

<222> 89..160

<221> sig_peptide

<222> 89..130

<223> Von Heijne matrix

score 4

seq HLGFI LSFHGLIA/NF

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ttcacattgg cttctttcac taaataac atg cat tta gga ttc att ctt tct 112

Met His Leu Gly Phe Ile Leu Ser

-10

ttc cat ggt ttg ata gct aat ttc ttt ttt tgt ctg aat gca cca gcg g 161

Phe His Gly Leu Ile Ala Asn Phe Phe Phe Cys Leu Asn Ala Pro Ala

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<210> 595

<211> 396

<212> DNA

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<222> 317..376

<223> Von Heijne matrix

score 4

seq GCVAAGVVIGAGA/AT

<221> misc_feature

<222> 149

<223> n=a, g, c or t

Oligonucleotide

<400> 595

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ctgcctggmt cccagcagga cgctgtgcc tttgggaaca aaggaatagt ctgcctggaa 120

tccctgcaga tcttggggcc ggaggcagnt ccaacccttg gagcaggaag aaacgcaaag 180

ttgtcaagaa ccaagtcgag ctgcctcaga gccggcccg agtagctgca gactccgccc 240

gcgacgtgtg cgcgcttctc tgggccagag cgagcctgtt ttgtgctcgg gttaagagat 300

ttgtccbagc tatacc atg ggc cgc act cgg gaa gct ggc tgc gtg gcc gct 352

Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala

-20

-15

-10

ggt gtg gtt atc ggg gct ggt gct gct act gtg tat aca gac tg 396

Gly Val Val Ile Gly Ala Gly Ala Ala Thr Val Tyr Thr Asp

-5

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<210> 596

<211> 407

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Glu	Gly	Leu	His	Gln	Gly	Leu	Cys	Leu	Pro	Gln	Arg	Val	His	Cys	Ser	
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ctg	ctc	ccg	gct	cct	gg											274
Leu	Leu	Pro	Ala	Pro												
					5											

<210> 598
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 <221> sig_peptide
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agtgtaaaca	ctggccatgt	gaagattgag	cctgtttgatg	gtttcttttg	tatcatagga											120	
tgccacgtca	ccaactaggg	aattctgccc	aatcagttga	gccaaatagt	gctgtcctat											180	
tgtaaaattg	ttaaatctgt	gtgcttgtgt	gtgtgcttgt	cagaatttgt	gaatcataga											240	
attgttttaa	ctggaagaag	accccccaaga	tcatctgctt	caacccttc	cttcctctct											300	
tttccagaga	ggttgcactt	tacttgagct	gtgactagga	tt atg cca	cat tct											354	
				Met Pro	His Ser												
				-20													
ttt gta agt	tgt aac cta	ttt ttg tct	gtr ttg aat	ttc ctt ttt	ttg											402	
Phe Val Ser	Cys Asn Leu	Phe Leu Ser	Val Leu Asn	Phe Leu Phe	Leu												
	-15		-10		-5												
cta agc ttt	agc aca															417	
Leu Ser Phe	Ser Thr																
	1																

<210> 599
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 <212> DNA
 <213> Homo sapiens

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ggcagcatag aaatggaaga aaaataccca gccagatcca gctcagagcc aagaaaatgt 120
acacaccaga tccccagcat tcccaattat cacaaaaggt gccttaattt ctatctacaa 180
gacaacccta caatcctcac aggccctgag ctgagtatag aaagttttct ggagtccat 239
atg gct gtt ttt ctc caa aag agg aaa cac aca atg aga cac cac cta 287
Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
-25 -20 -15
ctc ctc agt aca ctg gct act ata gca ggc aac att tac aga 329
Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
-10 -5 1

<210> 600
<211> 311
<212> DNA
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<220>
<221> CDS
<222> 169..309
<221> sig_peptide
<222> 169..246
<223> Von Heijne matrix
score 4
seq PVAVEALLRAVFG/VV

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gcgggcagaa acgggactgg cagtgccac acgtgtgcgt tctccccgtc cgcccgaagg 120
agctacctgt gcaccctgcc tccggctctc ctgagcagag agatcctg atg gct gac 177
Met Ala Asp
-25
tca gaa gca ctc ccc tcc ctt gct ggg gac cca gtg gct gtg gaa gcc 225
Ser Glu Ala Leu Pro Ser Leu Ala Gly Asp Pro Val Ala Val Glu Ala
-20 -15 -10
ttg ctc cgg gcc gtg ttt ggg gtt gtt gtg gat gag gcc att cag aaa 273
Leu Leu Arg Ala Val Phe Gly Val Val Val Asp Glu Ala Ile Gln Lys
-5 1 5
gga acc agt gtc tcc cag aag gtc tgc smg tgg aag ga 311
Gly Thr Ser Val Ser Gln Lys Val Cys Xaa Trp Lys
10 15 20

<210> 601
<211> 420
<212> DNA
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<220>
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<221> sig_peptide

<222> 159..266
 <223> Von Heijne matrix
 score 4
 seq LAELPVSSPLCHA/VL

<221> misc_feature
 <222> 365..366
 <223> n=a, g, c or t
 Oligonucleotide

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 ctaagccttt tctaccctct tctcaaagta gagccgaata tgattcagag gagagtctgg 60
 gaagtgatga tgatgacaat gatgatgatg atgatgtttt agcatcagat ttccatctcc 120
 aggaacattc taattcaaat tcatatagtt ggtccttg atg cgg ttg gcg atg gtg 176
 Met Arg Leu Ala Met Val
 -35
 caa ttg gtg ctc aac aat ttg aag act ttt tat ccc ttc gca gat cat 224
 Gln Leu Val Leu Asn Asn Leu Lys Thr Phe Tyr Pro Phe Ala Asp His
 -30 -25 -20 -15
 gat ctt gca gag ctt cca gtt agt tca cct ctt tgt cat gcg gtt cta 272
 Asp Leu Ala Glu Leu Pro Val Ser Ser Pro Leu Cys His Ala Val Leu
 -10 -5 1
 aaa act ctt caa tgt tgg gaa caa gtt ctt ctc cga cga ctt gaa atc 320
 Lys Thr Leu Gln Cys Trp Glu Gln Val Leu Leu Arg Arg Leu Glu Ile
 5 10 15
 cat ggt ggg cca cct caa aat tat atc gca agt cat acc gcc gan nag 368
 His Gly Gly Pro Pro Gln Asn Tyr Ile Ala Ser His Thr Ala Xaa Xaa
 20 25 30
 agt ttg tct gca ggt cct gca att ctt cgc cac aaa gct tta ctg gaa 416
 Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg His Lys Ala Leu Leu Glu
 35 40 45 50
 cct a 420
 Pro

<210> 602
 <211> 463
 <212> DNA
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<220>
 <221> CDS
 <222> 311..463

<221> sig_peptide
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 <223> Von Heijne matrix
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 seq LFILXYFXXYTLS/SG

<221> misc_feature
 <222> 353..354
 <223> n=a, g, c or t
 Oligonucleotide

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 acggggaact actggatatt tgaaagaagg aatttatctg tctatcttct atttatctat 180
 ctgtaatcta tcatctaata taggaaatga tagatctagg aagatgatag ctagataaat 240
 atcagtcata ttctatcat ctgggaaata gatttatctt gttttattat ttttaattaat 300
 taatttaaaa atg ttt aaa tta ttt tta ttt tta ttt att tta ttw tat 349

Met Phe Lys Leu Phe Leu Phe Leu Phe Ile Leu Xaa Tyr
 -20 -15 -10

ttc nng vat tac act tta agt tct ggg ata tat gtg cag aat gtg cag 397
 Phe Xaa Xaa Tyr Thr Leu Ser Ser Gly Ile Tyr Val Gln Asn Val Gln
 -5 1 5
 gtt tgt tac ata ggt ata cac atg cca tgg tgg ttt gct gca ccc atg 445
 Val Cys Tyr Ile Gly Ile His Met Pro Trp Trp Phe Ala Ala Pro Met
 10 15 20 25
 aac ctg tca tct gca cta 463
 Asn Leu Ser Ser Ala Leu
 30

<210> 603
 <211> 269
 <212> DNA
 <213> Homo sapiens

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 taattccatt ttccatgaa ctttttgaag tccocgtata cataactttt catggtgaga 120
 acacttataa tctactgtca gcaattttca aatataaaat atattattaa ctgtagtcac 180
 c atg ata tac agt aga tct ctt gaa ctt att cct ctt ttg tct gaa att 229
 Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile
 -20 -15 -10
 ttg tat gct ttg gcc aac atc tcc cca atc ccc cag acg g 269
 Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr
 -5 1 5

<210> 604
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<220>
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<221> sig_peptide
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 <223> Von Heijne matrix
 score 4
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 ttagggcaga gattaatgcc caccagaaag gtaactttga tgagggtagc aagcatgctt 120
 tcaactgaaaa gtattttttt ttcctctttt caagattctc ataattataa cccataaaac 180
 taagttagac ttgtttctta tgtgcattta tgatttaatt aacgagagta cactttgtat 240
 gacaaaatgc aattttaagg taaacactat ggagaataat ttcctttcct agtgaa atg 299
 Met
 gtg cac gtt ata ttt tat ttt gtt tta ttt cta ggg ata atg aca cag 347
 Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr Gln
 -15 -10 -5 1
 cgg g 351
 Arg

<210> 605
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 <212> DNA
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<220>
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<221> sig_peptide
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 score 4
 seq LIYFFQLHSCCHD/KV

<400> 605
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 Met His Lys Phe Phe Arg
 -25 -20
 cat ttc tat tca gat ttt ctg att tat ttc ttt cag ctc cat tca tgt 102
 His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe Phe Gln Leu His Ser Cys
 -15 -10 -5
 tgt cac gat aaa gtr act gcm cra agg gcc tat rtt cac tac agc agc 150
 Cys His Asp Lys Val Thr Ala Xaa Arg Ala Tyr Xaa His Tyr Ser Ser
 1 5 10
 ctc tta act cct tac ctc tct cag cac ccc tgc ccc cat ccc ggg 195
 Leu Leu Thr Pro Tyr Leu Ser Gln His Pro Cys Pro His Pro Gly
 15 20 25

<210> 606
 <211> 426
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 63..425

<221> sig_peptide
<222> 63..140
<223> Von Heijne matrix
score 4
seq LLRELRYLSAATG/HP

<221> misc_feature
<222> 174
<223> n=a, g, c or t
Oligonucleotide

<400> 606
ggaggagggg ttttcagggt cgtaggacgc cgttgggcac cacgctcgga gaagacagga 60
ca atg gcg gcc tta ggg tcc ccg tgc cgc act ttt cga gga ctt ctg 107
Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu
-25 -20 -15
cgg gag ttg cgc tac ctg agc gcg gcc acc ggc cac cct atc gcg aca 155
Arg Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr
-10 -5 1 5
ccg cgg cct atc ggt acc ntt gtg aag gct ttc cgt gca cat cgg gtc 203
Pro Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val
10 15 20
acc agt gaa aag ttg tgc aga gcc caa cat gag ctt cat ttc caa gct 251
Thr Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala
25 30 35
gcc acc tat ctc tgc ctc ctg cgt asa tcc gga aac atg tgg ccc tac 299
Ala Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr
40 45 50
atc agg aat ttc atg gca agg gtg agc gct cgg tgg agg agt ctg ctg 347
Ile Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu
55 60 65
gct tgg tgg gtc tca agt tgc ccc atc agc ctg gag gga agg gct ggg 395
Ala Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly
70 75 80 85
agc cat gaa cat gga gaa tat cct tgg atg c 426
Ser His Glu His Gly Glu Tyr Pro Trp Met
90 95

<210> 607
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 71..160

<221> sig_peptide
<222> 71..154
<223> Von Heijne matrix
score 4

seq VSLFLLVVLYHYA/AV

<400> 607
 agttccggtc caggtctctg acttcggggt tgttcgctgg tggcgtcgga gccgagccgg 60
 actggtcagg atg atc acg gac gtg cag ctc gcc atc ttc gcc aac atg 109
 Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met
 -25 -20
 ctg ggc gtg tcg ctc ttc ttg ctt gtc gtt ctc tat cac tac gcg gcc 157
 Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala
 -15 -10 -5 1
 gtg g 161
 Val

<210> 608
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 283..357
 <221> sig_peptide
 <222> 283..336
 <223> Von Heijne matrix
 score 4
 seq LSFLCSLSQNALN/IS

<400> 608
 tgaaccttgc ttttatacaa atcacttttt tgttatttga ggaacaagat aacattttct 60
 tggcaggatt actatagtcc cccaacaag ctctaccama gaagataata gaacttattg 120
 agcttaaatg aattatagga magttcctga aaagtccaar gtaaagtgtga agagaaccg 180
 attctcttaa cctcacccaa ccagcactt gattctccct tgtttcctgg tttcataca 240
 cacactggga aaggamaagg aagaagaaac aaggatgtcg tt atg gct gaa gga 294
 Met Ala Glu Gly
 -15
 gct ttg agc ttc ctt tgc tct tta tcg caa aat gca ttg aat att tcc 342
 Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala Leu Asn Ile Ser
 -10 -5 1
 ctc att tct cgt aag 357
 Leu Ile Ser Arg Lys
 5

<210> 609
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..201
 <221> sig_peptide
 <222> 133..180

<223> Von Heijne matrix
 score 4
 seq SFLLCFTLVGTQL/RN

<400> 609
 ttatatgttc tgcttatggg actttgcatg ttctacaaac tacaagtatc tttttctact 60
 ctgaattgaa tttagctctg tttacgggtt tcttttctgt gagcagaagt tcttaatgat 120
 tactgtagtc aa atg tat cca tct ttt ctt tta tgc ttc aca ctc gta ggg 171
 Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly
 -15 -10 -5
 act cag tta aga aat tct tcc tta gcc atg 201
 Thr Gln Leu Arg Asn Ser Ser Leu Ala Met
 1 5

<210> 610
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..279
 <221> sig_peptide
 <222> 223..267
 <223> Von Heijne matrix
 score 4
 seq SCTVGCATASSWG/CT

<400> 610
 accgccttcc cacatcggat cgcagggctc ccaaaatggc gagtgagact gcggggactc 60
 gctgagcagc ggagggggag cgtgcagarm mgctgcggcc ctcacagtcc ggagcccggc 120
 cgtgccgtgc cgtaggggaac atgcactttt ccattcccga aaccgagtcc cgcagcgggg 180
 acagcggcgg ctccgcctac gtggcctata acattcacgt ga atg gag tcc tgc 234
 Met Glu Ser Cys
 -15
 act gtc ggg tgc gct aca gcc agc tcc tgg ggc tgy acg agc agg gg 281
 Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys Thr Ser Arg
 -10 -5 1

<210> 611
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..240
 <221> sig_peptide
 <222> 28..156
 <223> Von Heijne matrix
 score 4
 seq AAWCSLVLSFCRL/HK


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<400> 611
agcttcgagg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg      54
                               Met Ala Met Ser Phe Glu Trp Pro Trp
                               -40                               -35

cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act      102
Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr
                               -30                               -25                               -20

cgg cag aag cag ctg gcc gcc tgg tgc tcg ctg gtc ctg tcc ttc tgc      150
Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys
                               -15                               -10                               -5

cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc      198
Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser
                               1                               5                               10

ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg g      241
Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val
15                               20                               25

```

```

<210> 612
<211> 176
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 106..174

<221> sig_peptide
<222> 106..147
<223> Von Heijne matrix
      score 3.90000009536743
      seq RLHVHSLSPFSFA/CL

```

```

<400> 612
aagagccttg gaacatctct ctgaagaata aaacaaatct tttctgcatg tataatcgat      60
ataaatttga ttatattgta ctttttatct cgtgtgtgtg tgtac atg aga tta cat      117
                               Met Arg Leu His

gta cat tcc ctt tct ccc ttt tcc ttt gct tgt ctc cct ttt ctg tcc      165
Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu Pro Phe Leu Ser
-10                               -5                               1                               5

ccc ccg ctg gg      176
Pro Pro Leu

```

```

<210> 613
<211> 342
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 258..341

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```

<221> sig_peptide
<222> 258..335

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<223> Von Heijne matrix
 score 3.90000009536743
 seq RMCILQLLSAVLY/RF

<400> 613
 catttctatk aaaatacaaaa tttaaggctg tagatttaat atgtagtatg ttcattrrgt 60
 tccaaataca ttctaatttc cactgtgatt tctwctttga ctcmtgaawt atttagvagg 120
 tgwttttgwh ttabdwattt ctgactgtat ggggattttc tagttagttt wctactctta 180
 atttgccttc agagamaata ctccacaaga tttcagtcctt tcaattttgt tgcaacttgc 240
 tacaaaacttg gcctaac atg ttg cat ttt wta tat atg atc caw gtg tgc 290
 Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys
 -25 -20
 ttg gaa aga atg tgc att ctg caa ttg ttg agt gct gtg ttg tat aga 338
 Leu Glu Arg Met Cys Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg
 -15 -10 -5 1
 ttt g 342
 Phe

<210> 614
 <211> 154
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..152

<221> sig_peptide
 <222> 48..137
 <223> Von Heijne matrix
 score 3.90000009536743
 seq VGLLDTPLGAVSA/HH

<221> misc_feature
 <222> 17
 <223> n=a, g, c or t
 Oligonucleotide

<400> 614
 agtcggagcgc aaggvcntgg cggasagaac ggattgcagg gtcagcc atg tca tct 56
 Met Ser Ser
 -30
 gag cct ccc cca cca cca cag ccc ccc acc cat caa gct tca gtc ggg 104
 Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala Ser Val Gly
 -25 -20 -15
 ctg ctg gac acc ccc ctc gga gcc gtg agc gct cac cat ccc ctc tgc 152
 Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His Pro Leu Cys
 -10 -5 1 5
 cc 154

<210> 615
 <211> 272
 <212> DNA
 <213> Homo sapiens

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<220>
<221> CDS
<222> 185..271

<221> sig_peptide
<222> 185..244
<223> Von Heijne matrix
      score 3.90000009536743
      seq FLTSISFLALVLW/NV

<400> 615
caactataat agctttttaa cttgtttctc tttccttttc cttcatttca gtccatctta      60
ttatctttga caaaataatt tctctgatgc ctgactgcct gccccccaac aacaaagctt      120
ttattatact tcctaactaa tcaactatwm cyttacccat ctagccaaag tagactaccc      180
atat atg ttt ctt gac cat gtc agg ttt tta acc tcc ata tct ttt ctt      229
      Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu
      -20                -15                -10
gct ctg gtc ctg tgg aat gtc ttt ctc aac tct acc cgt ctg g      272
Ala Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu
-5                1                5

<210> 616
<211> 114
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..113

<221> sig_peptide
<222> 36..92
<223> Von Heijne matrix
      score 3.90000009536743
      seq PALLTSSELPALA/SQ

<400> 616
agggttttttag tcttgacctc ttgacctgct tatag atg aga gaa aag cca caa      53
                        Met Arg Glu Lys Pro Gln
                        -15
cca gcg ctc ctg act tca agt gar ctg cct gcc ttg gcc tct caa ata      101
Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro Ala Leu Ala Ser Gln Ile
      -10                -5                1
cat tgc cgc gtc c      114
His Cys Arg Val
      5

<210> 617
<211> 171
<212> DNA
<213> Homo sapiens

<220>

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<220>

<221> CDS

<222> 97..255

<221> sig_peptide

<222> 97..201

<223> Von Heijne matrix

score 3.90000009536743

seq CTFLSLSLHPWGG/FF

<400> 619

acttcagaac tgggggagag ggagaggact ggaggcgga ggggtggccgc tggccagtgc 60

gcactcttct ctctgcatcc ccttccctgc ggcccc atg tgc ctg aac ccc gcc 114

Met Cys Leu Asn Pro Ala

-35 -30

tgc tcg gga ccg ctt tcc ctc cgt tcc cct cgg ctt ccc cct ctc ttt 162

Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro Arg Leu Pro Pro Leu Phe

-25 -20 -15

tgc act ttt ctt tcc ctt tct ttg cat ccc tgg ggg ggt ttc ttt ttg 210

Cys Thr Phe Leu Ser Leu Ser Leu His Pro Trp Gly Gly Phe Phe Leu

-10 -5 1

tgt gcc tgg att tct bct ttc ctc ccg tgg gtg tgt gtg tgk gcg gg 257

Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp Val Cys Val Xaa Ala

5 10 15

<210> 620

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 47..349

<221> sig_peptide

<222> 47..313

<223> Von Heijne matrix

score 3.90000009536743

seq RLLVACCLADIFR/IY

<400> 620

agcggagtak ygagtcggca acccggaggg tagaaatatt tctgtc atg gct cat 55

Met Ala His

tca aag act agg acc aat gat gga aaa att aca tat ccg cct ggg gtc 103

Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro Pro Gly Val

-85 -80 -75

aag gaa ata tca gat aaa ata tct aaa gag gag atg gtg aga cga tta 151

Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu

-70 -65 -60 -55

aag atg gtt gtg aaa act ttt atg gat atg gac cag gac tct gaa gaa 199

Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu

-50 -45 -40

gaa aag gag ctt tat tta aac cta gct tta cat ctt gct tca gat ttt 247

Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala Ser Asp Phe	
-35 -30 -25	
ttt ctc aag cat cct gat aaa gat gtt cgc tta ctg gta gcc tgc tgc	295
Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val Ala Cys Cys	
-20 -15 -10	
ctt gct gat att ttc agg att tat gct cct gaa gct cct tac aca tcc	343
Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro Tyr Thr Ser	
-5 1 5 10	
cct aag gg	351
Pro Lys	

<210> 621
 <211> 118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..117

<221> sig_peptide
 <222> 40..93
 <223> Von Heijne matrix
 score 3.90000009536743
 seq IAWTATPSSAAFA/QA

<400> 621	
atatcctgcc tgmgcctggg mcgggtggag gtgtcctgc atg gmg tct tgt gaa	54
Met Xaa Ser Cys Glu	
-15	
atc gcg tgg act gca aca ccc agc agc gcg gcc ttt gca caa gct ttt	102
Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala Phe Ala Gln Ala Phe	
-10 -5 1	
ccc aca gcc tgc aac a	118
Pro Thr Ala Cys Asn	
5	

<210> 622
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..220

<221> sig_peptide
 <222> 83..157
 <223> Von Heijne matrix
 score 3.90000009536743
 seq LLYILSRSSGRRG/KN

<400> 622	
aaagatttga aggaagatgt aagctttacc aaaattaaaa agtaaagga gtaagtgggg	60

```

ggaaaagggtg cagaacagtg ta atg tgt cac tac ttg tgg aaa aaa tta tac      112
                        Met Cys His Tyr Leu Trp Lys Lys Leu Tyr
                        -25                    -20

tca aca ctt ttg tat ata ctc agc aga tct tct gga aga aga ggt aag      160
Ser Thr Leu Leu Tyr Ile Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys
-15                    -10                    -5                    1
aat ctg ata act gca gtt gcc tcc agg gca ggg aat tta ggt gtc tgg      208
Asn Leu Ile Thr Ala Val Ala Ser Arg Ala Gly Asn Leu Gly Val Trp
                    5                    10                    15

aca gaa aag ggg g      221
Thr Glu Lys Gly
                    20

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<210> 623
<211> 432
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 344..430

```

```

<221> sig_peptide
<222> 344..424
<223> Von Heijne matrix
      score 3.90000009536743
      seq SRMVLLSSALLST/EN

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```

<221> misc_feature
<222> 348..349
<223> n=a, g, c or t
      Oligonucleotide

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```

<400> 623
gtttattgca ttttbcacaa ctcatataat ttaggcttat aagtagctgt atcctggttt      60
ggtttcactt gttttaatta ttttttgatg atttaagaca ctagccatat ggattcaagt      120
tttttagttt ttattttcct acaccatacc atagtagaac tattactgtt gttatttata      180
ttttttaaaa aattcacttg tttttctoga gaatttgatg ctgattttta tgttatactg      240
cataattcag taatttcaca cattaacaac atccagggtc atgtgaggat gagttttcta      300
gcttctgaaa tgttctgagg atgtaatttt ttaataagag gaa atg tnn tct cac      355
                        Met Xaa Ser His
                        -25

```

```

aga cta ttt ggg tgt ttt cca agt gac ttg tca cga atg gtt ttg ctc      403
Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg Met Val Leu Leu
                    -20                    -15                    -10

tct agt gca ctt ctg agt aca gaa aac ca      432
Ser Ser Ala Leu Leu Ser Thr Glu Asn
                    -5                    1

```

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<210> 624
<211> 233
<212> DNA
<213> Homo sapiens

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<220>
 <221> CDS
 <222> 91..231

<221> sig_peptide
 <222> 91..153
 <223> Von Heijne matrix
 score 3.90000009536743
 seq YLCLHLCAFSTEG/WM

<400> 624
 agaggaaaga gaaaaacatg taacatgtaa caaattgttt tcctaaatga caactcagaa 60
 caatagaagg cattagaaga gaccttccat atg cgc cca tca cat tct tca gcc 114
 Met Arg Pro Ser His Ser Ser Ala
 -20 -15
 tac cta tgt ctg cac ctt tgt gct ttc agt act gaa ggt tgg atg aac 162
 Tyr Leu Cys Leu His Leu Cys Ala Phe Ser Thr Glu Gly Trp Met Asn
 -10 -5 1
 cgt ctg tcc tct tct cta agg ctg gct cct cta cct ttg tac cct ttt 210
 Arg Leu Ser Ser Ser Leu Arg Leu Ala Pro Leu Pro Leu Tyr Pro Phe
 5 10 15
 tgc cta ccc agc aat tca ccc ca 233
 Cys Leu Pro Ser Asn Ser Pro
 20 25

<210> 625
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..378

<221> sig_peptide
 <222> 10..57
 <223> Von Heijne matrix
 score 3.90000009536743
 seq RLVWLGLRAPLGG/RQ

<400> 625
 aaggaagaa atg tgg tcg cgg ttg gtg tgg ctg ggm ctt cgg gcc cct ctg 51
 Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu
 -15 -10 -5
 ggt ggg cgc cag ggc ttc acc tcc aag gcg gat cct cag ggc agt ggc 99
 Gly Gly Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly
 1 5 10
 cgg atc acg gct gcg gtg atc gag cac ctg gag cgt cta gcg ctt gtg 147
 Arg Ile Thr Ala Ala Val Ile Glu His Leu Arg Leu Ala Leu Val
 15 20 25 30
 gac ttc ggc agc cgc gag gca gtg gcg cga ctg gag aaa gct atc gcc 195
 Asp Phe Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala
 35 40 45
 ttc gcc gac cgg cta cgc gcc gtg gac aca gac ggg gtg gag ccc atg 243

Phe	Ala	Asp	Arg	Leu	Arg	Ala	Val	Asp	Thr	Asp	Gly	Val	Glu	Pro	Met	
		50						55					60			
gaa	tcg	gtc	ctg	gag	gac	aga	tgt	cta	tac	ctg	aga	tcc	gac	aat	gtg	291
Glu	Ser	Val	Leu	Glu	Asp	Arg	Cys	Leu	Tyr	Leu	Arg	Ser	Asp	Asn	Val	
		65					70					75				
gta	gaa	ggc	aac	tgt	gct	gat	gaa	tta	cta	caa	aac	tcc	cat	cgc	gtc	339
Val	Glu	Gly	Asn	Cys	Ala	Asp	Glu	Leu	Leu	Gln	Asn	Ser	His	Arg	Val	
		80				85					90					
gtg	gag	gag	tac	ttt	gtg	gcc	ccc	cca	ggg	aat	atc	tct	tt			380
Val	Glu	Glu	Tyr	Phe	Val	Ala	Pro	Pro	Gly	Asn	Ile	Ser				
95					100					105						

<210> 626
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..275

<221> sig_peptide
 <222> 27..269
 <223> Von Heijne matrix
 score 3.90000009536743
 seq AIVTCKSLASIHA/LP

<400> 626																
atcctggttt	tgggacagcg	gcaatc	atg	gcg	cca	cct	gtg	aga	tac	tgc	atc					53
			Met	Ala	Pro	Pro	Val	Arg	Tyr	Cys	Ile					
			-80								-75					
ccc	ggc	gaa	cgt	ctg	tgt	aac	ttg	gag	gag	ggc	agc	ccg	ggc	agc	ggc	101
Pro	Gly	Glu	Arg	Leu	Cys	Asn	Leu	Glu	Glu	Gly	Ser	Pro	Gly	Ser	Gly	
		-70				-65					-60					
acc	tac	acc	cgc	cac	ggc	tac	atc	ttt	tcg	tcg	ctw	rcc	ggc	tgt	ctg	149
Thr	Tyr	Thr	Arg	His	Gly	Tyr	Ile	Phe	Ser	Ser	Leu	Xaa	Gly	Cys	Leu	
	-55				-50						-45					
atg	aag	agc	agc	gag	aat	ggc	gcg	ctt	cca	gtg	gtg	tct	gta	gtg	aga	197
Met	Lys	Ser	Ser	Glu	Asn	Gly	Ala	Leu	Pro	Val	Val	Ser	Val	Val	Arg	
	-40				-35				-30				-25			
gaa	aca	gag	tcc	cag	tta	ctg	cca	gat	gtg	gga	gct	att	gta	acc	tgt	245
Glu	Thr	Glu	Ser	Gln	Leu	Leu	Pro	Asp	Val	Gly	Ala	Ile	Val	Thr	Cys	
			-20					-15					-10			
aag	tct	cta	gca	tca	att	cac	gct	ttg	cca	a						276
Lys	Ser	Leu	Ala	Ser	Ile	His	Ala	Leu	Pro							
		-5						1								

<210> 627
 <211> 415
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 174..413

<221> sig_peptide

<222> 174..353

<223> Von Heijne matrix

score 3.90000009536743

seq RLLVARLHMASLA/RR

<221> misc_feature

<222> 7

<223> n=a, g, c or t

Oligonucleotide

<400> 627

accgga	gtg	gagcct	ggga	gccttg	acgt	tagga	acgaa	gtcta	acctg	gatctg	ggagc	60				
cgggtg	agat	caaatt	ggga	atgctt	tcat	aatga	acgtc	aaccag	tcag	ttccac	ctgt	120				
gccacatt	ttt	gggcag	cccc	agcccat	tcta	cccagg	gtat	catcag	tcca	gct	atg	176				
										Met						
										-60						
gtg	ggc	aat	cag	ggt	cca	cag	ccc	cgg	cca	ttc	cct	atg	gag	cct	aca	224
Val	Gly	Asn	Gln	Gly	Pro	Gln	Pro	Pro	Pro	Phe	Pro	Met	Glu	Pro	Thr	
			-55					-50					-45			
atg	gcc	cag	tac	cag	gct	atc	agc	aaa	cac	ctc	ccc	aag	gta	tgt	caa	272
Met	Ala	Gln	Tyr	Gln	Ala	Ile	Ser	Lys	His	Leu	Pro	Lys	Val	Cys	Gln	
			-40					-35					-30			
gag	ccc	cac	ctt	cct	cgg	ggg	cac	ctc	cag	cct	caa	cag	cac	agg	ctc	320
Glu	Pro	His	Leu	Pro	Arg	Gly	His	Leu	Gln	Pro	Gln	Gln	His	Arg	Leu	
			-25					-20					-15			
ctt	gtg	gcc	agg	ctg	cat	atg	gcc	agt	ttg	gca	agg	aga	tgt	aca	gaa	368
Leu	Val	Ala	Arg	Leu	His	Met	Ala	Ser	Leu	Ala	Arg	Arg	Cys	Thr	Glu	
			-10					-5			1				5	
tgg	gcc	aag	ctc	cac	tgt	tca	gat	gca	agg	ctg	ccc	tgg	gtc	tca	gc	415
Trp	Ala	Lys	Leu	His	Cys	Ser	Asp	Ala	Arg	Leu	Pro	Trp	Val	Ser		
			10					15					20			

<210> 628

<211> 318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 214..318

<221> sig_peptide

<222> 214..297

<223> Von Heijne matrix

score 3.90000009536743

seq GVAGVCFRRSDA/SE

<221> misc_feature

<222> 8

<223> n=a, g, c or t

Oligonucleotide

<400> 628
 amattgmknkh hataractct taccatcatt ttaactggat aaaaagtgaa gtgtctaaag 60
 atgtatatat ttsgcacgtt tgarttcaca agaggaagaa caawtttcta gccasgawac 120
 catgahagga ttccaaacag agattaaact tgtcctttga ggataggtaa tgagtccaga 180
 attggtgggt tcttggtttt gctgacttca aga atg aag cca cag acc ctc gca 234
 Met Lys Pro Gln Thr Leu Ala

-25
 gtg agt gtt aca gtt ctt aaa gat ggt gtg gct gga gtt tgt ttc ttc 282
 Val Ser Val Thr Val Leu Lys Asp Gly Val Ala Gly Val Cys Phe Phe
 -20 -15 -10
 aga cgt tca gat gcg tct gaa gtt tct tcc ttc tgg 318
 Arg Arg Ser Asp Ala Ser Glu Val Ser Ser Phe Trp
 -5 1 5

<210> 629
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..169
 <221> sig_peptide
 <222> 29..157
 <223> Von Heijne matrix
 score 3.90000009536743
 seq KCLFLSFAHFLMG/RT

<400> 629
 cattttgact ggtgtaagat gatattctc atg gtg gtt ttg att tgc ctt tct 52
 Met Val Val Leu Ile Cys Leu Ser
 -40
 ctc atg atc agt aat act gag ctt ttt ttc ata cgc ttc ttg act gca 100
 Leu Met Ile Ser Asn Thr Glu Leu Phe Phe Ile Arg Phe Leu Thr Ala
 -35 -30 -25 -20
 tgt atg cct tct ttt gaa aag tgt ctg ttc tta tct ttt gcc cac ttc 148
 Cys Met Pro Ser Phe Glu Lys Cys Leu Phe Leu Ser Phe Ala His Phe
 -15 -10 -5
 ttg atg gga aga acc cac cgt g 170
 Leu Met Gly Arg Thr His Arg
 1

<210> 630
 <211> 196
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..194

<221> sig_peptide

<222> 87..152

<223> Von Heijne matrix
score 3.90000009536743
seq SLLSDILFANIFS/HS

<400> 630

```
gccatttgta tatatttgav aaatatctat tcaaatacat tgcctgcttt aaaatactgt      60
tattggctctt tttatcattg gattgt atg agt tct tta tat att ttg gat att      113
                               Met Ser Ser Leu Tyr Ile Leu Asp Ile
                               -20                               -15

agt ctc tta tca gat ata tta ttt gca aat att ttc tcc cat tct tgg      161
Ser Leu Leu Ser Asp Ile Leu Phe Ala Asn Ile Phe Ser His Ser Trp
                               -10                               -5                               1

gac gtc ttt cca ctt tct ttt ctt ttc ttt tct tt      196
Asp Val Phe Pro Leu Ser Phe Leu Phe Phe Ser
                               5                               10
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<210> 631

<211> 339

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 53..337

<221> sig_peptide

<222> 53..304

<223> Von Heijne matrix
score 3.90000009536743
seq SLLLIILLPNTQD/LR

<400> 631

```
agttccgacg aaaaatggcg gggctctcctg agttgggtggg ccttgaccct cc atg gga      58
                               Met Gly

caa gga gct cgc ggc tgg cac aga gag cca ggc ctt ggt ctc cgc cac      106
Gln Gly Ala Arg Gly Trp His Arg Glu Pro Gly Leu Gly Leu Arg His
                               -80                               -75                               -70

tcc ccg aga aga ctt tcg ggt gcg ctg cac ctc gaa gcg ggc tgt gac      154
Ser Pro Arg Arg Leu Ser Gly Ala Leu His Leu Glu Ala Gly Cys Asp
                               -65                               -60                               -55

cga aat gct aca act gtg cgg ccg ctt cgt gca aaa shc ggg gac gct      202
Arg Asn Ala Thr Thr Val Arg Pro Leu Arg Ala Lys Xaa Gly Asp Ala
                               -50                               -45                               -40                               -35

ctg ccg gag gag att cgg gag ccc gct ctg cga gat gcg cag tgg gta      250
Leu Pro Glu Glu Ile Arg Glu Pro Ala Leu Arg Asp Ala Gln Trp Val
                               -30                               -25                               -20

cgg gac cag tta gcc agt tct tta ctc atc atc ctc tta ccc aac acc      298
Arg Asp Gln Leu Ala Ser Ser Leu Leu Ile Ile Leu Leu Pro Asn Thr
                               -15                               -10                               -5

cag gat ctt agg att cag aaa gat ccc aca cca ggc ccg gg      339
Gln Asp Leu Arg Ile Gln Lys Asp Pro Thr Pro Gly Pro
                               1                               5                               10
```

[illegible]

```
<221> sig_peptide
<222> 171..314
<223> Von Heijne matrix
      score 3.79999995231628
      seq NSLLLLLCLYIYP/HS
```

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<221> misc_feature
<222> 376..377
<223> n=a, g, c or t
      Oligonucleotide
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[illegible]

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<210> 633
<211> 154
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 54..152
```

<221> sig peptide

<222> 54..143

<223> Von Heijne matrix
score 3.79999995231628
seq XFVFVCXLLKCMS/VP

<400> 633

```
cagttaagtg tatctgtgtg tgagcaagtt tatatgtgta cacatgtttg ccc atg      56
                                         Met
                                         -30
tgt act tgt ctt tgt gtg tgt ctg tat atg tay aat atg caa ttt tta      104
Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe Leu
                    -25                    -20                    -15
kyt ttt gtg ttt gtk tgc gww ttg cta aag tgt atg agt gtg cct ttg      152
Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro Leu
                    -10                    -5                    1
tg                                                                    154
```

<210> 634

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 34..390

<221> sig_peptide

<222> 34..126

<223> Von Heijne matrix
score 3.79999995231628
seq PVCLLVLMAGSG/KT

<221> misc_feature

<222> 224

<223> n=a, g, c or t
Oligonucleotide

<400> 634

```
ctctatggtc gggtaggtgg ggccaggagg aag atg gcg gcg tcc gca gct gcc      54
                                         Met Ala Ala Ser Ala Ala Ala
                                         -30                    -25
gct gag ctc cag gct tct ggg ggt ccg cgg cac cca gtg tgt ctg ttg      102
Ala Glu Leu Gln Ala Ser Gly Gly Pro Arg His Pro Val Cys Leu Leu
                    -20                    -15                    -10
gtg ttg gga atg gcg gga tcc ggg aaa acc act ttt gta cag agg ctc      150
Val Leu Gly Met Ala Gly Ser Gly Lys Thr Thr Phe Val Gln Arg Leu
                    -5                    1                    5
aca gga cac ctg cat gcc caa ggc act cca ccg tat gtg atc aac ctg      198
Thr Gly His Leu His Ala Gln Gly Thr Pro Pro Tyr Val Ile Asn Leu
                    10                    15                    20
gat cca gca gta cat gaa gtt ccc tnt cct gcc aat att gat att cgt      246
Asp Pro Ala Val His Glu Val Pro Xaa Pro Ala Asn Ile Asp Ile Arg
                    25                    30                    35                    40
gat act gta aag tat aaa gaa gta atg aaa caa tat gga ctt gga ccc      294
```

Asp	Thr	Val	Lys	Tyr	Lys	Glu	Val	Met	Lys	Gln	Tyr	Gly	Leu	Gly	Pro	
				45					50					55		
aat	ggc	ggc	ata	gtg	acc	tca	ctc	aat	ctc	ttt	gst	acc	aga	ttt	gat	342
Asn	Gly	Gly	Ile	Val	Thr	Ser	Leu	Asn	Leu	Phe	Xaa	Thr	Arg	Phe	Asp	
			60					65					70			
cag	gtg	atg	aaa	tta	ttg	aga	agg	ccc	aga	aca	tgt	cca	aat	atg	tgt	390
Gln	Val	Met	Lys	Leu	Leu	Arg	Arg	Pro	Arg	Thr	Cys	Pro	Asn	Met	Cys	
			75				80					85				

<210> 635
 <211> 137
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..135

<221> sig_peptide
 <222> 22..81
 <223> Von Heijne matrix
 score 3.79999995231628
 seq VLLTHGLIHYSFT/HH

<400>	635																
caacatgcag	gtttgttact	t	atg	tat	gca	tgt	gcc	atg	ttg	gtg	tta	tta					51
			Met	Tyr	Ala	Cys	Ala	Met	Leu	Val	Leu	Leu					
			-20				-15										
act	cat	gga	ctc	atc	cat	tac	tca	ttt	act	cat	cat	tta	cat	tac	gta		99
Thr	His	Gly	Leu	Ile	His	Tyr	Ser	Phe	Thr	His	His	Leu	His	Tyr	Val		
-10			-5						1					5			
ttt	atc	cta	att	ctt	ccc	ctc	cca	ccc	ccg	cca	cag	gg					137
Phe	Ile	Leu	Ile	Leu	Pro	Leu	Pro	Pro	Pro	Pro	Gln						
			10				15										

<210> 636
 <211> 172
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..172

<221> sig_peptide
 <222> 38..109
 <223> Von Heijne matrix
 score 3.79999995231628
 seq SMCLLLDVSSXKS/TD

<400>	636																
catcttgtag	aaaaaagtta	caaattaaca	aaaaaga	atg	ggc	ttt	ctt	ggc	agc								55
				Met	Gly	Phe	Leu	Gly	Ser								
								-20									

```

ccc aga cag aga aac tca atg tgt ttg ctt tta gac gtc agc tct rcc      103
Pro Arg Gln Arg Asn Ser Met Cys Leu Leu Leu Asp Val Ser Ser Xaa
      -15                      -10                      -5
aag agc aca gat aat tth cya rtc gww wtt ttg att att tat tat ctg      151
Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa Leu Ile Ile Tyr Tyr Leu
      1                      5                      10
att acc aga aaa ggg cca ggg      172
Ile Thr Arg Lys Gly Pro Gly
15                      20

```

```

<210> 637
<211> 253
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 100..252

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```

<221> sig_peptide
<222> 100..228
<223> Von Heijne matrix
      score 3.79999995231628
      seq FNIFLAAPSPVWQ/PQ

```

```

<400> 637
acaagcactg caatgcagca accattgacc taactatgct tccttctcca ggatcatctca      60
agcagaccccc tcaactctgaa gcccccgat ccaagcagg atg agc tgc caa mct      114
                        Met Ser Cys Gln Xaa
                        -40

```

```

mag ctt gct cdg acc ttg act tgg ctc atg atc cgt gga aga cat ccc      162
Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile Arg Gly Arg His Pro
      -35                      -30                      -25
tac ctg acc cgt cga tca gcc cga aac ttc aac atc ttt ttg gca gct      210
Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn Ile Phe Leu Ala Ala
      -20                      -15                      -10
ccg tcc cca gtt tgg cag cct cag agg acc cgc cga ccc cag k      253
Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg Arg Pro Gln
      -5                      1                      5

```

```

<210> 638
<211> 185
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 32..184

```

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<221> sig_peptide
<222> 32..133
<223> Von Heijne matrix
      score 3.79999995231628
      seq FHQMALXPPTSRA/QA

```


<400> 638
acgcggcaca cagtcgccagt gctcagtcac c atg tgt cct gca tgg ctc cca 52
Met Cys Pro Ala Trp Leu Pro
-30
tgt tgg acg gca cag acg gaa cat ctc gat cgt tac agg aag ttc cac 100
Cys Trp Thr Ala Gln Thr Glu His Leu Asp Arg Tyr Arg Lys Phe His
-25 -20 -15
cag atg gcg ctg tyt cca ggg aca tct agg gca cag gcc tta ctt tat 148
Gln Met Ala Leu Xaa Pro Gly Thr Ser Arg Ala Gln Ala Leu Leu Tyr
-10 -5 1 5
aac gaa gtc cta gag aga ttt atg ttc acc cgg ctg c 185
Asn Glu Val Leu Glu Arg Phe Met Phe Thr Arg Leu
10 15

<210> 639
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..204

<221> sig_peptide
<222> 73..126
<223> Von Heijne matrix
score 3.79999995231628
seq RICTFLLPSHSTS/GP

<400> 639
ttggatgacc ttaatgcttc aggacttagt aagaaataag cccgagtact tgtgaaatgt 60
taggctttgt tg atg aat gtc atg aag aga ata tgt acc ttt ctg ttg cct 111
Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro
-15 -10
tca cac tct acc tct ggc cct ctg tgc tgt tca aat gcc cat ctt cct 159
Ser His Ser Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro
-5 1 5 10
gct acc tcc tct acc ttg aaa cat tgc agg gct tgg agg gaa gcg bv 206
Ala Thr Ser Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
15 20 25

<210> 640
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..506

<221> sig_peptide
<222> 21..383
<223> Von Heijne matrix

score 3.79999995231628
seq SLATLPFLSTVVT/DK

<221> misc_feature
<222> 495
<223> n=a, g, c or t
Oligonucleotide

<400> 640
aagtcacatg agccacaaaa atg gtg gtg ttc ggg tat gag gct ggg act aag 53
Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
-120 -115
cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag 101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
-110 -105 -100 -95
gtt ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta 149
Val Phe Lys Met Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu
-90 -85 -80
gaa gat gca aaa ctc aga aga cca atg gtc ata gaa atc atagaa aaa 197
Glu Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys
-75 -70 -65
aat ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg 245
Asn Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met
-60 -55 -50
gcg aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc 293
Ala Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe
-45 -40 -35
ctg ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat 341
Leu Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr
-30 -25 -20 -15
gca tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag 389
Ala Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys
-10 -5 1
ctt ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac 437
Leu Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn
5 10 15
tgt gtt ttc aga agc tca ctg att ggc ata gtt tgt ggw gtt ttc tat 485
Cys Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr
20 25 30
ccc agt tct ntg gct ttt act a 507
Pro Ser Ser Xaa Ala Phe Thr
35 40

<210> 641
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 295..483

<221> sig_peptide
<222> 295..408

<223> Von Heijne matrix
score 3.79999995231628
seq LVVCVSVTVFVWS/CC

<221> misc_feature
<222> 54
<223> n=a, g, c or t
Oligonucleotide

<400> 641
accattcgga agaggcggag tcttcttccg aggaccattc ggaagaaggc gganctacct 60
ctcatcagga ccagtctgac tgcacctgca tccttagctc agagcatccc cggagcatct 120
taagagctga gcgcastgac aactaggggc cggaccgtcg caggaggcgt ccgctggata 180
ccttccccct tccctgacct agagctctac agctgctgcc tcggtactga ccgagggttc 240
ccagagctgt ctyaccattg caaaaacgtt atagcaacag cctctgatta cgac atg 297
Met
gct gag atc acc aat atc cga cct agc ttt gat gtg tca ccg gtg gtg 345
Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val Val
-35 -30 -25
gcc ggc ctc atc ggg gcc tct gtg ctg gtg gtg tgt gtc tcg gtg acc 393
Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val Thr
-20 -15 -10
gtc ttt gtc tgg tca tgc tgc crc cag cag gca gag aag aag cac aag 441
Val Phe Val Trp Ser Cys Cys Xaa Gln Gln Ala Glu Lys Lys His Lys
-5 1 5 10
aac cca cca tac aag ttt att cac atg ctc aaa ggc wtc agc 483
Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
15 20 25

<210> 642
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 235..309

<221> sig_peptide
<222> 235..279
<223> Von Heijne matrix
score 3.79999995231628
seq ILTMLILLIHEHG/IF

<400> 642
attratctat gtgtctgttg ttatacgaat atcatgctgt tttggtttct atatccttgt 60
aatatgtttt gaagtcagggt agtgtgatgc ctccagattt gttctttttg gtcaggattg 120
ctttggctgw tttgggttcw wttwtgggtc catacaaatt ttaggattat tttttctatg 180
tctgtgaaaa gtggcatggg tattacattc aatctgtaga ttgctttgga tagt atg 237
Met
-15
gtc att tta act atg tta att ctt tta atc cat gag cat ggt att ttc 285
Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile Phe
-10 -5 1

ttt tca ctt gtt tgt gtc ctc ttc
Phe Ser Leu Val Cys Val Leu Phe
5 10

309

<210> 643
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..245

<221> sig_peptide
<222> 147..233
<223> Von Heijne matrix
score 3.79999995231628
seq LTHHTCTPPSTA/HP

<221> misc_feature
<222> 61
<223> n=a, g, c or t
Oligonucleotide

<400> 643
aacagacccc acccggcaca acctgctcac atacacacac acaataacac acacccaatc 60
nyacgcacccc sactcagcat aacctgctca cacaatcaca cacacaatca cacacaccct 120
accaggtaca gccactcag acacac atg ttc tca cac aat cac tca tac aca 173
Met Phe Ser His Asn His Ser Tyr Thr
-25
tac aca cca cag cac agc ccg ctc aca cac aca cac aca tgc acc cca 221
Tyr Thr Pro Gln His Ser Pro Leu Thr His Thr His Thr Cys Thr Pro
-20 -15 -10 -5
ccc agc aca gct cac cca cgc ggg 245
Pro Ser Thr Ala His Pro Arg Gly
1

<210> 644
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..209

<221> sig_peptide
<222> 144..188
<223> Von Heijne matrix
score 3.79999995231628
seq XMILLCFLAVSNF/NK

<400> 644
atactctttc tacattctgc tccgctttag ctgcgagagt ttaccaactc aaatctggcc 60

caagcctgga cagtctagat aaggaagcgg atcacaaaaa caaattggtc tgtgtgtgtg 120
 tgcggtgcgtg cagcgcgctg tgt atg ttt kat atg att tta ctt tgt ttt ttg 173

Met Phe Xaa Met Ile Leu Leu Cys Phe Leu
 -15 -10

gca gtt tcg aat ttt aat aaa ctt tta tgg gga gva ag 211
 Ala Val Ser Asn Phe Asn Lys Leu Leu Trp Gly Xaa
 -5 1 5

<210> 645
 <211> 98
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..98

<221> sig_peptide
 <222> 6..83
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LPLACFSLFGXLP/QG

<400> 645
 ttcaa atg ttt tta att tta ggg aaa ttt tct cga gtt atg ggt tta cca 50
 Met Phe Leu Ile Leu Gly Lys Phe Ser Arg Val Met Gly Leu Pro
 -25 -20 -15

ctt gct tgc ttc tct ctc ttt ggc wtt ctt cct cag ggg ctc ctt atc 98
 Leu Ala Cys Phe Ser Leu Phe Gly Xaa Leu Pro Gln Gly Leu Leu Ile
 -10 -5 1 5

<210> 646
 <211> 347
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 258..347

<221> sig_peptide
 <222> 258..314
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LAXLPGXXHGGLS/AV

<221> misc_feature
 <222> 294
 <223> n=a, g, c or t
 Oligonucleotide

<400> 646
 ctttcttttc cggayycagc agtggcgccct aaagtctgcg aggaggaagt cgcctctgtg 60
 ccccgagatt cagaggtcta aggaagagga gataaatata tgaaggtgct gtttggcaca 120

```

gaatttaata gggaagaaaag agacagtata actcaccagt gctgggtctc atcatcctgc      180
aatttcdgaa caactatgaa tacaaaaaga attttaaaat cccagtcctg cctagaaagg      240
ggaagtcatc tctaaat atg gtg gcc ctg ggg cag ctg gcc tdc ctg cca      290
                Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro
                -15                                -10
ggc nbc tdc cat ggg ggc ctt tct gca gtg act gtg gtt ctt ccc att      338
Gly Xaa Xaa His Gly Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile
                -5                                1                                5
tta ctc tgt      347
Leu Leu Cys
    10

```

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<210> 647
<211> 143
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 78..143

<221> sig_peptide
<222> 78..122
<223> Von Heijne matrix
      score 3.79999995231628
      seq VSFVCLLFERNVYS/NL

```

```

<400> 647
aaactggggt gagatgatat ctcaatgtag ttttcattta catctctaata gatcaataat      60
gttgagcaat ttttcat atg ccc gtt tca ttt gtc tgt ctt ctt ttc aga      110
                Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg
                -15                                -10                                -5
aat gtt tat tca aat cta ttg cct tct ttt ttt      143
Asn Val Tyr Ser Asn Leu Leu Pro Ser Phe Phe
                1                                5

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<210> 648
<211> 232
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 41..232

<221> sig_peptide
<222> 41..121
<223> Von Heijne matrix
      score 3.79999995231628
      seq LPLLLPAHHGRHG/SG

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<400> 648
aaaaagtgct cgggacaagg mcatagggct gagagtagcc atg ggc tct gga gga      55
                Met Gly Ser Gly Gly

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<400> 650
ggagtggaca cggagggggcc tagaggaggg ccctagaggg gcggaggggc cgatggaaag 60
ggaaaggtgg cctgtcctcc cctcccgaca ccaggggagg agccccagcc ccgcgacgag 120
gaggaagcgg actgragctg ctgaggcagt ttgacctggc ctggcagtac gggccctgca 180
ccgggatcac acggctgcag cgctgggtgc gggccaagca gatgggcttg gaggctcccc 240
cagaggtgtg gcaggtgctg aagaccacc ccggagaccc ccgcttccag tgcagtctct 300
ggcatctcta tcccct atg agg cac cac gta aga yct cct gcc ctt agc tct 352
Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser
-20 -15 -10
ctt gct cac cac cca aga acc tca gga cag aag cga gag ccc att gct 400
Leu Ala His His Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala
-5 1 5
cct gct cag ctc agc ccg g 419
Pro Ala Gln Leu Ser Pro
10

<210> 651
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..396
<221> sig_peptide
<222> 52..270
<223> Von Heijne matrix
score 3.79999995231628
seq LAGNLALSPTGNA/KK

<400> 651
ttggaagtgg tgtggagacg gaggacagga gcagtgccca agcagcgagg g atg ctg 57
Met Leu
atc ttg aat ggc ttc cgg ggc cat gcc aca gat tcc gtg aag aac tcc 105
Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys Asn Ser
-70 -65 -60
atg gaa agc atg aac act gac atg gtg atc atc cca ggg ggt ctg acc 153
Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly Leu Thr
-55 -50 -45 -40
tca cag ctt cag gtg ctg gat gtc gtg gtc tac aag cca ctg aat gac 201
Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu Asn Asp
-35 -30 -25
agt gtg cgg gcc cag tac tcc aac tgg ctt ctg gct ggg aac ctg gcg 249
Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn Leu Ala
-20 -15 -10
ctg agc cca acc ggg aat gct aag aag cca ccc ctg ggc ctc ttt ctg 297
Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu Phe Leu
-5 1 5
gag tgg gtc atg gtc gcg tgg aat agc atc tca agt gag tcc atc gtc 345
Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Glu Ser Ile Val
10 15 20 25
caa ggg whc aaa gaa gtg cca tat ctc crg caa ctt gga gga gga aga 393

Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly Gly Arg
30 35 40

cga 396
Arg

<210> 652
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..168

<221> sig_peptide
<222> 67..141
<223> Von Heijne matrix
score 3.79999995231628
seq YCLSNCLLXXSWG/LH

<400> 652
tgtatacaca taaccagata ttctcctaag tttttcaaaa taatagaaac agatattttg 60
ggattc atg atc tgt acc act gtt tat att acc atg gct cct tac tgt 108
Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys
-25 -20 -15
cta tca aac tgt tta ctt thw caw agt tgg ggc ctg cat ttg tat aga 156
Leu Ser Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg
-10 -5 1 5
ttt cta gcc ccc at 170
Phe Leu Ala Pro

<210> 653
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..178

<221> sig_peptide
<222> 131..172
<223> Von Heijne matrix
score 3.79999995231628
seq VSLCVAALFPLQA/YG

<400> 653
agagtacctg aaaaccttag agaaccctgg ggaaatatatt atagccaggc ttcttggaga 60
ctctgggaac aggaaagtca ggaaccctgc ctttcaggaa ctgctgtatc tcagtcggct 120
tcttcatttc atg gtt tct ctc tgt gta gct gct tta ttt cct ctt cag 169
Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln
-10 -5
gct tac ggg 178
Ala Tyr Gly

1

<210> 654
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..119

<221> sig_peptide
<222> 36..107
<223> Von Heijne matrix
score 3.79999995231628
seq FVYLLLRNLXSYS/LP

<400> 654
tgtgggttttg attggcattt cctgatcat tactg atg ttg agc att ttt tca 53
Met Leu Ser Ile Phe Ser
-20
ttt ttt tgt agg cca ttt gta tat ctt ctt ttg aga aat ctc krt tca 101
Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu Leu Arg Asn Leu Xaa Ser
-15 -10 -5
tat tct ttg ccc acc acg gg 121
Tyr Ser Leu Pro Thr Thr
1

<210> 655
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..370

<221> sig_peptide
<222> 89..319
<223> Von Heijne matrix
score 3.79999995231628
seq LGLQCDAVNLAFG/RR

<400> 655
acttcgccat ttctctccgg aagtgcggat cccagcggcg gtcgtgtagc tgagcagscc 60
tggggcttgg ttctatgtcc ctgtggct atg ttt cca gtg tcc tot ggg tgt 112
Met Phe Pro Val Ser Ser Gly Cys
-75 -70
ttc caa gag caa caa gaa acg aat aaa tct ctg ccc cgc agc gcc tcc 160
Phe Gln Glu Gln Gln Glu Thr Asn Lys Ser Leu Pro Arg Ser Ala Ser
-65 -60 -55
acc cca gag acc cgg acc aag ttc aca cag gac aat ctg tgc cry gcc 208
Thr Pro Glu Thr Arg Thr Lys Phe Thr Gln Asp Asn Leu Cys Xaa Ala
-50 -45 -40

cag cgc gag cgc ctg gac tcg gcc aac ctg tgg gtc ctk gtg gac tgc	256
Gln Arg Glu Arg Leu Asp Ser Ala Asn Leu Trp Val Leu Val Asp Cys	
-35 -30 -25	
atc ctt cgc gac acc tcc gag gac ctg gga ctc cag tgt gac gcc gtg	304
Ile Leu Arg Asp Thr Ser Glu Asp Leu Gly Leu Gln Cys Asp Ala Val	
-20 -15 -10	
aac ctg gcc ttc ggg cgc cgc tgt gag gaa ctg gag gac gcg cgg cac	352
Asn Leu Ala Phe Gly Arg Arg Cys Glu Glu Leu Glu Asp Ala Arg His	
-5 1 5 10	
aag ctg cag yac cac ctg	370
Lys Leu Gln Xaa His Leu	
15	

<210> 656
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..196
 <221> sig_peptide
 <222> 137..181
 <223> Von Heijne matrix
 score 3.79999995231628
 seq LVHSFLWLSSILY/IY

<400> 656	
attgtatcgt tcttatgcct ttgcatcctc atagcttagc tcccacatat cagtgagaac	60
atacaatggt tggttttcca ttctgaggt acttcaactta gaataatagt ctccaatctc	120
atccaggtca ctgcaa atg cca ttg gtt cat tcc ttc tta tgg ctg agt agt	172
Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser	
-15 -10 -5	
atc cta tat ata tac cac ctg cgg g	197
Ile Leu Tyr Ile Tyr His Leu Arg	
1 5	

<210> 657
 <211> 246
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..246
 <221> sig_peptide
 <222> 79..150
 <223> Von Heijne matrix
 score 3.79999995231628
 seq XVFXFXFLXRXLX/XX

<400> 657

tttttgacat	cytattaata	gccattctgg	ctggtgtcag	gtggatatctc	attgtgggtt	60
cgattttgga	tttctcta	atg att agt aat ggt aag ttt ttt tgt ttt ttt	111			
		Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe				
		-20 -15				
ttk gtt ttt kgt ttt tkg ttt ttg ara cgg asy ttg cyc tkg ycg ccc	159					
Xaa Val Phe Xaa Phe Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro						
-10 -5 1						
agg ctg gag tgc aat ggm aar ayc tgc gcy cac tgm aac ctc cgc ctc	207					
Arg Leu Glu Cys Asn Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu						
5 10 15						
ctg agt yca agc aat tcy ctk gcc tca gcc ccc cga ggg	246					
Leu Ser Xaa Ser Asn Ser Leu Ala Ser Ala Pro Arg Gly						
20 25 30						

<210> 658
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..333
 <221> sig_peptide
 <222> 31..300
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LRVRLTLPHSIRS/DS

<221> misc_feature
 <222> 320
 <223> n=a, g, c or t
 Oligonucleotide

<400> 658	
acacgcgcct cttcacgagg tggaaacaag atg gag gat tgc gcc tgc gcc tgc	54
	Met Glu Asp Ser Ala Ser Ala Ser
	-90 -85
ctg tct tct gca gcc gct act gga acc tcc acc tgc act cca gcg gcc	102
Leu Ser Ser Ala Ala Ala Thr Gly Thr Ser Thr Ser Thr Pro Ala Ala	
-80 -75 -70	
ccg aca gca cgg aag cag ctg gat aaa gaa cag gtt aga aag gca gtg	150
Pro Thr Ala Arg Lys Gln Leu Asp Lys Glu Gln Val Arg Lys Ala Val	
-65 -60 -55	
gac gct ctc ttg acg cat tgc aag tcc agg aaa aac aat tat ggg ttg	198
Asp Ala Leu Leu Thr His Cys Lys Ser Arg Lys Asn Asn Tyr Gly Leu	
-50 -45 -40 -35	
ctt ttg aat gag aat gaa agt tta ttt tta atg gtg gta tta tgg aaa	246
Leu Leu Asn Glu Asn Glu Ser Leu Phe Leu Met Val Val Leu Trp Lys	
-30 -25 -20	
att cca agt aaa gaa ctg agg gtc aga ttg acc ttg cct cat agt att	294
Ile Pro Ser Lys Glu Leu Arg Val Arg Leu Thr Leu Pro His Ser Ile	
-15 -10 -5	
cga tca gat tca gaa gat atc tgt tna ttt acg aag gat gg	335

Arg Ser Asp Ser Glu Asp Ile Cys Xaa Phe Thr Lys Asp
 1 5 10

<210> 659
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..196

<221> sig_peptide
 <222> 20..106
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LIELNLXSPVALQ/WP

<400> 659
 attcaacaag caatcaggt atg aat gca gaa ggg gct tcc cca gga aaa gaa 52
 Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu
 -25 -20
 acg aac aca gga aca ttg ata gag cta aat ctg mcc agc cct gta gcc 100
 Thr Asn Thr Gly Thr Leu Ile Glu Leu Asn Leu Xaa Ser Pro Val Ala
 -15 -10 -5
 ctc cag tgg cca ctt tcc agc ccc tct tgc ctg agg atc ctc agc aac 148
 Leu Gln Trp Pro Leu Ser Ser Pro Ser Cys Leu Arg Ile Leu Ser Asn
 1 5 10
 aag gtg ccc agg aac ctg agg tgg cag aaa cac tac tcc acc cac cag g 197
 Lys Val Pro Arg Asn Leu Arg Trp Gln Lys His Tyr Ser Thr His Gln
 15 20 25 30

<210> 660
 <211> 272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..270

<221> sig_peptide
 <222> 28..216
 <223> Von Heijne matrix
 score 3.70000004768372
 seq MAAAAALRAPAQs/SV

<400> 660
 attttgccct gtcaggtcca tccggcg atg ctg ggt ctg gac gag ctc ggg agg 54
 Met Leu Gly Leu Asp Glu Leu Gly Arg
 -60 -55
 agt ggt tgt ggc cat tgc aca cag gcg gat ctg agg ttc ggc gac gcc 102
 Ser Gly Cys Gly His Cys Thr Gln Ala Asp Leu Arg Phe Gly Asp Ala
 -50 -45 -40

gct ggy csc gaa ccc cgg gmc agg mca acg cac agg aac acc gcc gca	150
Ala Gly Xaa Glu Pro Arg Xaa Arg Xaa Thr His Arg Asn Thr Ala Ala	
-35 -30 -25	
gcc cgc gtt ccc ccc ccg ccc aga gtc atg gcg gca gca gcc gct ctg	198
Ala Arg Val Pro Pro Pro Pro Arg Val Met Ala Ala Ala Ala Ala Leu	
-20 -15 -10	
agg gcg cct gct cag agc agt gtg acc ttt gaa gat gtg gct gta aac	246
Arg Ala Pro Ala Gln Ser Ser Val Thr Phe Glu Asp Val Ala Val Asn	
-5 1 5 10	
ttt tcc ctg gag gaa tgg agt ctt ct	272
Phe Ser Leu Glu Glu Trp Ser Leu	
15	

<210> 661
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 263..409

<221> sig_peptide
 <222> 263..340
 <223> Von Heijne matrix
 score 3.70000004768372
 seq WGNLSFHLQEAHG/SE

<400> 661	
tgaaaacaaa catctactaa tgttgtcaga tggtaggaa gcaagattct gcaactatag	60
agggttaagt tttcttttgt tctgtgggtc ctctctaaaa ctctaagatc ttgaggggtg	120
catttcagaa agtgcagcgt gacccgcagt ttgtgggaag ccattggagct cggcactgcc	180
atcctaatac ttcttaaagc acaaaacccc agagacaatc tgggggtcagg agagtgggaag	240
gggcttgtct gccacactgg tg atg agt gcc ctg aaa gac ttc aga gaa ttt	292
Met Ser Ala Leu Lys Asp Phe Arg Glu Phe	
-25 -20	
ctg aac tgg tgg gga aac ctc tct ttt cat ctt cag gaa gct cat gga	340
Leu Asn Trp Trp Gly Asn Leu Ser Phe His Leu Gln Glu Ala His Gly	
-15 -10 -5	
agt gaa att gca gaa atg gga gct ggt att cta gag gaa aaa aat tat	388
Ser Glu Ile Ala Glu Met Gly Ala Gly Ile Leu Glu Glu Lys Asn Tyr	
1 5 10 15	
ggv caa caa wat cac tgt aac ta	411
Gly Gln Gln Xaa His Cys Asn	
20	

<210> 662
 <211> 146
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..145

<221> sig_peptide
 <222> 38..127
 <223> Von Heijne matrix
 score 3.70000004768372
 seq PPSLFLSLPPSL/PP

<400> 662
 awbwcccgcc cacacgtggc caacctttgc gttttta atg tct ctw ccc cct ttt 55
 Met Ser Leu Pro Pro Phe
 -30 -25
 ttc cac cct tct ccc gct ccc tct ctc gct ccc cct ccc tcc ctc ttt 103
 Phe His Pro Ser Pro Ala Pro Ser Leu Ala Pro Pro Pro Ser Leu Phe
 -20 -15 -10
 ctt tcc ctc cct ccc tct ctt tct ccc cct cta ccc gcc cgg g 146
 Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro Leu Pro Ala Arg
 -5 1 5

<210> 663
 <211> 65
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..63

<221> sig_peptide
 <222> 10..48
 <223> Von Heijne matrix
 score 3.70000004768372
 seq MFFLCGFLYLCFI/SF

<400> 663
 caatatgct atg ttt ttc ctt tgt ggt ttt ctg tat cta tgt ttt atc tca 51
 Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser
 -10 -5 1
 ttt ttt ttt ttt tt 65
 Phe Phe Phe Phe
 5

<210> 664
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..182

<221> sig_peptide
 <222> 30..155
 <223> Von Heijne matrix
 score 3.70000004768372

seq ALGIFLCPGETLS/AS

<400> 664
 cgggatgccg gagccctcgg gccttgagg atg aag gca ggc ccc tgc tcc tgc 53
 Met Lys Ala Gly Pro Cys Ser Cys
 -40 -35
 cag gag gga ggg agg cag tgg gct cat ggg tcg gtg cct ttg cag ccg 101
 Gln Glu Gly Gly Arg Gln Trp Ala His Gly Ser Val Pro Leu Gln Pro
 -30 -25 -20
 aca gca cgc ctt gcg gcc ctg ggg atc ttt ctg tgc ccc ggc gag acc 149
 Thr Ala Arg Leu Ala Ala Leu Gly Ile Phe Leu Cys Pro Gly Glu Thr
 -15 -10 -5
 ctt tcg gcc tca ctg cat tgg aac ccc att ggg 182
 Leu Ser Ala Ser Leu His Trp Asn Pro Ile Gly
 1 5

<210> 665
 <211> 320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..318
 <221> sig_peptide
 <222> 160..228
 <223> Von Heijne matrix
 score 3.70000004768372
 seq TNLLCLTFQRCQS/YN

<400> 665
 tacatcagaa accagaggcg gaaaactttc cacggtgata tgcataaaca aatatttcat 60
 attttttaca gaaagtctgg ctattgccta tagaaagaca aaaactggta acagccttat 120
 tccagctaaa tttgaatgcc aggttgacac taatcatgg atg ctt tcc cag agc 174
 Met Leu Ser Gln Ser
 -20
 ttt cag aaa aac aaa acc aac ctg ttg tgt tta act ttc caa aga tgt 222
 Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu Thr Phe Gln Arg Cys
 -15 -10 -5
 cag agt tac aat tgg ctg aat att ttt gaa gct aca tat atg acg act 270
 Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala Thr Tyr Met Thr Thr
 1 5 10
 ctc ttc att tca gta att aam aca aat ttt tta aaa aga tac ctc ctg 318
 Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu Lys Arg Tyr Leu Leu
 15 20 25 30
 gg 320

<210> 666
 <211> 273
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 180..272

<221> sig_peptide
<222> 180..254
<223> Von Heijne matrix
score 3.70000004768372
seq QLLGCMVLYDCFS/FK

<400> 666
aagttgttgc atgtgtcaat ggttggtcct ttttatttct gagtaatgtt ccatgatatg 60
aatgtaccac agtttgttta accattcacc cactgaagga cgtttggatt gtttctaagt 120
tttgactgtg gcaagtaaag atgctatgaa cattcatgta cacatgaatt tgtaggcat 179
atg ttt tta ttt tgc tgg gag aaa agc cca aga atg cag ttg ctg ggt 227
Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly
-25 -20 -15 -10
tgt atg gta ttg tat gat tgt ttt tct ttt aag aaa ctg ccg ggg g 273
Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly
-5 1 5

<210> 667
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..148

<221> sig_peptide
<222> 8..97
<223> Von Heijne matrix
score 3.70000004768372
seq FVCFHFVFCVFC/NV

<400> 667
attttgt atg tct ttt ata tct gtt att ttt cct tta atc ott tta aac 49
Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn
-30 -25 -20
cgt ttt tca ttt gtt tgt ttc ttt cat gtc ttt tac tgt gtt ttc tgc 97
Arg Phe Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys
-15 -10 -5
aac gtc tct tct ttg ttc tcc tat cag ttt ott ott cat ttc tgt gat 145
Asn Val Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp
1 5 10 15
gac t 149
Asp

<210> 668
<211> 122
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
 <222> 16..120

<221> sig_peptide
 <222> 16..108
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LGMGMGFFSGVKS/WI

<400> 668
 caaggaatta cagaa atg cat gaa tac tta cct aga aac ttt cat gac ttt 51
 Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe
 -30 -25 -20
 aat tct ccc aac tct aaa tta ggc atg gga atg ggc ttt ttc tca ggt 99
 Asn Ser Pro Asn Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly
 -15 -10 -5
 gtc aaa tct tgg att gga ggt ga 122
 Val Lys Ser Trp Ile Gly Gly
 1

<210> 669
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..286

<221> sig_peptide
 <222> 38..145
 <223> Von Heijne matrix
 score 3.70000004768372
 seq ILMRDFSPSGIFG/AF

<400> 669
 tcgcgcgggtc ccgcacagcg gacaccagga ctccaaa atg gcg tca rtt gta cca 55
 Met Ala Ser Xaa Val Pro
 -35
 gtg aag gac aag aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc 103
 Val Lys Asp Lys Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser
 -30 -25 -20 -15
 tgg atc ttg atg cgg gac ttc agt cct agt ggc att ttc gga gcg ttt 151
 Trp Ile Leu Met Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe
 -10 -5 1
 caa aga ggt tac tac cgg tac tac aac aag tac atc aat gtg aag aag 199
 Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys
 5 10 15
 ggg agc atc tcg ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt 247
 Gly Ser Ile Ser Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe
 20 25 30
 agc tac tcc ttt tcc tac aag cat ctc aag cac gag tcg gg 288
 Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys His Glu Ser
 35 40 45

<210> 670
 <211> 160
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..160

<221> sig_peptide
 <222> 89..142
 <223> Von Heijne matrix
 score 3.70000004768372
 seq GALLWMAWDGQLS/RP

<400> 670
 cgtcaacatt cttttcattc tgggcctgag cgcgtggatc aagcogctgc ccttgcaact 60
 gctgagcctg aagctggact tgccggtg atg gtg ata tcg gcc ggg gca ctg 112
 Met Val Ile Ser Ala Gly Ala Leu
 -15
 ctg tgg atg gcg tgg gac ggc cag ctc agc cgc ccc gaa ggc gcc cgt 160
 Leu Trp Met Ala Trp Asp Gly Gln Leu Ser Arg Pro Glu Gly Ala Arg
 -10 -5 1 5

<210> 671
 <211> 137
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..136

<221> sig_peptide
 <222> 44..97
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LELLGSSYNPISA/SP

<400> 671
 gaattttctt cttctgctca ggctggagta caatggcaca atc atg gtt cac tgt 55
 Met Val His Cys
 -15
 aat ctt gaa ctc ctg ggc tca agt tat aat ccc atc tca gcc tct cca 103
 Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile Ser Ala Ser Pro
 -10 -5 1
 gta gct agg act ata tca tgc ccc gct att gtg g 137
 Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val
 5 10

<210> 672
 <211> 493
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 111..491

<221> sig_peptide

<222> 111..374

<223> Von Heijne matrix

score 3.70000004768372

seq CDLLLARFGLIQS/MK

<400> 672

gcccgcgctt gttgtgctga ggccgagggg gtcgccatth	tggatggtga accctgaagt	60
cggtgtctgc tgcgttcacg gcaggattcg gttaggagga	acagcacagc atg ctg	116
	Met Leu	
ggc tct gga ttt aaa gct gag cgc tta aga gtg	aat ttg aga tta gtc	164
Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val	Asn Leu Arg Leu Val	
-85	-80 -75	
ata aat cgc ctt aaa cta ttg gag aaa aag aaa	acg gaa ctg gcc cag	212
Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys	Thr Glu Leu Ala Gln	
-70	-65 -60 -55	
aaa gca agg aag gag att gct gac tat ctg gct	gct ggg aaa gat gaa	260
Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala	Ala Gly Lys Asp Glu	
-50	-45 -40	
cga gct cgg atc cgt gtg gag cac att atc cgg	gaa gac tac ctc gtg	308
Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg	Glu Asp Tyr Leu Val	
-35	-30 -25	
gag gcc atg gag atc ctg gag ctg tac tgt gac	ctg ctg ctg gct cgg	356
Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp	Leu Leu Leu Ala Arg	
-20	-15 -10	
ttt ggc ctt atc cag tct atg aag gaa cta gat	tct ggt ctg gct gaa	404
Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp	Ser Gly Leu Ala Glu	
-5	1 5 10	
tct gtg tct aca ttg atc tgg gct gct cct cga	ctc cag tca gaa gtg	452
Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg	Leu Gln Ser Glu Val	
15	20 25	
gct gag ttg aaa ata gtt gct gat cag ctc tgt	cca agt at	493
Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys	Pro Ser	
30	35	

<210> 673

<211> 263

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 102..263

<221> sig_peptide

<222> 102..230

<223> Von Heijne matrix

score 3.70000004768372

seq VWCLXLKLVPAIC/IS

<400> 673

tcccagcaga aggggagcg cctggctgtc agcagcgtgt gcctcaggag ggatctgcgg 60
tgacgggggtt gttacttcag taggatgagg aagagtcaca a atg cgg ggt tgg mmg 116
Met Arg Gly Trp Xaa
-40

gct cct gct tgg aga sgh ytg arc acy agg aga cta cca atg ggg agc 164
Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg Leu Pro Met Gly Ser
-35 -30 -25

agg cac ggt gcc agc ccg gcc tct gcc gtc tgg tgt ctg tmc ctc aag 212
Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp Cys Leu Xaa Leu Lys
-20 -15 -10

tta gtc cca gct ttg tgc att agc ggg ctc acc ctc gga atc cag gga 260
Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr Leu Gly Ile Gln Gly
-5 1 5 10

ttc 263
Phe

<210> 674

<211> 263

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..261

<221> sig_peptide

<222> 115..216

<223> Von Heijne matrix

score 3.70000004768372

seq RLILXFHDNTWG/ST

<221> misc_feature

<222> 136,139..140

<223> n=a, g, c or t

Oligonucleotide

<400> 674

gtcatttatg ccatattctg tccactagaa atgaattact aagtctggcc caaactcaag 60
tggaggcgaa ttaagctgca tctcataagg gaaagagtat cgaagaactt ctgt atg 117
Met

tat ttt aaa acc act aca nta nnb cat agt gca cat atg ctt ctg caa 165
Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu Gln
-30 -25 -20

att tgc ttt ttt cgc tta aca atc tta gkt ttc cat gac aat aca tgg 213
Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr Trp
-15 -10 -5

ggg tca act tca ttc tct twa gtt gck gca atg cta ttc cac tac cgg 261
Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr Arg
1 5 10 15

gg 263

<210> 675
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..107

<221> sig_peptide
 <222> 30..101
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LLFLFFLFLFFFF/FF

<400> 675
 tgcactggca cacactcaca gctctgacc atg tca tca aac ata cag aga ctg 53
 Met Ser Ser Asn Ile Gln Arg Leu
 -20
 ggc ttc cct ctg ctt ttt ctt ttt ttt ctt ttt ctt ttt ttt ttt 101
 Gly Phe Pro Leu Leu Phe Leu Phe Phe Leu Phe Leu Phe Phe Phe
 -15 -10 -5
 ttt ttt 107
 Phe Phe
 1

<210> 676
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..276

<221> sig_peptide
 <222> 70..270
 <223> Von Heijne matrix
 score 3.70000004768372
 seq LVLPLPMLPTSNR/KR

<400> 676
 gtcacagcac cctcctgaaa actgcagctt ccttctcacc ttgaagaata atcctagaaa 60
 actcacaaa atg tgt gat gct ttt gta ggt acc tgg aaa ctt gtc tcc agt 111
 Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser
 -65 -60 -55
 gaa aac ttt gat gat tat atg aaa gaa gta gga gtg ggc ttt gcc acc 159
 Glu Asn Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr
 -50 -45 -40
 agg aaa gtg gct ggc atg gcc aaa cct aac atg atc atc agt gtg aat 207
 Arg Lys Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn
 -35 -30 -25
 ggg gat gtg atc acc att ccc cac ctg gtc ctc ccc ctt ccc atg ctg 255
 Gly Asp Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu


```

ccaagacgta tgag atg ama ggc ttc ttc tgt ctg tgt gcg ttt aac tca      170
                Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser
                -15                      -10                      -5

ttt ctc ctt agc ccc gag ggg      191
Phe Leu Leu Ser Pro Glu Gly
                1

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<210> 679
<211> 235
<212> DNA
<213> Homo sapiens

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```

<220>
<221> CDS
<222> 31..234

```

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<221> sig_peptide
<222> 31..228
<223> Von Heijne matrix
      score 3.59999990463257
      seq LTSFLSIXIFVNP/TR

```

```

<400> 679
atttttcacc actgcatagt gttacattgt atg att ttc cca cat tgc atg tac      54
                        Met Ile Phe Pro His Cys Met Tyr
                        -65                      -60

tgt tta gag tgt ata act aag aat gga ttg cta ggt tta aag gtg ctt      102
Cys Leu Glu Cys Ile Thr Lys Asn Gly Leu Leu Gly Leu Lys Val Leu
                -55                      -50                      -45

cca ctc tat ggg ata atg cta att ttt ttc cct aaa gtg gtt tat aac      150
Pro Leu Tyr Gly Ile Met Leu Ile Phe Phe Pro Lys Val Val Tyr Asn
                -40                      -35                      -30

aat caa ccc ttg cac tac aag tca gta atg gtg ttt cag ttg act tca      198
Asn Gln Pro Leu His Tyr Lys Ser Val Met Val Phe Gln Leu Thr Ser
                -25                      -20                      -15

ttc ttg tcg att tka att ttt gtc aac ccc act cgg g      235
Phe Leu Ser Ile Xaa Ile Phe Val Asn Pro Thr Arg
-10                      -5                      1

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<210> 680
<211> 410
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 173..409

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<221> sig_peptide
<222> 173..334
<223> Von Heijne matrix
      score 3.59999990463257
      seq LMAXLLTVEVTHP/NS

```


<221> misc_feature
 <222> 305
 <223> n=a, g, c or t
 Oligonucleotide

<400> 680
 taatcgaaaa gctcagtgcg caggcgcgaa gaagctggca ggggcacgag ccggggggcgg 60
 gtttgaagac gcgtcgttgg gttttggagg ccgtgaaaca gccgtttgag tttggctgcg 120
 ggtggagaac gtttgtcagg ggcccggcca agaaggaggc ccgcctgtta cg atg gtg 178
 Met Val
 tcc atg agt ttc aag cgg aac cgc agt gac cgg ttc tac agc acc cgg 226
 Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser Thr Arg
 -50 -45 -40
 tgc tgc ggc tgt tgc cat gtc cgc rcc ggg acg atc atc ctg ggg acc 274
 Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu Gly Thr
 -35 -30 -25
 tgg tac atg gta gta aac cta ttg atg gca nbt ttg ctg act gtg gaa 322
 Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr Val Glu
 -20 -15 -10 -5
 gtg act cat cca aac tcc atg cca gct gtc aac att cag tat gaa gtc 370
 Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr Glu Val
 1 5 10
 atc ggt aat tac tat tcg tct gag aga atg gct gat aat g 410
 Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
 15 20 25

<210> 681
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..302

<221> sig_peptide
 <222> 21..113
 <223> Von Heijne matrix
 score 3.59999990463257
 seq STFALTIXRXXSC/SS

<221> misc_feature
 <222> 102
 <223> n=a, g, c or t
 Oligonucleotide

<400> 681
 gagttkgact gtgaagaaac atg gcg gcc gcg acg ttg act tcg aaa ttg tac 53
 Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr
 -30 -25
 tcc ctg ctg ttc cgc agg acc tcc acc ttc gcc ctc acc atc akc cgt 101
 Ser Leu Leu Phe Arg Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg
 -20 -15 -10 -5
 ngg gsg tca tgt tct tcg rgc gcg cct tcg atc aag gcg cgg acg cta 149

Xaa	Xaa	Ser	Cys	Ser	Ser	Xaa	Ala	Pro	Ser	Ile	Lys	Ala	Arg	Thr	Leu	
			1					5					10			
tct	acg	acc	aca	tca	acg	agg	gga	agc	tgt	gga	aac	aca	tca	agc	aca	197
Ser	Thr	Thr	Thr	Ser	Thr	Arg	Gly	Ser	Cys	Gly	Asn	Thr	Ser	Ser	Thr	
		15					20				25					
agt	atg	aga	aca	agt	agt	tcc	ttg	gag	gcc	ccc	atc	cag	gcc	aga	agg	245
Ser	Met	Arg	Thr	Ser	Ser	Ser	Leu	Glu	Ala	Pro	Ile	Gln	Ala	Arg	Arg	
	30					35				40						
acc	agg	tcc	acc	cag	cag	ctg	ttt	gcc	cag	agc	tgg	agc	ctc	agc	dtg	293
Thr	Arg	Ser	Thr	Gln	Gln	Leu	Phe	Ala	Gln	Ser	Trp	Ser	Leu	Ser	Xaa	
45				50						55				60		
aag	atg	atg	c													303
Lys	Met	Met														

<210> 682
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..327

 <221> sig_peptide
 <222> 79..201
 <223> Von Heijne matrix
 score 3.599999990463257
 seq LHTSVTLFLLSYC/DC

<221> misc_feature
 <222> 258
 <223> n=a, g, c or t
 Oligonucleotide

<400> 682	
agatgattcc ctgattctcc agagagatta cacacttcgt ttgtggctaa ggttactgtg	60
acccaatgaa agaagaaa atg aaa gcc ata aag aaa agt ctt aca gaa gaa	111
Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu	
-40 -35	
gaa tac ctg tac ctg gac ttt tct cac caa aca gaa gga tgc atc ttt	159
Glu Tyr Leu Tyr Leu Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe	
-30 -25 -20 -15	
cct ctt cat aca tct gta act tta ttt ctg tta tct tac tgt gac tgt	207
Pro Leu His Thr Ser Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys	
-10 -5 1	
aaa atc ttt aaa att tgc tta gtt gtc acc aaa gag gtg agt aga gat	255
Lys Ile Phe Lys Ile Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp	
5 10 15	
avn tca cta cta aga gat gac ctg atc cag gat gtt gaa ata cag att	303
Xaa Ser Leu Leu Arg Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile	
20 25 30	
att tca agg cag gag ctc cca cca a	328
Ile Ser Arg Gln Glu Leu Pro Pro	
35 40	

<210> 683
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 386..445

<221> sig_peptide
 <222> 386..427
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FLCVCYFIRKSTS/FF

<221> misc_feature
 <222> 307
 <223> n=a, g, c or t
 Oligonucleotide

<400> 683
 ttaacatctt ccactgaaaa gaaaagataa tgatataaat aaagcaattt aaatcaagtc 60
 taaggatatag gaaggatattt aagaaagaag caaacattct ctagatgttg ttatccaaaa 120
 tatattctct tttgcagttt actgaaataa tttcttcagt gtgtgggaat ttcctttgca 180
 tccagcttta ctatagagat gacatcacac caacagtgac acgacttggt tacaagaggg 240
 tggataaac agcaaatgtt cttccttaaa acagatttct tgttgaactt caacagaaaa 300
 agaagcngta aatgtagaag gaagaacagg agatagtctt taacatgtag ggtaaaatct 360
 aaggtagagg agagagcagc tgata atg ttt tta tgt gtt tgc tac ttt att 412
 Met Phe Leu Cys Val Cys Tyr Phe Ile
 -10
 agg aag tct act tcc ttc ttt tcc ata tct agt ag 447
 Arg Lys Ser Thr Ser Phe Phe Ser Ile Ser Ser
 -5 1 5

<210> 684
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..217

<221> sig_peptide
 <222> 5..139
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AWWLLLPVWKLGG/QL

<400> 684
 tcaa atg ggg aag ccg aga ggt ggt gag atg ctt gag gtt gta aag act 49
 Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr
 -45 -40 -35

gtc tcc act ttc act ttg gga ggg tgg aaa ggg act gct cct gtg tcc	97
Val Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser	
-30 -25 -20 -15	
tgc gcc tgg tgg ctg ctt ctc cca gtt tgg aag ctg gga ggg cag ctt	145
Cys Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu	
-10 -5 1	
gag cgc agg aag aat cca aag gaa tac tgt ctt ggc tcc tgg gtg tgg	193
Glu Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp	
5 10 15	
ctc agt cct cag ctg gct cca agg	217
Leu Ser Pro Gln Leu Ala Pro Arg	
20 25	

<210> 685
 <211> 132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..130

<221> sig_peptide
 <222> 77..124
 <223> Von Heijne matrix
 score 3.59999990463257
 seq FTFISTLLFVFLG/VV

<400> 685	
tgaaatccta gcttgaatat ttacattagt cttgtttctc aaacttgact ctttggtttg	60
atcgacatctt tcccta atg ctg att ttc acc ttt att tct act ttg ctg ttt	112
Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe	
-15 -10 -5	
gta ttc ttg gga gtt gtg gg	132
Val Phe Leu Gly Val Val	
1	

<210> 686
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 120..260

<221> sig_peptide
 <222> 120..230
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PGSGLC SMAAVQA/GN

<400> 686	
acatctcctt ggccccgcc cactcccgcg gggctattgt ccccggtaaa ctgcagtttc	60

tggttcgaga	ctccaatcct	gtttogaatt	gctgcttgct	gcccccttggg	ctgggggata	119
atg gaa gtt ctt tcb mtt ccc aac tct ttc cag acc caa gca ctc tgg	167					
Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp						
-35 -30 -25						
gac tca ctc cat agt cca gga gtt cca ggt tcc gga tta tgt tcc atg	215					
Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met						
-20 -15 -10						
gca gca gtc caa gca gga aac caa gcc atc tac tct gcc tcg ggg	260					
Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly						
-5 1 5 10						

<210> 687
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 332..472

<221> sig_peptide
 <222> 332..457
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LLTQAGFPRRGEA/AP

<400> 687	
tgtgtatgtg tgaaaatcag gaagagccag cggggagtggt gtgttgccat cgcgtctccg	60
cctgcagggg cgggacccca ggaggaggga gaggacagag ccaactgcaga ggaccagact	120
gggaaaacaa cgatatggca ggagccagtc ttggggcccg cttctaccgg cagatcaaaa	180
gacatccggg gctgggacag aaagaacaac ccggagccct ggaaccgcct gagccccaat	240
gaccaatata agttccttgc agtttccact gactataaga agctgaagaa ggaccggcca	300
gacttctaag ccaggctggg ctgccagtgc c atg caa gcc aca gcc agc cag	352
Met Gln Ala Thr Ala Ser Gln	
-40	

ccc atc cac ttc ttc crs tcc tcc ccg cag gcc cca agg cat cac tcc	400
Pro Ile His Phe Phe Xaa Ser Ser Pro Gln Ala Pro Arg His His Ser	
-35 -30 -25 -20	
ggc cac cct gtc ccg cta ctg ctt aca cag gcc ggg ttc cca cgc aga	448
Gly His Pro Val Pro Leu Leu Leu Thr Gln Ala Gly Phe Pro Arg Arg	
-15 -10 -5	
ggg gag gct gct cca ccc cta ctc c	473
Gly Glu Ala Ala Pro Pro Leu Leu	
1 5	

<210> 688
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..106

<221> sig_peptide
 <222> 5..94
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LCTFTLNLTAVRT/IX

<400> 688
 acac atg cga ggg tak aac tgh gtg ttc agg gtt ttc tct gaa agc ctg 49
 Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu
 -30 -25 -20
 aag gga ttg tgt acw ttt aca ttg aac ttg act gca gtt aga acc att 97
 Lys Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile
 -15 -10 -5 1
 arc cta gat g 107
 Xaa Leu Asp

<210> 689
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 258..377

<221> sig_peptide
 <222> 258..353
 <223> Von Heijne matrix
 score 3.59999990463257
 seq RLTISTXLSTSXX/FM

<400> 689
 aaacacaaca accagattcc tcctctaaag aagcccctgg gagcacagct catcaccatg 60
 gactggacct ggaggttcct ctttttggtg acagcagcta cagatgtcca gtcccaggtc 120
 cagctgggtgc aagtctgggt actgaggtga agaggcctgg gtctcgggtg aaggtctcct 180
 gtaagacttc tggaggcacc ttcagtagta atgccatcac gtgggtgcga caggcccctg 240
 gacaagggct tgagtgg atg ggr agg atc atc ccc atg gtt gaa aaa gcg 290
 Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala
 -30 -25
 gac acc gca cag aag ttc cag ggc aga ctc act att agt aca dkv cta 338
 Asp Thr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu
 -20 -15 -10
 tcg acg agc asa gsc ttc atg gaa ctg agc agt ctg aga 377
 Ser Thr Ser Xaa Xaa Phe Met Glu Leu Ser Ser Leu Arg
 -5 1 5

<210> 690
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..388

<221> sig_peptide
 <222> 53..253
 <223> Von Heijne matrix
 score 3.59999990463257
 seq IIMVFVFICFCYL/HY

<400> 690
 ataaattcag tagttacctt agtagacaaa tcatttgaac caagttgagg ac atg aat 58
 Met Asn
 ctt gtt att tgt gtc cta ctt ttg tcc att tgg aaa aat aat tgc atg 106
 Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn Cys Met
 -65 -60 -55 -50
 act aca aac caa acc aat gga tct tct act aca gga gat aaa cct gtt 154
 Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys Pro Val
 -45 -40 -35
 gaa tca atg cag aca aaa ttg aac tac ctt aga aga aat cta ctc att 202
 Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu Leu Ile
 -30 -25 -20
 tta gtt ggt att atc atc atg gtt ttt gtc ttt atc tgt ttt tgt tat 250
 Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe Cys Tyr
 -15 -10 -5
 ctc cat tat aat tgt ctg agc gat gat gcg tcc aaa gca gga atg gtc 298
 Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly Met Val
 1 5 10 15
 aag aaa aaa ggc ata gca gcc aag tca tct aaa aca tca ttc agt gaa 346
 Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe Ser Glu
 20 25 30
 gcc aag aca gcc tct caa tgc agt tca gaa aca caa acc ggg 388
 Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly
 35 40 45

<210> 691
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 304..408

<221> sig_peptide
 <222> 304..387
 <223> Von Heijne matrix
 score 3.59999990463257
 seq IFFSLTSLGCKFS/KL

<400> 691
 cttgacttct gtgcactcac aggettgatc aacaccacaa ggaagctgcc aaggccatcc 60
 tctgaaacca cagcccagc tctatgttgg ccccttttag ccatggctgg aatggctgag 120
 acacaggaca ccaagtcctt aggtgtaca cagcactggg accctgggcc ctgcccattg 180
 aacaattttt tcttcctaaa tcttcaggcc tgtgatggga ggggctaccg caaaggtctc 240
 tgacatgccc cagatacatt ttccctattg tcttggggat taacatttgg ctccctcgta 300
 ctt atg caa att tct gca gcc agc ttg aat ttc tcc tca aaa aat gga 348

Met	Gln	Ile	Ser	Ala	Ala	Ser	Leu	Asn	Phe	Ser	Ser	Lys	Asn	Gly		
			-25					-20					-15			
att	ttc	ttt	tct	tta	aca	ttg	tca	ggc	tgc	aaa	ttt	tcc	aaa	ctt	tta	396
Ile	Phe	Phe	Ser	Leu	Thr	Leu	Ser	Gly	Cys	Lys	Phe	Ser	Lys	Leu	Leu	
			-10					-5				1				
tgc	cct	ttt	ggg													408
Cys	Pro	Phe	Gly													
5																

<210> 692
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..321

<221> sig_peptide
 <222> 106..261
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LVWDCLLPSPFF/LL

<221> misc_feature
 <222> 284..285
 <223> n=a, g, c or t
 Oligonucleotide

<400> 692																
tgttacctgt	gtgcatatat	tatatctact	taagttttat	tctaaataag	gagcttgtga											60
tarttgtttc	cgttttgtaa	ttagaaggta	ttatatgttc	ctatc atg	att ttt gag											117
				Met	Ile Phe Glu											
				-50												

cct	gtg	ggt	ctg	aaa	cca	gtg	ttt	cta	aat	att	ttt	ttc	ttt	tca	cat	165
Pro	Val	Val	Leu	Lys	Pro	Val	Phe	Leu	Asn	Ile	Phe	Phe	Phe	Ser	His	
			-45					-40				-35				

cat	gta	ttt	aca	gtg	ttt	ttc	agt	ggg	agt	cat	ggt	gac	atc	ctg	agt	213
His	Val	Phe	Thr	Val	Phe	Phe	Ser	Gly	Ser	His	Val	Asp	Ile	Leu	Ser	
		-30				-25					-20					

cgc	aca	ggt	ctt	ggt	tgg	gac	tgt	ctt	ctt	cct	cct	cct	tcc	ttc	ttc	261
Arg	Thr	Val	Leu	Val	Trp	Asp	Cys	Leu	Leu	Pro	Pro	Pro	Ser	Phe	Phe	
	-15				-10					-5						

ctc	ctt	ctt	ctt	tct	tct	tcc	tnn	tcc	ttv	ctc	ctc	ctt	vct	dct	tct	309
Leu	Leu	Leu	Leu	Ser	Ser	Ser	Xaa	Ser	Xaa	Leu	Leu	Leu	Xaa	Xaa	Ser	
1			5					10					15			

tcc	tcc	tcc	cgg	g												322
Ser	Ser	Ser	Arg													
			20													

<210> 693
 <211> 153
 <212> DNA
 <213> Homo sapiens


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<220>
<221> CDS
<222> 93..152

<221> sig_peptide
<222> 93..134
<223> Von Heijne matrix
      score 3.59999990463257
      seq LVPLLSHLLFKFT/WP

<400> 693
cttttttagt aggggagctt gataatggaa aacagtatga ggaattgtca cactgtatga      60
gatttttaaac taaggcataa gaatgaaacc gg atg tta gtt cct ctt tta tca      113
                                   Met Leu Val Pro Leu Leu Ser
                                   -10
cac ttg ctc ttc aag ttt acc tgg cca aaa tkg tcc cag g      153
His Leu Leu Phe Lys Phe Thr Trp Pro Lys Xaa Ser Gln
      -5                               1                               5

<210> 694
<211> 234
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..232

<221> sig_peptide
<222> 23..169
<223> Von Heijne matrix
      score 3.59999990463257
      seq FGVLSGLXQXVSP/GK

<400> 694
aagcgcgggga cgcwrcaaag tc atg gac cgc aac ccc tcg ccg ccg ccg      52
                                   Met Asp Arg Asn Pro Ser Pro Pro Pro Pro
                                   -45                               -40

ggt cgc gac aag gag gag gag gag gag gtg gcc ggt gga gac tgc ata      100
Gly Arg Asp Lys Glu Glu Glu Glu Glu Val Ala Gly Gly Asp Cys Ile
      -35                               -30                               -25

ggg agc acg gtc tac agc aaa cac tgg ctc ttc ggc gtc ctc agc gga      148
Gly Ser Thr Val Tyr Ser Lys His Trp Leu Phe Gly Val Leu Ser Gly
      -20                               -15                               -10

ctc akc cag rtt gtt agc cct gga aaa cac caa aat cta ggc tca grt      196
Leu Xaa Gln Xaa Val Ser Pro Gly Lys His Gln Asn Leu Gly Ser Xaa
      -5                               1                               5

gmt gag gag cag ctg acg gag ctt gat gaa cga aat gg      234
Xaa Glu Glu Gln Leu Thr Glu Leu Asp Glu Arg Asn
10                               15                               20

<210> 695
<211> 455

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 344..454

<221> sig_peptide
<222> 344..412
<223> Von Heijne matrix
score 3.59999990463257
seq LGCHFFSLALLNT/GP

<221> misc_feature
<222> 285,342..343
<223> n=a, g, c or t
Oligonucleotide

<400> 695
tggttatatgg gtctcttgaa gacaatatac agttgggtct ttcttcttta ttcaacttac 60
cactctgtgc cttttaagtg gggcatttag ctaakwtaca ttcaagggtta atattgatat 120
gtgcatatgt gatcctgtca tsatgttamc tggctggttat tcagactaga ttgtgtagtt 180
tttttatagt gtgtcagtag ttacgttttg tgggtgggtcag tgacagtgat ttttttcccc 240
atgttttagca tccctttaag gacctattgt aaagcagggtc tagtngtaac aaatttcctt 300
ggcatttact tatcaggaaa ggatcttttt ttctcctttg cnn atg aag ctt agt 355
Met Lys Leu Ser
-20
ttg gct gga tat gaa att ctt ggt tgt cat ttc ttt tct tta gca ctg 403
Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe Ser Leu Ala Leu
-15 -10 -5
cta aat aca ggc ccc caa tat ctt ttg gct tat agg gtt tct gct gaa 451
Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg Val Ser Ala Glu
1 5 10
agg t 455
Arg

<210> 696
<211> 153
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..151

<221> sig_peptide
<222> 8..127
<223> Von Heijne matrix
score 3.59999990463257
seq ITALSQSLQPLRK/LP

<400> 696
agacaag atg gcg acg tcc gtg ggg cac cga tgt ctg gga tta ctg cac 49
Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His

-40	-35	-30	
ggg gtc gcg ccg tgg cgg agc agc ctc cat ccc tgt gag atc act gcc			97
Gly Val Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala			
-25	-20	-15	
ctg agc caa tcc cta cag ccc tta cgg aag ctg cct ttt aga gcc tct			145
Leu Ser Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser			
-10	-5	1	5
ygc acg gg			153
Xaa Thr			

<210> 697
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 116..493

<221> sig_peptide
 <222> 116..262
 <223> Von Heijne matrix
 score 3.59999990463257
 seq YCLVTLVFFYSSA/SF

<400> 697			
aaaagctgac gacttcggtc tgcgccgga gtgcatgagc tgccgatgtg gtgcttagtg	60		
attgcgggtt cggtcgctct cccgtgttcc ccgggctggg tatttgccctc gcacc atg	118		
	Met		
gcg ccc aag ggc aaa gtg ggc acg aga ggg aag aag cag ata ttt gaa	166		
Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe Glu			
-45	-40	-35	
gag aac aga gag act ctg aag ttc tac ctg cgg atc ata ctg ggg gcc	214		
Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly Ala			
-30	-25	-20	
aat gcc att tac tgc ctt gtg acg ttg gtc ttc ttt tac tca tct gcc	262		
Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser Ala			
-15	-10	-5	
tca ttt tgg gcc tgg ttg gcc ctg ggc ttt agt ctg gca gtg tat ggg	310		
Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr Gly			
1	5	10	15
gcc agc tac cac tct atg agc tcg atg gca cga gca gcg ttc tct gag	358		
Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser Glu			
20	25	30	
gat ggg gcc ctg atg gat ggt ggc atg gac ctc aac atg gag cag ggc	406		
Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln Gly			
35	40	45	
atg gca gag cac ctt aag gat gtk atc cta ctg aca gcc atc gtg cag	454		
Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln			
50	55	60	
gtg ctc agc tgc ttc tct ctg tat gtc tgg tcc ttc tgg	493		
Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp			
65	70	75	

<210> 698
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..172

<221> sig_peptide
 <222> 8..94
 <223> Von Heijne matrix
 score 3.59999990463257
 seq AFNKAVWFTPCSC/QE

<400> 698
 aacaaag atg gcg gcg gtg act gtg acg gtg acg aag acg gcg gcg gcg 49
 Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala
 -25 -20
 gcg acg gca ttt aac aag gcg gtg tgg ttt act cca tgc agt tgt cag 97
 Ala Thr Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln
 -15 -10 -5 1
 gag gta agt agc agg ctg ccg gct cgg acg gcg gcg acg cgg cag gac 145
 Glu Val Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp
 5 10 15
 agg gcg gat aag aag gag cgg ccc tgt gg 174
 Arg Ala Asp Lys Lys Glu Arg Pro Cys
 20 25

<210> 699
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..300

<221> sig_peptide
 <222> 199..255
 <223> Von Heijne matrix
 score 3.59999990463257
 seq PGSAICLWHSTLG/GX

<221> misc_feature
 <222> 261
 <223> n=a, g, c or t
 Oligonucleotide

<400> 699
 attttgtctc ggcagcgggtg gccgwagctc catcgcatatt tatgtttctg gcgagaagg 60
 aacggagttt tcatcaggta gattggtttt trtgcgggcgcg tcctccaccg ttctctccag 120
 gacagcacct agtcgtggcc ggaggagtct catagctgtc agaaagaata agactgattt 180
 tatgggaaaa ttaagcag atg ctc cag ttt gag aaa cct gga tct gcg atc 231

	Met	Leu	Gln	Phe	Glu	Lys	Pro	Gly	Ser	Ala	Ile					
					-15					-10						
tgt	ttg	tgg	cac	agc	act	ttg	gga	ggy	ymn	ggc	ggg	cgt	gag	att	gds	279
Cys	Leu	Trp	His	Ser	Thr	Leu	Gly	Gly	Xaa	Gly	Arg	Glu	Ile	Xaa		
			-5				1				5					
agt	ttg	aga	cca	gcc	tgc	ggg										300
Ser	Leu	Arg	Pro	Ala	Cys	Gly										
	10					15										

<210> 700
 <211> 159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..157

<221> sig_peptide
 <222> 86..139
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LAILLKWVSNSKS/FL

<400>	700															
ttttatagct	atcacaaatg	agattgcttt	cttaatTTTT	tttcagatta	atcatagtta	60										
acaaatagaa	actattgatt	ttygt	atg	ttg	att	tcg	tat	ctt	gca	att	tta	112				
			Met	Leu	Ile	Ser	Tyr	Leu	Ala	Ile	Leu					
						-15					-10					
cta	aaa	tgg	gtt	agc	aat	tct	aag	agt	ttt	ttg	gtg	aag	gca	tcg	gg	159
Leu	Lys	Trp	Val	Ser	Asn	Ser	Lys	Ser	Phe	Leu	Val	Lys	Ala	Ser		
			-5				1					5				

<210> 701
 <211> 274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..273

<221> sig_peptide
 <222> 46..90
 <223> Von Heijne matrix
 score 3.59999990463257
 seq LQTLAFWSAYVPC/QT

<400>	701															
agtgtgtccg	gaattggtgg	gttcttggtc	tcactgagtt	ctaga	atg	aag	ctg	cag	57							
			Met	Lys	Leu	Gln										
						-15										
acc	ctc	gca	ttc	tgg	tca	gcc	tat	gtg	cca	tgc	cag	acc	cag	gac	cgg	105
Thr	Leu	Ala	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg	

-10	-5	1	5	
gat gcc ccg cgc ctc acc ctg gag cag att gac ctc ata cgc cgc atg				153
Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg Met				
10	15	20		
tgt gcc tcc tat tct gag ctg gag ctt gtg acc tcg gct aaa gct ctg				201
Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys Ala Leu				
25	30	35		
aac gac act cag aaa ttg gcc tgc ctc atc ggt gta gag ggt ggc cac				249
Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His				
40	45	50		
tcg ctg gac aat agc ctc tcc agg g				274
Ser Leu Asp Asn Ser Leu Ser Arg				
55	60			

<210> 702
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..175

<221> sig_peptide
 <222> 107..148
 <223> Von Heijne matrix
 score 3.5
 seq PACLSSFVIPSELL/SP

<400> 702	
ttgcttttcta agacacttac tttcatcggc acttttcagat ttttgaatta tacttttctca	60
atttgatttt tcaagtgagt tattaggata taggtgggag tggaga atg cct gcc	115
	Met Pro Ala
tgc ctt tct tcc ttt gtc att ccc tct ctc ctt tct ccc tcc tcc cct	163
Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro Ser Ser Pro	
-10	-5
ccc tcc ata ggg	175
Pro Ser Ile Gly	

<210> 703
 <211> 298
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 197..298

<221> sig_peptide
 <222> 197..244
 <223> Von Heijne matrix
 score 3.5
 seq SFAGSCTILGASS/HS

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<400> 703
ttttcatgtg tctgttggct gcataaatgt cttcttctga gaagtgtctg ttcataacct 60
tcgcccactt gttgatgagg ttgttttttt cttgtaaatt tgtttgtgtt cattgtaagt 120
tctggatatt agccctttgt cagatgagta gattgtaaaa atttctccc attctacagg 180
ttgcctgttc actctg atg gta gtt tct ttt gct ggt tct tgc aca att cta 232
                Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu
                -15                -10                -5

ggc gcc agt agc cat tca ttc ccc att gaa gtc agc ctg ttc cca gtg 280
Gly Ala Ser Ser His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val
                1                5                10

gac tgt ggc ttc ctc ttg 298
Asp Cys Gly Phe Leu Leu
                15

```

```

<210> 704
<211> 136
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS
<222> 41..136

<221> sig_peptide
<222> 41..100
<223> Von Heijne matrix
        score 3.5
        seq AVSQSWLAAPSTS/WV

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```

<400> 704
ttcttattaa agatttattt ttgtagagac agatgtctca atg tgt tgc cca ggc 55
                Met Cys Cys Pro Gly
                -20

tgg aac gca gtg tcg caa tct tgg ctc gct gca cct tcc acc tcc tgg 103
Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala Pro Ser Thr Ser Trp
-15                -10                -5                1

gtt caa gag att ctc gta ctt cag cct cca ggg 136
Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
                5                10

```

```

<210> 705
<211> 433
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS
<222> 225..431

<221> sig_peptide
<222> 225..386
<223> Von Heijne matrix
        score 3.5
        seq IRCPLIFLXXVSG/TX

```

<400> 705
agaggactay gcgagagcgt ctacggttgt gccaaaggaa aaaaaatggt cctaagaaaa 60
gagtatacaa agttgtgttc atcaaagtct ggaacccaaa ggtgtccctc caaagctgta 120
cacgacagag aaaacgcgaa ctgaaagaag aagcaggtcc caaggggcca ggcgcctcct 180
ccacctctc ctctctctag gattaacctc catttcagct aatc atg gga gag att 236

Met Gly Glu Ile

aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa 284
Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys
-50 -45 -40 -35

aab dtw atk gtg gat gat gat gac agt aag ata tgg tcg chc tat gac 332
Xaa Xaa Xaa Val Asp Asp Asp Ser Lys Ile Trp Ser Xaa Tyr Asp
-30 -25 -20

gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg cyc yct gtc 380
Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Xaa Xaa Val
-15 -10 -5

agt gga act gha gat gtc ttt ttc cgg cag att ttg gct ctg act gga 428
Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly
1 5 10

tgg gg 433
Trp
15

<210> 706

<211> 419

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 284..418

<221> sig_peptide

<222> 284..331

<223> Von Heijne matrix

score 3.5

seq SHSHLSLVGHSRA/CG

<400> 706
attgaaaatc attaaaaatc ttagcaattg ttttaaatta tctaattttt ttctccaaat 60
aatatctatt ttagcagcca aatcaccaca aatcattggt ttttatcttt agttgtgggt 120
gcacagcggg tgcgtgtatt ttggggcatg tgagggtgtct tgatgcgttc atgcagtgtg 180
taacagtcac atcagggtaa atgggacatc tttcacctca agcatttata cttcgtgtta 240
tggacaccct cagctggaaa ggggggctgc gtcgtgagta tga atg gat gca agt 295

Met Asp Ala Ser
-15

cat agc cac ctg agc ctg gtg ggg cac agc agg gcc tgt gga gtc aca 343
His Ser His Leu Ser Leu Val Gly His Ser Arg Ala Cys Gly Val Thr
-10 -5 1

tcc cgg cct cat gct cgg cat agg gga cgc tgc tta ggt cca tgc agt 391
Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu Gly Pro Cys Ser
5 10 15 20

cgc tca ggg ccc agg ctg tgc agc gcc a 419
Arg Ser Gly Pro Arg Leu Cys Ser Ala

<210> 707
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 200..382

<221> sig_peptide
 <222> 200..301
 <223> Von Heijne matrix
 score 3.5
 seq LISHDPWPRGAFA/LS

<221> misc_feature
 <222> 365
 <223> n=a, g, c or t
 Oligonucleotide

<400> 707
 gttacttatg gttgagagag aatatttttc agattttatt ggacattgat atttgtaaatt 60
 tgttcattcc ttttgcccag ttttctattg agtgggttcat agtttctcat gggatatccaa 120
 gagttctgga tatgtagagg tggaggggtca atctcatcay ttccttggtt taaaaatctt 180
 ccatggtttt gtcatcact atg ggc tca aac gcc gtg gtg tgg cat aca aag 232
 Met Gly Ser Asn Ala Val Val Trp His Thr Lys
 -30 -25
 ccc tca ctt ctg aac cac cct gct tcc agc ctc atc tcc cat gat ccc 280
 Pro Ser Leu Leu Asn His Pro Ala Ser Ser Leu Ile Ser His Asp Pro
 -20 -15 -10
 tgg cca cgc ggt gcg ttt gcg ctt tca tgt cca agt gct tcc ttc atg 328
 Trp Pro Arg Gly Ala Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met
 -5 1 5
 ttg ttt tct tcc tta caa tgc cct ttc cct tat tgd naa aca gag tgc 376
 Leu Phe Ser Ser Leu Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys
 10 15 20 25
 aac gwg 382
 Asn Xaa

<210> 708
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 215..382

<221> sig_peptide
 <222> 215..268
 <223> Von Heijne matrix
 score 3.5

seq ACLFRAVADQVYG/DQ

<400> 708

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aagtgacgct acaggggcca gctatgctcc cgggagtgtt gatgttttcc agtcattccg      60
gctgacagcg ttcaagttgg aatcctggag gggaggtgtt tttcctgtcg tacgtgggac      120
aggccacgct gtccgtccgc agtaccgacg cctgcagcag gagcattggg ttgaaaaggc      180
cctacgagac aagaagggct tcatcatcaa gcag atg aag gag gat ggc gcc tgt      235
                               Met Lys Glu Asp Gly Ala Cys
                               -15
```

```
ctc ttc cgg gct gta gct gac cag gtg tat gga gac cag gac atg cat      283
Leu Phe Arg Ala Val Ala Asp Gln Val Tyr Gly Asp Gln Asp Met His
-10                               -5                               1                               5
```

```
gag gtt gtg cga aag cat trc atg gac tat ctg atg aag aat gcc gac      331
Glu Val Val Arg Lys His Xaa Met Asp Tyr Leu Met Lys Asn Ala Asp
10                               15                               20
```

```
tay ttc tcc arc tat gtc aca gag gac ttt acc acc tac att akc agg      379
Tyr Phe Ser Xaa Tyr Val Thr Glu Asp Phe Thr Thr Tyr Ile Xaa Arg
25                               30                               35
```

```
aag cg      384
Lys
```

<210> 709

<211> 149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..147

<221> sig_peptide

<222> 76..138

<223> Von Heijne matrix

score 3.5

seq VLIMIXEAXNVWC/GD

<221> misc_feature

<222> 123..124

<223> n=a, g, c or t

Oligonucleotide

<400> 709

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acctaataatt aaaaatcttc ttctctaaaa gtggcatata accctgatca agaggtcatg      60
ggctcagttt gatat atg gtt cac ctc att ctt act gaa gtc ctc att atg      111
                               Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met
                               -20                               -15                               -10
```

```
atc akc gag gcn nsg aat gtg tgg tgt ggg gat tgg gg      149
Ile Xaa Glu Ala Xaa Asn Val Trp Cys Gly Asp Ser
-5                               1
```

<210> 710

<211> 167

<212> DNA

<213> Homo sapiens

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<220>
<221> CDS
<222> 15..167

<221> sig_peptide
<222> 15..155
<223> Von Heijne matrix
      score 3.5
      seq CLXFGILASEVYS/WN

<400> 710
atatttcatg gcga atg tac cac aat tta ttt gct ctg ttg ttg ata gac      50
                Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp
                -45                                -40
att cat gtt gtt cta gtt ttt tac tgc ctg gat ctc tta atg att cat      98
Ile His Val Val Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His
-35                                -30                                -25                                -20
att ttc tat tgt aaa tac tgc ctt gka ttt ggk att tta gca agt gaa      146
Ile Phe Tyr Cys Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu
                -15                                -10                                -5
gtc tat tct tgg aac att tac      167
Val Tyr Ser Trp Asn Ile Tyr
                1

<210> 711
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..215

<221> sig_peptide
<222> 84..170
<223> Von Heijne matrix
      score 3.5
      seq SPLCSXSSGYCXA/FP

<400> 711
ccgcttttgg ctgcatcagc cggggattgc cggcgccagg tgctgggggc gactcggaca      60
gogggagcgt ggggtggagt agg atg gag tct ccc tcc cga gct ggg ggt gtr      113
                Met Glu Ser Pro Ser Arg Ala Gly Gly Val
                -25                                -20
grc ctm vga aag gct gct tcg ccg ctg tgt tcg gmv agc tct gga tac      161
Xaa Leu Xaa Lys Ala Ala Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr
                -15                                -10                                -5
tgc rgg gct ttt ccg cgg agg agc gcc cgc cgg cat ctg cat ccg gga      209
Cys Xaa Ala Phe Pro Arg Arg Ser Ala Arg Arg His Leu His Pro Gly
                1                                5                                10
cac ggg      215
His Gly
15

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<210> 712
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..241

<221> sig_peptide
 <222> 59..133
 <223> Von Heijne matrix
 score 3.5
 seq LISLSVLMPVQHS/PD

<400> 712
 actatccttt cctcattgaa ttgctgtgat acctttgttg caaatcagct gtctgcag 58
 atg tgg agg tat gtt tct aga ctt tct tct gtt cca ttg atc agc ttg 106
 Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
 -25 -20 -15 -10
 tct gtc ttg atg cca gta cag cac tcc cct gat ttt tgt agc ttt att 154
 Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
 -5 1 5
 gta agt aca gtt atc cct tgg ttt cct tgg gga att ggt ccc agg acc 202
 Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
 10 15 20
 ctc atg gat ata aaa atc ctg gga tgc tgc agt cca ggg 241
 Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
 25 30 35

<210> 713
 <211> 376
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 276..374

<221> sig_peptide
 <222> 276..365
 <223> Von Heijne matrix
 score 3.5
 seq NLLKLSSHSPCTCA/CK

<221> misc_feature
 <222> 154,217
 <223> n=a, g, c or t
 Oligonucleotide

<400> 713
 tatgtacatt tgtcaaaact cagaaaatgt atatataata tgtgtgcata tgattttaag 60
 tagttttaca taaaaagata agcaaattatt ggatgctggt taacactaag catgctgaaa 120

tatttagagg gaagagtatt attgtctaca atyngcttta aagacaccaa aaataaggtg	180
grttaattwa wkggsywwgg grmdwtggat aaatggnkag awatgtgata aagcaagtct	240
aatagaattt tgtggcagaa tctaattggcg gctat atg gat gtt agc tgt aaa	293
Met Asp Val Ser Cys Lys	
-30 -25	
att ctt tac aat gtg att gaa aaa ttt tgc aat aat ctg ttg aag ctt	341
Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys Asn Asn Leu Leu Lys Leu	
-20 -15 -10	
tct tcc cat tcc cct act tgt gct tgc aaa cta aa	376
Ser Ser His Ser Pro Thr Cys Ala Cys Lys Leu	
-5 1	

<210> 714
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 216..302
 <221> sig_peptide
 <222> 216..275
 <223> Von Heijne matrix
 score 3.5
 seq SHLSGSSLQLCVA/QF

<400> 714	
gtatgtgtga tttgatttta tttgcccttt gaactatgac ccaatactcc ccaaacctgt	60
tattcagttt ttgccagag ttattatattc tggggaataa acagaggaca cacaccaga	120
ggctgccagt agcaaaaatc actgtaattc aaaaagcatg acactacggt agtgaaatta	180
tcacactttt ctttgcatag agcagttttac ttgtg atg att ttc aaa gat gtg	233
Met Ile Phe Lys Asp Val	
-20 -15	
ttc tcc cac ttg tca ggt tca tct ctt caa ctg tgt gtc gca caa ttt	281
Phe Ser His Leu Ser Gly Ser Ser Leu Gln Leu Cys Val Ala Gln Phe	
-10 -5 1	
ctc gaw ctc agt gct gtt gac at	304
Leu Xaa Leu Ser Ala Val Asp	
5	

<210> 715
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 91..240
 <221> sig_peptide
 <222> 91..222
 <223> Von Heijne matrix
 score 3.5

seq SFSFLFFFFLSFF/FF

<400> 715

gtttgtgatt aagtgatttc ctctagtggg atgctttgac tctcttttag cttttgtgta 60
aatactatag gtttttgctt tgtgggtaac atg aag ctt aca aaa aat atc tta 114
Met Lys Leu Thr Lys Asn Ile Leu
-40

twa gta ata ata ggc tgt ttt aag ctg ata gcc tac aaa aac tct gta 162
Xaa Val Ile Ile Gly Cys Phe Lys Leu Ile Ala Tyr Lys Asn Ser Val
-35 -30 -25

ctg tac ttt tac tct aac ttc tca ttt tct ttt ctt ttc ttt ttt ttc 210
Leu Tyr Phe Tyr Ser Asn Phe Ser Phe Ser Phe Leu Phe Phe Phe Phe
-20 -15 -10 -5

ctt tct ttc ttt ttt ttc ttt ttt ttt tt 242
Leu Ser Phe Phe Phe Phe Phe Phe Phe Phe
1 5

<210> 716

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 100..375

<221> sig_peptide

<222> 100..360

<223> Von Heijne matrix

score 3.5

seq VAGXMLAPGGTLA/DD

<400> 716

ctggcgtyag ttccgggtcgc agaggagaca ccgccgcagt tgccgggtaca tcgggggattt 60
ctggctcttt cctcttcgcc ttaaattcgg gtgtctttt atg aat aat caa aag 114
Met Asn Asn Gln Lys
-85

cag caw rag cca acg cta tca ggc cag cgt ttt aaa act aga aaa aga 162
Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg
-80 -75 -70

gat gaa aaa gag agg ttt gac cct act cag ttt caa gac tgt att att 210
Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile
-65 -60 -55

caa ggc tta act gaa acc ggt act gat ttg gaa gca gta gct aag ttt 258
Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu Ala Val Ala Lys Phe
-50 -45 -40 -35

ctt gat gct tct gga gca aaa ctt gat tac cgt cga tat gca gaa aca 306
Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr
-30 -25 -20

ctc ttt gac att ctg gtg gct ggt kga atg ctg gcc cca ggt ggt aca 354
Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu Ala Pro Gly Gly Thr
-15 -10 -5

ctg gca gat gac atg atg cvg 375
Leu Ala Asp Asp Met Met Xaa

1

5

<210> 717
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 324..428

<221> sig_peptide
 <222> 324..374
 <223> Von Heijne matrix
 score 3.5
 seq LEIKLPFLPFAQQ/ID

<400> 717
 aacagtctat ttctgtttgt aaatattagt atttctgtgg attctgtact tgttccttgt 60
 tatcctttca ttctcttagg ttcatttggg ctgatggatt caggtaacct tgaaattctg 120
 atagtttcaa aatcttttat ctccagggtt gatctctctt gtgaactctg gaactgtatt 180
 cccaattgtc aattggacat cctacgtat gggacctcag atatttcaaa catgatgtgt 240
 ccaagtctgt atcacttctg gccatcatat tgttctttta tttttccaaa tttcacatca 300
 ccagtaacaa actagctgtg atc atg gca gat agc ctg gaa ata aaa ctc ccc 353
 Met Ala Asp Ser Leu Glu Ile Lys Leu Pro
 -15 -10
 ttt tta ccc ttt gca cag caa att gac atc aaa tcc tgt ttc tac ttt 401
 Phe Leu Pro Phe Ala Gln Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe
 -5 1 5
 ttt ttt ttw aac wat kgc ttc cct agg g 429
 Phe Phe Xaa Asn Xaa Xaa Phe Pro Arg
 10 15

<210> 718
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..348

<221> sig_peptide
 <222> 4..108
 <223> Von Heijne matrix
 score 3.5
 seq ATAAATAASATTG/AS

<221> misc_feature
 <222> 155
 <223> n=a, g, c or t
 Oligonucleotide

<400> 718

tga atg gac aga aaa tgg acc tgg aag aga ggg caa agg tca cat ctg	48
Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu	
-35 -30 -25	
gag tca ggc cag gct gcc ccg gcc act gca gca gct acg gca gca tct	96
Glu Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Ala Thr Ala Ala Ser	
-20 -15 -10 -5	
gcc aca acg ggg gca agt gtg tgg aga agc aca atg ggc wac ctg tgt	144
Ala Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys	
1 5 10	
gat tgc acc anb dca cct tat gaa ggg ccc ttt tgc aaa aaa gag gtt	192
Asp Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val	
15 20 25	
tct gct gtt ttt gag gct ggc acg tcg gtt act tac atg ttt caa gaa	240
Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu	
30 35 40	
ccc tat cct gtg acc aag aat ata agc ctc tca tcc tca gct att tac	288
Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr	
45 50 55 60	
aca gat tca gct cca tcc aag gaa aac att gca ctt agc ttt gtg aca	336
Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr	
65 70 75	
acc caa gca ccg gg	350
Thr Gln Ala Pro	
80	

<210> 719
 <211> 305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..305

<221> sig_peptide
 <222> 84..212
 <223> Von Heijne matrix
 score 3.5
 seq VLSIKHLPPQLRA/FQ

<400> 719	
gttttttccct ttctatttca gcctgactgc cggaatcaga gccgcgggtg agatccccag	60
ccctgtgagc ctgtaggagt aga atg gct ccc caa atg tat gag ttc cat ctg	113
Met Ala Pro Gln Met Tyr Glu Phe His Leu	
-40 -35	
cca tta tcc cca gag gag ttg ttg aaa agt gga ggg gtg aat cag tat	161
Pro Leu Ser Pro Glu Glu Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr	
-30 -25 -20	
gtt gtg caa gag gta ctg tcc atc aaa cat ctt cca cca cag ctt aga	209
Val Val Gln Glu Val Leu Ser Ile Lys His Leu Pro Pro Gln Leu Arg	
-15 -10 -5	
gct ttt cag gct gcc ttt cga gct cag ggg ccc ctg gct atg ctg cag	257
Ala Phe Gln Ala Ala Phe Arg Ala Gln Gly Pro Leu Ala Met Leu Gln	
1 5 10 15	

cac ttt gat act atc tac agc att ttg cat cac ttt cga agt ata gat	305
His Phe Asp Thr Ile Tyr Ser Ile Leu His His Phe Arg Ser Ile Asp	
20 25 30	

<210> 720
 <211> 257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..257

<221> sig_peptide
 <222> 6..50
 <223> Von Heijne matrix
 score 3.5
 seq AVQVVGSWPSVQP/RE

<400> 720	
aaaag atg gct gct gtg caa gtt gtc ggt tgc tgg cct tcc gtg cag ccg	50
Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro	
-15 -10 -5	
cgg gag gca ccg cgg gaa gca atc cct gag cga ggc aat ggg ttt cgc	98
Arg Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg	
1 5 10 15	
ctc ttg tct gcc agg ctc tgc gcc ctg cgc ccg gat gac agc agc tcc	146
Leu Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser	
20 25 30	
gcc cgm acc gag atc cac ctg mtc ttc gat cag ctc atc tcc gag aac	194
Ala Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn	
35 40 45	
tac agc gag ggc agt ggc gtg gcc ccg gag gac gtw agt gct ctt ctt	242
Tyr Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu	
50 55 60	
gtc cag gct tgc ggg	257
Val Gln Ala Cys Gly	
65	

<210> 721
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 217..360

<221> sig_peptide
 <222> 217..306
 <223> Von Heijne matrix
 score 3.5
 seq FLFFLQFSFPLYL/LF

<221> misc_feature
 <222> 316,319
 <223> n=a, g, c or t
 Oligonucleotide

<400> 721
 ggcatgttta tatactcatt ccctggatgat tgtattttgc atacttgatt tttacctaag 60
 cttttatctt ttttccttta ttttctgttg ctttgtcttt ttgtaatgcc tcctggggca 120
 atttctttga tttttatctt gcagttcttc tattgagttt tgcatgttgg ctatcatgtt 180
 ttaaattttc atttttcata gtattctgtc ctatgg atg ttt cat ggc tgt cat 234
 Met Phe His Gly Cys His
 -30 -25
 att tta tct ttt ctg agg ata tca act aga ggt ttt ctt ttt ttt ctt 282
 Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg Gly Phe Leu Phe Phe Leu
 -20 -15 -10
 caa ttt tcc ttt cct ctg tat tat ctc ttt cgg ngg ntt ttc cct cag 330
 Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe Arg Xaa Xaa Phe Pro Gln
 -5 1 5
 tct ttc atg ttg gag gca ttt gtc aga tgt 360
 Ser Phe Met Leu Glu Ala Phe Val Arg Cys
 10 15

<210> 722
 <211> 191
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..189
 <221> sig_peptide
 <222> 64..141
 <223> Von Heijne matrix
 score 3.5
 seq LVLVAPWVPPLLL/AF

<400> 722
 ttctctctctt gtgaaggcag ctctcagat ccaggaggta tctgcacgga cctcatttat 60
 gtt atg tat aga cat tcc aaa cag cgt aat aat gtc cca tgc ctt gta 108
 Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val
 -25 -20 -15
 ctc tac gcc cct tgg gtc cct ccc ctc ctc cta gct ttc tgg ggc tgg 156
 Leu Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp
 -10 -5 1 5
 tgg ctc ctg gag cag ggt ctt ttt ttt ttt ttt tt 191
 Trp Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe
 10 15

<210> 723
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..473

<221> sig_peptide
 <222> 63..212
 <223> Von Heijne matrix
 score 3.5
 seq ITYGVFLCIDCSG/SH

<400> 723
 ttttttttttc gtcgactctt accggttggc tgggccagct gcgcgcgggc tcacagctga 60
 cg atg ggg gac ccc agc aag cag gac atc ttg acc atc ttc aag cgc 107
 Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg
 -50 -45 -40
 ctc cgc tcg gtg ccc act aac aag gtg tgt ttt gat tgt ggt gcc aaa 155
 Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys
 -35 -30 -25 -20
 aat ccc agc tgg gca agc ata acc tat gga gtg ttc ctt tgc att gat 203
 Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp
 -15 -10 -5
 tgc tca ggg tcc cac cgg tca ctt ggt gtt cac ttg agt ttt att cga 251
 Cys Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg
 1 5 10
 tct aca gag ttg gat tcc aac tgg tca tgg ttt cag ttg cga tgc atg 299
 Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met
 15 20 25
 caa gtc gga gga aac gct agt gca tct tcc ttt ttt cat caa cat ggg 347
 Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly
 30 35 40 45
 tgt tcc acc aat gac acc aat gcc aag tac aac agt cgt gct gct cag 395
 Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln
 50 55 60
 ctc tat agg gag aaa atc aaa tcg ctc gcc tct caa gca aca cgg aag 443
 Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys
 65 70 75
 cat ggc act gat ctg tgg ctt gat agt tgt 473
 His Gly Thr Asp Leu Trp Leu Asp Ser Cys
 80 85

<210> 724
 <211> 139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..137
 <221> sig_peptide
 <222> 60..125
 <223> Von Heijne matrix
 score 3.5
 seq LLLHLVVFHQRTLI/SL

<400> 724
 ttttagcattc aagccgtgat tagtgctttc ttttctcccc agcctgcctt tcagaacag 59
 atg cct ctc cct ccc aat cag tcc cct cta ctg ctg cac ctg gtg ttt 107
 Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
 -20 -15 -10
 cat caa agg acc ctg att tcc ctc ccg ccg cc 139
 His Gln Arg Thr Leu Ile Ser Leu Pro Pro
 -5 1

<210> 725
 <211> 187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..187
 <221> sig_peptide
 <222> 125..163
 <223> Von Heijne matrix
 score 3.5
 seq MFLTFFFCTQVHG/PS

<400> 725
 ttttcgggaa ctctcactct ctcataaact actttattac catcccacca tatcctgtcc 60
 tttttttttg gctacttag atctgttttc ctttcttgcc ttaaattggga attgctagag 120
 gmat atg ttt cta act ttt ttt ttc tgc aca caa gtt cat ggt cct tct 169
 Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser
 -10 -5 1
 ata ctt gat agc cca gct 187
 Ile Leu Asp Ser Pro Ala
 5

<210> 726
 <211> 207
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..206
 <221> sig_peptide
 <222> 39..80
 <223> Von Heijne matrix
 score 3.5
 seq VTLWIFQFFLCLT/CK

<221> misc_feature
 <222> 154
 <223> n=a, g, c or t
 Oligonucleotide

<400> 726
aatataaata ccaaatacat aaatagtttt ggtgttag atg gtc act tta tgg att 56
Met Val Thr Leu Trp Ile
-10
ttt caa ttt ttc ttg tgt ttg act tgt aaa gct tat aat tta aga aac 104
Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys Ala Tyr Asn Leu Arg Asn
-5 1 5
tgt aat gat ggg aag ggh wga gsm tca gwg gtg ctt gga ttg gaa caa 152
Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa Val Leu Gly Leu Glu Gln
10 15 20
mnr cta cct gaa tct gct ggt atg gta caw ttt tta ggt ttg aaa cac 200
Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa Phe Leu Gly Leu Lys His
25 30 35 40
agg tgg g 207
Arg Trp

<210> 727
<211> 164
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..164
<221> sig_peptide
<222> 54..95
<223> Von Heijne matrix
score 3.5
seq VLWAGPXVPLLCA/AX

<400> 727
agacaatggg gmmaatgtca cacatcacag accaagaggc ctaggaggav aag atg 56
Met
gtt ttg tgg gct ggg ccc akc gtc ccc ctg ctg tgt gca gcc tas gga 104
Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa Gly
-10 -5 1
ctt ggt gcc ctg cat ccc aga tgc tct agt caa ggc ttg agg ctt gcr 152
Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu Ala
5 10 15
sct tct gaa gcc 164
Xaa Ser Glu Ala
20

<210> 728
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..321

<221> sig_peptide
 <222> 139..261
 <223> Von Heijne matrix
 score 3.5
 seq FNIGLLWVPXXXG/AV

<400> 728
 catggaaatc actccaatca gaccggcccg aggatacgtt ttcttgtgat ccgcagcagc 60
 gccattagca tcataaacca ggtgattggc tggatctact ttgtggcctg gtccatctcc 120
 ttctaccctc aggtgmtc atg aat tgg agg cgg aaa agt gtc att ggt ctg 171
 Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu
 -40 -35
 agc ttc gac ttc gtg gct ctg aac ctg acg ggc ttc gtg gcc tac agt 219
 Ser Phe Asp Phe Val Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser
 -30 -25 -20 -15
 gta ttc aac atc ggc ctc ctc tgg gtg ccc twc wtc daa gga gca gtt 267
 Val Phe Asn Ile Gly Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val
 -10 -5 1
 tct cct caa ata ccc caa cgg agt gaa ccc cgt gaa cag caa cga cgt 315
 Ser Pro Gln Ile Pro Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg
 5 10 15
 ctt ctt 321
 Leu Leu
 20

<210> 729
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..471

<400> 729
 gacttccctc tagaatcctc caac atg gag cct ctt gca gct tac ccg cta 51
 Met Glu Pro Leu Ala Ala Tyr Pro Leu
 1 5
 aaa tgt tcc ggg ccc aga gca aag gta ttt gca gtt ttg ctg tct ata 99
 Lys Cys Ser Gly Pro Arg Ala Lys Val Phe Ala Val Leu Leu Ser Ile
 10 15 20 25
 gtt cta tgc aca gta acg cta ttt ctt cta caa cta aaa wtc ctc aaa 147
 Val Leu Cys Thr Val Thr Leu Phe Leu Leu Gln Leu Lys Xaa Leu Lys
 30 35 40
 cct aaa atc aac agc ttt tat gcc ttt gaa gtg aag gat gca aaa gga 195
 Pro Lys Ile Asn Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly
 45 50 55
 aga act gtt tct ctg gaa aag tat aaa ggc aaa gtt tca cta gtt gta 243
 Arg Thr Val Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val
 60 65 70
 aac gtg gcc agt gac tgc caa ctc aca gac aga aat tac tta ggg ctg 291
 Asn Val Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu
 75 80 85
 aag gaa ctg cac aaa gag ttt gga cca tcc cac ttc agc gtg ttg gct 339

Lys	Glu	Leu	His	Lys	Glu	Phe	Gly	Pro	Ser	His	Phe	Ser	Val	Leu	Ala		
90					95					100					105		
ttt	ccc	tgc	aat	cag	ttt	gga	gaa	tcg	gag	ccc	cgc	cca	agc	aag	gaa		387
Phe	Pro	Cys	Asn	Gln	Phe	Gly	Glu	Ser	Glu	Pro	Arg	Pro	Ser	Lys	Glu		
				110					115					120			
gta	gaa	tct	ttt	gca	aga	aaa	aac	tac	gga	gta	act	ttc	ccc	atc	ttc		435
Val	Glu	Ser	Phe	Ala	Arg	Lys	Asn	Tyr	Gly	Val	Thr	Phe	Pro	Ile	Phe		
			125					130					135				
cac	aag	att	aag	att	cta	gga	tct	gaa	gga	gaa	ctg	c					472
His	Lys	Ile	Lys	Ile	Leu	Gly	Ser	Glu	Gly	Glu	Leu						
		140					145										

<210> 730

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..465

<400> 730

actcgggggag	actccaaaca	gtgagcctag	agctggagac	tagcgttaac	cggcggggcg		60
gccgggtttt	atg aat gaa gct atg gct aca gat tcc cca aga aga ccc agt		111				
	Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser						
	1	5	10				
cgt tgt act ggt gga gtt gtg gtt cgc ccc cag gct gtc aca gag cag			159				
Arg Cys Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln							
15		20	25	30			
tcc tac atg gaa agt gtt gtg act ttt ctg cag gat gtt gtg cca cag			207				
Ser Tyr Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln							
	35	40	45				
gct tac agt gga aca cct cta aca gaa gaa aag gag aaa ata gtc tgg			255				
Ala Tyr Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp							
	50	55	60				
gtc aga ttt gaa aat gca gat tta aat gat aca tca aga aat ctg gaa			303				
Val Arg Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu							
	65	70	75				
ttt cat gaa ata cat agt act ggg agt gaa ccg cct ttg ttg att atg			351				
Phe His Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met							
	80	85	90				
att ggc tac agt gat gga atg cag gtc tgg agc atc cct atc akt ggc			399				
Ile Gly Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly							
95	100	105	110				
gaa sac aag agc tct tct ctg ttc gac atg gcc caa ttc gag cgg cta			447				
Glu Xaa Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu							
	115	120	125				
gaa tct tgc ctg ctc cac			465				
Glu Ser Cys Leu Leu His							
	130						

<210> 731

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 207..344

<400> 731

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agacgcgacg gtgctgggat cccgggaggg akcggaacgg acctgggctt ggtcgcctcc      60
aagccggcgg gaccgagtgc tttaggccgc tygaaagaaa gttgctccga cccgggaaaa      120
ggagaagatg aaggaagcca aggatgcccg ctataccaat gggcacctct tcaccaccat      180
ttcagtttca ggcattgacca tgtgct atg cct gta aca aga gca tca cag cca      233
                        Met Pro Val Thr Arg Ala Ser Gln Pro
                        1               5
agg aag ccc tca tct gcc caa caa cag aaa gcg gcc ctg ctg aak aac      281
Arg Lys Pro Ser Ser Ala Gln Gln Gln Lys Ala Ala Leu Leu Xaa Asn
10               15               20               25
aac acc gcc ttg cag tcc gtt tct ctt cga agt aag aca acc atc cgg      329
Asn Thr Ala Leu Gln Ser Val Ser Leu Arg Ser Lys Thr Thr Ile Arg
                30               35               40
gag cgg cca agc tcg g      345
Glu Arg Pro Ser Ser
                45
```

<210> 732

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 274..396

<400> 732

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agcaaccaag tcgcacctgg agctgtccta gcgcctagtt ctctcccggc cgcagagctg      60
gccgccccagg gggagtgcga gagtttggaa gatctctcta acacctctcg gccaaactta      120
gaagtgtata agatcagctt tatctttcca aatggagaca agtatgatgg tgactgtaca      180
agaacatctt ctggaatcta cgagagaaat ggaataggta ttcataccac tcctaattgg      240
attgtctaca caggaagctg gaaagatgac aag atg aat ggt ttt gga aga ctt      294
                        Met Asn Gly Phe Gly Arg Leu
                        1               5
gag cat ttt tca gga gca gta tat gaa gga caa ttt aag gat aat atg      342
Glu His Phe Ser Gly Ala Val Tyr Glu Gly Gln Phe Lys Asp Asn Met
10               15               20
ttt cat gga ctg ggg act tac aca ttc cca aat ggg gca aag tat act      390
Phe His Gly Leu Gly Thr Tyr Thr Phe Pro Asn Gly Ala Lys Tyr Thr
25               30               35
gga att tc      398
Gly Ile
40
```

<210> 733

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 49..441

<400> 733

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ggaagttctt gggagcgcca gttccgtctg tgtgttcgag tggacaaa atg gcg aag      57
                               Met Ala Lys
                               1
atc gcc aag act cac gaa gat att gaa gca cag att cga gaa att caa      105
Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg Glu Ile Gln
   5                               10                               15
ggc aag aag gca gct ctt gat gaa gct caa gga gtg ggc ctc gat tct      153
Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly Leu Asp Ser
  20                               25                               30                               35
aca ggt tat tat gac cag gaa att tat ggt gga agt gac agc aga ttt      201
Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp Ser Arg Phe
   40                               45                               50
gct gga tac gtg aca tca att gct gca act gaa ctt gaa gat gat gac      249
Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu Asp Asp Asp
   55                               60                               65
gat gac tat tca tca tct acg agt ttg ctt ggt cag aag aag cca gga      297
Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys Lys Pro Gly
   70                               75                               80
tat cat gcc cct gtg gca ttg ctt aat gat ata cca cag tca aca gaa      345
Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln Ser Thr Glu
   85                               90                               95
cag tat gat cca ttt gct gag cac aga cct cca aag att gca gac cgg      393
Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile Ala Asp Arg
  100                               105                               110                               115
gaa gat gaa tac aaa aag cat agg cgg acc atg ata att tcc cag agc      441
Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile Ser Gln Ser
   120                               125                               130
gt                                                                443
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<210> 734

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 128..373

<400> 734

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gagaagccgc agtctcgaga gcgtcaacga ggtgtttcgg tagtctcttg ccatcctttc      60
tgccgacccg gtgtcgctgg gctgcacccc gggcggggac gtccgcctgg caaggagggg      120
ggccaag atg ccg atc aat aaa tca gag aag cca gaa agc tgc gat aat      169
      Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn
      1                               5                               10
gtg aag gtt gtt gtt agg tgc cgg ccc ctc aat gag aga gag aaa tca      217
Val Lys Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser
  15                               20                               25                               30
atg tgc tac aaa cag gct gtc agt gtg gat gag atg agg gga act atc      265
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30

35

<210> 737
 <211> 160
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..158

<400> 737
 tgaatgactg gctatatt atg ggc acc cat gtt ttt gct ata aat aaa cgt 50
 Met Gly Thr His Val Phe Ala Ile Asn Lys Arg
 1 5 10
 aca tat gta att tca aga gac cga gaa tta tca act gca aag ccc awr 98
 Thr Tyr Val Ile Ser Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa
 15 20 25
 tgt agc agt cta ctc acg gcc cct gta ctt tgc tac tgg agg gcc tgt 146
 Cys Ser Ser Leu Leu Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys
 30 35 40
 cct ctg caa acc ca 160
 Pro Leu Gln Thr
 45

<210> 738
 <211> 234
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 66..233

<400> 738
 gttgttagtt ttcttttttag ctgaattacc cactcacatc cttattatatt tatgccactg 60
 atttc atg ttt tgt ttt cta ttt tca tgg tgg ctt aga gga ggt ctt cat 110
 Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His
 1 5 10 15
 gta tta tta aac aca tgc tta tat gta cct tat ggg tat ttg tca ctt 158
 Val Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu
 20 25 30
 att tgt tta ctt tgt tta tgg tat ctt aat cta tac aaa ttc tca att 206
 Ile Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile
 35 40 45
 ttc ttt tct ttt ctt tct ttt ttt ttt t 234
 Phe Phe Ser Phe Leu Ser Phe Phe Phe
 50 55

<210> 739
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 424..588

<400> 739

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atcaaaagaa ctcttatata caggagccca ggcaccatac tgtcttttcg aggtaggagt      60
cgactcctgt gaggtatggt gctgggtgca gatgcagtgt ggctctggat agcaccttat      120
ggacagttgt gtccccaagg aaggatgaga atagctactg aagtcctaaa gagcaagcct      180
aactcaagcc attggcacac aggcattaga cagaaagctg gaagttgaaa tggaggagtc      240
caacttgccct ggaccagctt aatgggtctg ctcttggtta cgtttttata catggatgac      300
ttgcttgggt atggagagtc ggcttgacta cactgtgtgg agcaagtttt aaagaagcaa      360
aggactcaga attcatgatt gaagaaatgc aggcagacct gttatcctaa actagggttt      420
tta atg acc aca aca agc aag cat gca gct tac tgc ttg aaa ggg tct      468
    Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser
      1          5          10          15
tgc ctc amc caa gct aga gtg cag tgg cct ttg aag cwt act aca gcc      516
Cys Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala
      20          25          30
tca aac ttc tgg gct caa gtg atc ctc agc ctc cca gtg gtc ttt gta      564
Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val
      35          40          45
gac tgc ctg atg gag tmt cat ggc a      589
Asp Cys Leu Met Glu Xaa His Gly
      50          55

```

<210> 740
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..388

<400> 740

```

aaaaaacgct gttggaaatc tcgcg atg gag gga gga gga ggt ata ccc cta      52
                        Met Glu Gly Gly Gly Gly Ile Pro Leu
                        1          5
gaa aca ctt aaa gaa gaa agt cag tca aga cat gtt cta cct gca agt      100
Glu Thr Leu Lys Glu Glu Ser Gln Ser Arg His Val Leu Pro Ala Ser
      10          15          20          25
ttt gaa gtc aac agt ttg cag aaa agc aac tgg ggg ttc tta ctt act      148
Phe Glu Val Asn Ser Leu Gln Lys Ser Asn Trp Gly Phe Leu Leu Thr
      30          35          40
ggg ctt gtg ggt ggc acc ctg gtg gct gtg tac gct gta gcc acg ccg      196
Gly Leu Val Gly Gly Thr Leu Val Ala Val Tyr Ala Val Ala Thr Pro
      45          50          55
ttt gta acg cca gcc ctt cga aaa gtc tgt ttg cca ttt gta cct gca      244
Phe Val Thr Pro Ala Leu Arg Lys Val Cys Leu Pro Phe Val Pro Ala
      60          65          70
act atg aag cag att gaa aat gtt gtg aaa atg ttg cga tgc cga aga      292
Thr Met Lys Gln Ile Glu Asn Val Val Lys Met Leu Arg Cys Arg Arg
      75          80          85
gga tcc ctt gtg gac atc ggt agt ggg gac gga cgc att gtc ata gcg      340

```

Gly	Ser	Leu	Val	Asp	Ile	Gly	Ser	Gly	Asp	Gly	Arg	Ile	Val	Ile	Ala	
90					95					100					105	
gct	gcg	aag	aaa	ggg	ttc	ama	gca	ggt	ggt	tat	gaa	tta	aac	cca	tgg	388
Ala	Ala	Lys	Lys	Gly	Phe	Xaa	Ala	Val	Gly	Tyr	Glu	Leu	Asn	Pro	Trp	
				110					115						120	

<210> 741
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..476

<400> 741																
agtgcgcctc	taag	atg	gcg	acg	cct	ttg	gcg	gta	aat	tcg	gct	gct	agt		50	
		Met	Ala	Thr	Pro	Leu	Ala	Val	Asn	Ser	Ala	Ala	Ser			
		1				5					10					
cta	tgg	ggt	cct	tac	aaa	gac	att	tgg	cat	aaa	gtg	gga	aat	gct	ctt	98
Leu	Trp	Gly	Pro	Tyr	Lys	Asp	Ile	Trp	His	Lys	Val	Gly	Asn	Ala	Leu	
		15				20						25				
tgg	aga	aga	caa	cct	gaa	gct	ggt	cam	ctt	ctt	gat	aag	att	ttg	aag	146
Trp	Arg	Arg	Gln	Pro	Glu	Ala	Val	Xaa	Leu	Leu	Asp	Lys	Ile	Leu	Lys	
		30				35					40					
aaa	cac	aaa	cct	gac	ttc	atc	tca	ttg	ttc	aaa	aat	ccg	cca	aaa	aat	194
Lys	His	Lys	Pro	Asp	Phe	Ile	Ser	Leu	Phe	Lys	Asn	Pro	Pro	Lys	Asn	
					50					55					60	
ggt	caa	cag	cat	gag	aag	ggt	cag	aaa	gcc	agt	aca	gag	gga	gtc	gcc	242
Val	Gln	Gln	His	Glu	Lys	Val	Gln	Lys	Ala	Ser	Thr	Glu	Gly	Val	Ala	
				65					70					75		
att	cag	ggt	caa	cag	gga	act	cga	ctt	ctt	cct	gaa	cag	ctc	att	aaa	290
Ile	Gln	Gly	Gln	Gln	Gly	Thr	Arg	Leu	Leu	Pro	Glu	Gln	Leu	Ile	Lys	
			80					85					90			
gaa	gcc	ttt	att	ctc	agt	gac	ctt	ttt	gat	att	gga	gaa	ttg	gca	gct	338
Glu	Ala	Phe	Ile	Leu	Ser	Asp	Leu	Phe	Asp	Ile	Gly	Glu	Leu	Ala	Ala	
		95					100					105				
ggt	gag	ctt	ctt	ctt	gct	gga	gag	cat	caa	cag	cca	cat	ttt	cct	ggc	386
Val	Glu	Leu	Leu	Leu	Ala	Gly	Glu	His	Gln	Gln	Pro	His	Phe	Pro	Gly	
		110				115					120					
ctt	acc	aga	gga	tta	gta	gct	ggt	ctt	ctg	tac	tgg	gat	gga	aag	cga	434
Leu	Thr	Arg	Gly	Leu	Val	Ala	Val	Leu	Leu	Tyr	Trp	Asp	Gly	Lys	Arg	
					130					135					140	
tgc	att	gcg	aat	tcc	ttg	aaa	gcc	ttg	ata	cag	tct	aga	cgg	gg		478
Cys	Ile	Ala	Asn	Ser	Leu	Lys	Ala	Leu	Ile	Gln	Ser	Arg	Arg			
				145					150							

<210> 742
 <211> 752
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 377..751

<400> 742

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atttcctgcc gtaagtatac agtgcctccg ggtcgcggtc attttgagcc cctgtctgga      60
tgacttcttg cggctgttct acccctcccc ctccccgcgt cggcctgmct gctgtcgtcg      120
ggaggtgggt gaggtgacgc aaacagcccc gttgttgccc tccgcgtatc ccctcaccac      180
ctttgcggcc atccacgact ttcgcacctt cgcgcatttt cctgcctgtg aggggtggaca      240
gatcgcgctc ggggtctcggc ctccctgagt cgggtgactg cgggaggcga cggagtgctt      300
ctgggggtgt gagctgggga agttcgtggt cacggatgcg tgtgggggtg ctgctcagtc      360
tgtaacggca ggaaag atg aat ggg agg gct gat ttt cga gag ccg aat gca      412
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Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala

1 5 10

```
gag gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca      460
```

Glu Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr

15 20 25

```
gag gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg      508
```

Glu Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp

30 35 40

```
ttc aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga      556
```

Phe Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly

45 50 55 60

```
tta att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc      604
```

Leu Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile

65 70 75

```
cct aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt      652
```

Pro Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu

80 85 90

```
tct tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc      700
```

Ser Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser

95 100 105

```
ccc ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca      748
```

Pro Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Ser Ser Pro

110 115 120

```
cct g      752
```

Pro

125

<210> 743

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 353..457

<221> misc_feature

<222> 438

<223> n=a, g, c or t

Oligonucleotide

<400> 743

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cctatcactg gagaatgggt ttggtgcttt gagctgtgtt totacataaa aaagaaggaa      60
```

tcaaagtgat gctgggtgtga caatataaca tttgaagctg ctccaaacaa ctttgactgt 120

aagaaaatgg ccaagagaat acaagaggct ctaaccaagg actctgactt cactaagcca 180
 ctgaaacatt cctggcacta cctacctcct gccttttcgt tatgggagga aaccctattg 240
 gttaggtcac tggtttaaaa cacgtccttt aaattgcaga ggaagaaaag gcttggaggt 300
 gataaaggaa tayagttcat tcccttsmtt atggtgatgg ttcataggc at atg cat 358

Met His
 1

atg tcc aaa ctc atc aac ttg tat aca tca rat atg tgc aat tta ctg 406
 Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn Leu Leu
 5 10 15

tmt atc cac cty mtc tym ata agc tgt tta ant aat aat aar rta aca 454
 Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys Xaa Thr
 20 25 30

tta cg 459
 Leu
 35

<210> 744
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..411

<400> 744
 atggggacgg ggctgttccc ggggaggctg tgatgggttg acaggtgcgt gacagtggga 60
 gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc 111
 Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala
 1 5 10

gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat 159
 Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
 15 20 25

gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta 207
 Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
 30 35 40

tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga 255
 Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
 45 50 55

ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct 303
 Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
 60 65 70 75

cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc 351
 Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
 80 85 90

cat gat tac agt gct gca gca gct ccc agt cca gtg cta gga aac att 399
 His Asp Tyr Ser Ala Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile
 95 100 105

ccc cca gga gat 411
 Pro Pro Gly Asp
 110

<210> 745
 <211> 404

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..403

<400> 745
 ctctggggcg gasggccacc atcttgaac gggaggcgga sagagtcgac tgggagcgac 60
 cgagcgggcc gccgcccgcg cc atg aac ccc gaa tat gac tac ctg ttt aag 112
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys
 1 5 10
 ctg ctt ttg att ggc gac tca ggc gtg ggc aag tca tgc ctg ctc ctg 160
 Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu
 15 20 25
 cggttt gct gat gac acg tac aca gag agc tac atc agc acc atc ggg 208
 Arg Phe Ala Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly
 30 35 40
 gtg gac ttc aag atc cga acc atc gag ctg gat ggc aaa act atc aaa 256
 Val Asp Phe Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys
 45 50 55
 ctt cag atc tgg gac aca gcg ggc cag gaa cgg ttc cgg acc atc act 304
 Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr
 60 65 70
 tcc agc tac tac cgg ggg gct cat ggc atc atc gtg gtg tat gac gtc 352
 Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val
 75 80 85 90
 act gac cag gaa tcc tac gcc ary gtg aag cag tgg ctg cag gag att 400
 Thr Asp Gln Glu Ser Tyr Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile
 95 100 105
 gac c 404
 Asp

<210> 746
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 336..428

<221> misc_feature
 <222> 393
 <223> n=a, g, c or t
 Oligonucleotide

<400> 746
 ggcttcttcc agtcacctcg gcccggatcg ggaagtgtca agcgggcgct ccccatctc 60
 gcgcgctatt accactgaac ccggaccccc taccagggtc cagggccagc cgccatgacg 120
 aacgtgtact ccttgatgg gattctggtg tttggtttgc tctttgtttg cacctgtgcc 180
 tacttcaaga aagtacctcg tctcaaaaacc tggctgctat cagagaagaa ggggtgtttgg 240
 ggtgtgtttt acaaagccgs tgtgattgga accaggctgc atgctgctgt ggcaattgct 300
 tgtgttgtaa tgggctttta cgtcctgttt ataaa atg aat tcc aaa gca scc 353

									Met	Asn	Ser	Lys	Ala	Xaa	
									1				5		
aag	tca	tca	act	gcc	aac	caa	ggg	gac	ggg	gat	gaa	gaa	nct	gtt	ggg
Lys	Ser	Ser	Thr	Ala	Asn	Gln	Gly	Asp	Gly	Asp	Glu	Glu	Xaa	Val	Gly
			10					15					20		
mga	mct	gaa	scc	agt	gta	gga	gag	ttc	a						
Arg	Xaa	Glu	Xaa	Ser	Val	Gly	Glu	Phe							
			25					30							

<210> 747
 <211> 179
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..178
 <221> misc_feature
 <222> 140
 <223> n=a, g, c or t
 Oligonucleotide

<400> 747															
gaaatataca ataccttatg ttgtatatta catt atg ttg tat agt acg ttg aaa															55
									Met	Leu	Tyr	Ser	Thr	Leu	Lys
									1				5		
cat	aca	cta	caa	tac	gtt	atc	att	aat	tgt	ggt	cac	cat	gct	gtg	caa
His	Thr	Leu	Gln	Tyr	Val	Ile	Ile	Asn	Cys	Gly	His	His	Ala	Val	Gln
			10					15				20			
aag	atc	tct	aaa	acg	tat	tcc	tcc	tgt	ctg	act	gaa	nyt	ttg	tat	cct
Lys	Ile	Ser	Lys	Thr	Tyr	Ser	Ser	Cys	Leu	Thr	Glu	Xaa	Leu	Tyr	Pro
			25				30				35				
ttg	cct	aat	atc	tcc	cca	atc	cct	cca	c						
Leu	Pro	Asn	Ile	Ser	Pro	Ile	Pro	Pro							
40							45								

<210> 748
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..382

<400> 748															
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ctttggcgct ggttcctgtg ggcaacttgg acacgactcc atg aat gat gag gtt															115
									Met	Asn	Asp	Glu	Val		
									1				5		
aac	cct	aga	aga	gtt	cta	gag	ctg	atg	ggt	agt	gaa	gta	act	caa	att
Asn	Pro	Arg	Arg	Val	Leu	Glu	Leu	Met	Gly	Ser	Glu	Val	Thr	Gln	Ile
				10					15				20		

gct tgt ggc aga caa cat acc cta gsm ttc gtg cct tct tct gga ctc	211
Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val Pro Ser Ser Gly Leu	
25 30 35	
atc tat gca ttt ggt tgt gga gca aga ggt caa tta gga act ggg cac	259
Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln Leu Gly Thr Gly His	
40 45 50	
act tgt aat gtt aag tgc cca tct cct gtc aag ggt tac tgg gct gcc	307
Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys Gly Tyr Trp Ala Ala	
55 60 65	
cac agt ggc cag ctt tca gcc cga gct gat cgc ttt aaa tat cat atc	355
His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg Phe Lys Tyr His Ile	
70 75 80 85	
gtt aag cag atc ttc tct gga gga gac c	383
Val Lys Gln Ile Phe Ser Gly Gly Asp	
90	

<210> 749
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 381..446

<400> 749	
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gggcgccttc cgcccggtc ccattcctgc cgcgctccag caaccttgaa gttttgcagc	120
gccagaaaag gaggcgagga aggcaggag tgtgtgagag gagggagcaa aaagctcacc	180
ctaaaacatt tttttcaagg agaaaagaaa aagggggggc gcaaaaatgg ctggggcaat	240
tatagaaaac atgagcacca agaagctgtg cattgttggt gggattctgc tcgtgttcca	300
aatcatcgcc tttctggtg gagccttgat tgctccagg sccacaacgg cagtgtccta	360
catgtcgggtg aaatgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt	413
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly	
1 5 10	
tcg gtg cct tgg gga ccc aat cat tgt gac aag	446
Ser Val Pro Trp Gly Pro Asn His Cys Asp Lys	
15 20	

<210> 750
 <211> 410
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..410

<400> 750	
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agaaataact tgctggcttg tctggagtca catggtgaca atttacagaa agtcatctct	120
gcagcttg atg ggc gac aac cct ttt caa oca aaa agt aat tca aaa atg	170
Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met	
1 5 10	

gca gaa ctg ttt atg gaa tgt gaa gaa gag gag ctg gaa cca tgg cag	218
Ala Glu Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln	
15 20 25 30	
aag aaa gta aaa gaa gtt gag gat gac gat gat gat gag cca atc ttt	266
Lys Lys Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe	
35 40 45	
gtt ggc gag ata tca agt tca aaa cca gca att tca aat att ttg aac	314
Val Gly Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn	
50 55 60	
aga gtt aac ccc agc tca tat tca agg gga cta aag aat ggt gca ctc	362
Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu	
65 70 75	
agt cga ggt att act gct gca ttc aag cct aca agt caa cac tac acg	410
Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr	
80 85 90	

<210> 751
 <211> 536
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 334..534
 <221> misc_feature
 <222> 148
 <223> n=a, g, c or t
 Oligonucleotide

<400> 751	
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tctcccaagg cagaggagat cgttgggttt caaggccccg cgggcatttc tcgcgggcc	120
tgcggagaga gttcttcact accacaancm arggaggat atgataggcg gccagtggat	180
ataactcctt tagaacaaag gaaattaact tttgataccc atgcattggg tcaggacttg	240
gaaactcatg gatttgacaa aacacaagca gaaacaattg tatcagcggt aactgcttta	300
tcaaatgtca gcttggtatc tatctataaa gag atg gtc act caa gct caa cag	354
Met Val Thr Gln Ala Gln Gln	
1 5	
gaa ata aca gta caa cag cta atg gct cat ttg gat gct atc agg aaa	402
Glu Ile Thr Val Gln Gln Leu Met Ala His Leu Asp Ala Ile Arg Lys	
10 15 20	
gac atg gtc atc cta gag aaa agt gaa ttt gca aat ctg aga gca gag	450
Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala Asn Leu Arg Ala Glu	
25 30 35	
aat gag aaa atg aaa att gaa tta gac caa gtt aag caa caa cta atg	498
Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val Lys Gln Gln Leu Met	
40 45 50 55	
cat gaa acc agt yga atc aga gca gat aat aaa ctg ga	536
His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys Leu	
60 65	

<210> 752
 <211> 139

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..138

<400> 752
cttggatcctt tgggtgttacc ttaa atg aaa ttt gga aat gtt agg atg tya 51
Met Lys Phe Gly Asn Val Arg Met Xaa
1 5
tct att caa ata ttt att gtg tcc atc tgg agc ttc ttc ctt ttc tat 99
Ser Ile Gln Ile Phe Ile Val Ser Ile Trp Ser Phe Phe Leu Phe Tyr
10 15 20 25
ggc aag tat aca tat att aga ctg atc ttg tcc caa ggc c 139
Gly Lys Tyr Thr Tyr Ile Arg Leu Ile Leu Ser Gln Gly
30 35

<210> 753
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..191

<400> 753
tattacagag tttgcagact gaaagagagt ctagctaagg cttgctcctc ataccagga 60
tttgatctaa tccaacaagc ctttgt atg acc ttt gac ctc agt gtg ttc agt 113
Met Thr Phe Asp Leu Ser Val Phe Ser
1 5
act ttg tca gat cac ttt tac tca tca ttg tcc aat act gca agg 161
Thr Leu Ser Asp His Phe Tyr Ser Ser Ser Leu Ser Asn Thr Ala Arg
10 15 20 25
aat ctg tat att tgt tta ttt cat atc aca ca 193
Asn Leu Tyr Ile Cys Leu Phe His Ile Thr
30 35

<210> 754
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..393

<400> 754
cggcctcgca cttccggtgg ggagattccg gcctggagct cccagggccg agcagacctt 60
gggacctgtg agcgtgcat ccaattaacc atgggaaggg tcagcaccag ccaccagccc 120
cttaggtgag gactctgcct ggggctctgc tgatggttcc gaatcatgga gctgcagaga 180
gtcctccag cctggagacg ttcttggtga aagctgtggt ctaactccac cggctcttcc 240
tgcacattgt attcaagagg ggtgcctgcc cccgctgact caggagctcc ggtgctgcag 300

ccgccacga atg ggg agg tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg 351
 Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala
 1 5 10
 gtg ttg acc ctg ggg ctg gtg ctt ctc tac tac tgc ttc tcc at 395
 Val Leu Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser
 15 20 25

<210> 755
 <211> 460
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 76..459

<400> 755
 agaaggctgt gcgtgctcct cgctttctcc gcggtcttcc gagcggtcgc gtgaactgct 60
 tcctgcaggc tggcc atg gcg ctt cac gtt ccc aag gct ccg ggc ttt gcc 111
 Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala
 1 5 10
 cag atg ctc aag gag gga gcg aaa cac ttt tca gga tta gaa gag gct 159
 Gln Met Leu Lys Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala
 15 20 25
 gtg tat aga aac ata caa gct tgc aag gag ctt gcc caa acc act cgt 207
 Val Tyr Arg Asn Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg
 30 35 40
 aca gca tat gga cca aat gga atg aac aaa atg gtt atc aac cac ttg 255
 Thr Ala Tyr Gly Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu
 45 50 55 60
 gag aag ttg ttt gtg aca aac gat gca gca act att tta aga gaa cta 303
 Glu Lys Leu Phe Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu
 65 70 75
 gaa gta cag cat cct gct gca aaa atg att gta atg gct tct cat atg 351
 Glu Val Gln His Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met
 80 85 90
 caa gag caa gaa gtt gga gat ggc aca aac ttt gtt ctg gta ttt gct 399
 Gln Glu Gln Glu Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala
 95 100 105
 gga gct ctc ctg gaa tta gct gaa gaa ctt ctg agg att ggc ctg tca 447
 Gly Ala Leu Leu Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser
 110 115 120
 gtt tca gag gtc a 460
 Val Ser Glu Val
 125

<210> 756
 <211> 142
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..140

<400> 756
aagcctgact tcagcgctcc cactctcggc cgacaccct c atg gcc aac cgt tac 56
Met Ala Asn Arg Tyr
1 5
acc atg gat ctg act gcc atc tac gag agc ctc ctg tgc ctg agc cct 104
Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro
10 15 20
gac gts acc ctc acc cac ttc gcc cac tgc aac ctc ca 142
Asp Val Thr Leu Thr His Phe Ala His Cys Asn Leu
25 30

<210> 757
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 158..361

<400> 757
atcttgtagg cggggacacg ccgaggtaac ttccagggtg cgccttcggt gtcttctcca 60
agctgtagtt ctacgtcccg acctccctat cataccacac tcttcagcga ccacgcaggc 120
actttcccg tccccagtat accataattg aagaaaa atg atg gaa gag agt gga 175
Met Met Glu Glu Ser Gly
1 5
ata gag aca aca cca cct ggg act cct cca cca aat cct gca ggg ctg 223
Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro Pro Asn Pro Ala Gly Leu
10 15 20
gct gct act gct atg tct tct acc cct gtt cca tta gcg gca acc agt 271
Ala Ala Thr Ala Met Ser Ser Thr Pro Val Pro Leu Ala Ala Thr Ser
25 30 35
tct ttt tct tct cca aat gta tcc tcc atg gag tcc ttc cca cca ctc 319
Ser Phe Ser Ser Pro Asn Val Ser Ser Met Glu Ser Phe Pro Pro Leu
40 45 50
gca tac tct act cct cag ccg ccc ctt cct cct gtg agg cct t 362
Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro Pro Val Arg Pro
55 60 65

<210> 758
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 219..368

<221> misc_feature
<222> 317
<223> n=a, g, c or t
Oligonucleotide

<400> 758

gaagaaggct cttacagcat ggccgccggt actgcagctg ccttagcggt tttgagtcag 60
 gagagccgaa cgccgggcccgg ggggtgcggg ggccctacggg tcccggcccc ggtcactatg 120
 gacagttttt tcttcggctg tgagctctcc ggccacaccc gctccttcac ctttaaggta 180
 gaggaagagg atgatgcgga sacgtgctgg cactaacc atg ctc tgc ctc acc gag 236
 Met Leu Cys Leu Thr Glu

1 5
 gga gcc aaa gac gag tgt aat gtg gta gaa gtt gtg gcc cgg aac cat 284
 Gly Ala Lys Asp Glu Cys Asn Val Val Glu Val Val Ala Arg Asn His
 10 15 20
 gac cat cag gag atc gca gtc cct gtg gcc aan ctc aag ctg tcc tgc 332
 Asp His Gln Glu Ile Ala Val Pro Val Ala Xaa Leu Lys Leu Ser Cys
 25 30 35
 caa ccc atg ctc agt ctg gat gac ttc cag ctc caa 368
 Gln Pro Met Leu Ser Leu Asp Asp Phe Gln Leu Gln
 40 45 50

<210> 759

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 36..452

<400> 759

agctcgctgc gcaggcgag tgagttcgac acacc atg ccg act gtc agc gtg 53
 Met Pro Thr Val Ser Val
 1 5
 aag cgt gat ctg ctc ttc caa gcc ctg ggc cgc acc tac act gac gaa 101
 Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly Arg Thr Tyr Thr Asp Glu
 10 15 20
 gaa ttt gat gaa cta tgt ttt gaa ttt ggt ctg gag ctt gat gaa att 149
 Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly Leu Glu Leu Asp Glu Ile
 25 30 35
 aca tct gag aag gaa ata ata agt aaa gaa caa ggt aat gta aag gca 197
 Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu Gln Gly Asn Val Lys Ala
 40 45 50
 gca gga gcc tct gat gtt gtt ctt tac aaa att gac gtc cct gcc aat 245
 Ala Gly Ala Ser Asp Val Val Leu Tyr Lys Ile Asp Val Pro Ala Asn
 55 60 65 70
 aga tat gat ctc ctg tgt ctg gaa gga ttg gtt cga gga ctt cag gtc 293
 Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu Val Arg Gly Leu Gln Val
 75 80 85
 ttc aaa gaa agg ata aag gct cca gtg tat aaa cgg gta atg cct gat 341
 Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr Lys Arg Val Met Pro Asp
 90 95 100
 gga aaa atc cag aaa ttg att atc aca gaa gag aca gct aag ata cgt 389
 Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu Glu Thr Ala Lys Ile Arg
 105 110 115
 cct ttt gcg gta gca gca gtt ctc cgt aat ata aag ttt act aaa gat 437
 Pro Phe Ala Val Ala Ala Val Leu Arg Asn Ile Lys Phe Thr Lys Asp
 120 125 130

cga tat gac agc ttc
Arg Tyr Asp Ser Phe
135

452

<210> 760
<211> 295
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..295

<400> 760
aagctgCGGT tcgaaaatss tgacagcaca gggcttcctg ggctctgcag agcaaactgg 60
aaagagctgg gatccaggca ct atg ttc tct gaa gaa ctg tgg ctg gaa aat 112
Met Phe Ser Glu Glu Leu Trp Leu Glu Asn
1 5 10
gag aaa aag tgt gct gtg gtt cgg aag tct aag cag ggc agg aaa cgc 160
Glu Lys Lys Cys Ala Val Val Arg Lys Ser Lys Gln Gly Arg Lys Arg
15 20 25
caa gaa ctg ctg gcc gta gcc ttc ggg gtg aag gtc cac acg ttc cga 208
Gln Glu Leu Leu Ala Val Ala Phe Gly Val Lys Val His Thr Phe Arg
30 35 40
ggc cca cac tgg tgt gaa tat tgt gcc aat ttc atg tgg ggg ctc atc 256
Gly Pro His Trp Cys Glu Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile
45 50 55
gcc caa ggg gtc cgg tgc tca gac tgt gga ttg aac gta 295
Ala Gln Gly Val Arg Cys Ser Asp Cys Gly Leu Asn Val
60 65 70

<210> 761
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..210

<400> 761
ttggccatttt ttttcctttg gctttgatatt gtgaactata tccaagactc attggagtaa 60
tagttaactg attgcagtgg atttcgaggt gtggcaacta gtggcaatgc tcatgcgaca 120
gtg atg gtg gtt ttc atg aca tat gta act tta ccc ttt ttt ttt tct 168
Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser
1 5 10 15
ttc atc tct tcc ctt ctt tca ttt ttt ttt ctt ttt cta ctc tc 212
Phe Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu
20 25

<210> 762
<211> 623
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> 474..623

<400> 762

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agtgaggaggt ttaggcaagt gcctgatttg ggtaatcgaa agcaccaggt gattgtattt      60
gatgactttt aagctttcat atgccgttat ttaataacctg tcaacttccaa atgagagatg      120
taagggcaac ggccgtttagc gttctgwttt ggatcagggt ctggagtgga cgcccctagc      180
ttaggggtcc ttctaggcag ccagaaacct gcggaaaatg gtagegatgg cggctgggcc      240
gagtgggtgt ctggtgccgg cgtttgggct acggttggtt ttggcgactg tgcttcaagc      300
ggtgtctgct tttggggcag agttttcatc ggaggcatgc agagagttrg gcttttctag      360
caacttgctt tgcagctctt gtgatcttct cggacagttc aacctgcttc agctggatcc      420
tgattgcaga ggatgstgtc aggaggaagc acaatttgaa accaaaaagc tgt atg      476
                                         Met
                                         1
cag gag cta ttc ttg aag ttt gtg gat gaa aat tgg gaa ggt tcc ctc      524
Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser Leu
      5              10              15
aag tcc aag tat gtc cgt ggt tca gac cct gta tta aag ctt ttg gac      572
Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu Asp
      20              25              30
gac aat ggg aac att gct gaa gaa ctg agc att ctc aaa tgg aca cag      620
Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr Gln
      35              40              45
aca
Thr
50
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<210> 763

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..261

<400> 763

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gacatccacg gggcgcgaggt gacacgcggg agggagagca gtgttctgct ggagccg      57
atg cca aaa acc atg cat ttc tta ttc aga ttc att gtt ttc ttt tat      105
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
      1              5              10              15
ctg tgg ggc ctt ttt act gct cag aga caa aag aaa gag gag agc acc      153
Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
      20              25              30
gaa gaa gtg aaa ata gaa gtt ttg cat cgt cca gaa aac tgc tct aag      201
Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
      35              40              45
aca agc aag aag gga gac cta cta aat gcc cat tat gac ggc tac ctg      249
Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
      50              55              60
gct aaa gac ggc
Ala Lys Asp Gly      261
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65

<210> 764
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..159

<400> 764
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Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr
1 5 10 15
att agc cac ggc ttt gca cgt ggt gtg agg agg ggt gtg gct att gtg 96
Ile Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val
20 25 30
ggc aag ggt ctg gaa tgg cat ggg tgt tgg tgg atg tgc cac gga tac 144
Gly Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr
35 40 45
agg att cta gcc ggg a 160
Arg Ile Leu Ala Gly
50

<210> 765
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 404..514

<400> 765
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tgcatectcc actccacaag aggctaggag ctgggggggag agaggcagtc cagccgcagg 120
gccacccgaa cagtctctcc tcctcacaga agcctggagc tgggcatcca agaagaagca 180
gcttcatttg ttttctggtg tcatcgtagg tggccaccta tggcttttgg gcttctcacc 240
tggggcgggg gggttctgca ccacctccc accctccttc ctccgtgtgg acgatagagc 300
cacatccagc accacggaca gtcgccgggc gaccaaagag aagaatgtac ttcattctggt 360
tgggctggat tccctctgat aagccttccc agttgactga aag atg agg cta ggc 415
Met Arg Leu Gly
1
tot agc aag ttg aag tca aac cag ctc ctt caa gaa gct ttg agc aga 463
Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu Ala Leu Ser Arg
5 10 15 20
atg aag tgg gga gga ccc agc ttc cag ccc agg aag ccc act gta cct 511
Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys Pro Thr Val Pro
25 30 35
gga gc 516
Gly

<210> 766

<211> 626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..238

<221> sig_peptide
 <222> 68..106
 <223> Von Heijne matrix
 score 15
 seq MLLLLLLLPLALG/DK

<221> misc_feature
 <222> 529
 <223> n=a, g, c or t
 Oligonucleotide

<400> 766
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 cccagac atg ctg ctg ctg ctg ctg ctg ctg ccc ctt gct ctg ggg gac 109
 Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp
 -10 -5 1
 aaa ggg gat gga ggg aga cag aca ata tgg gga tgg tta ctt gct gca 157
 Lys Gly Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala
 5 10 15
 agt gca gga gct ggt gac ggt gca gga ggg cct gtg tgt cca tgt gcc 205
 Ser Ala Gly Ala Gly Asp Gly Ala Gly Gly Pro Val Cys Pro Cys Ala
 20 25 30
 ctg ctc ctt ctc cta ccc cca gga tgg ctg gac tgactctgac ccagttcatg 258
 Leu Leu Leu Leu Leu Pro Pro Gly Trp Leu Asp
 35 40
 gctactgggt cccggcaggg aatgatataa gctggaaggc tccagtggcc acaaacaacc 318
 cagcttgggc agtgcaggag gaaactcggg accgattcca mctycyttgg ggaccacag 378
 accaaaaatt gcactctgag catcagagat gccagaatga gtgatgcggg gagatacttc 438
 ttctgtatgg agaaaggaaa tataaaatgg aattataaat atgaccagct ctctgtgaac 498
 gtgayagcct tgaccacag gcccaacats nktatccccg gtaccctgga gtctggctgc 558
 ttccagaatc tgacctgctc tgtgccctgg gcctgtgagc aggggacgcc ccctatgac 618
 tcttgat 626

<210> 767
 <211> 473
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..344

<221> sig_peptide
 <222> 60..113
 <223> Von Heijne matrix
 score 10.3000001907349

seq VLMLAALLLHCYA/DS

<400> 767

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acagcaactt ccttgatccc tgccacgcac gactgaacac agacagcagc cgcctcgcc 59
atg aag ctg ctg atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc 107
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
      -15      -10      -5
tat gca gat tct ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc 155
Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
      1      5      10
atc aat tcc gac ata tct ata cct gaa tac aaa gag ctt ctt caa gag 203
Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
      15      20      25      30
ttc ata gac agt gat gcc gct gca gag gct atg ggg aaa ttc aag cag 251
Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
      35      40      45
tgt ttc ctc aac cag tca cat aga act ctg aaa aac ttt gga ctg atg 299
Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
      50      55      60
atg cat aca gtg tac gac agc att tgg tgt aat atg aag agt aat 344
Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
      65      70      75
taactttacc caaggcggtt ggctcagagg gctacagact atggccagaa ctcatctgtt 404
gattgctaga aaccactttt ctttcttggt ttgtctkttt atgwggaaam tgctagacaa 464
ctgttgaaa 473

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<210> 768

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 218..502

<221> sig_peptide

<222> 218..310

<223> Von Heijne matrix

score 9.19999980926514

seq RLLLATVLQAVSA/FG

<400> 768

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agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcaccagc gattgtattt 60
gatgactttt aagctttcat atgccgttat ttaataacctg tcaacttccaa atgagagatg 120
taagggcaac ggccgtagc gttctgwtgt ggatcaggct ctggagtgga cgcccctagc 180
ttaggggtcc ttctaggcag ccagaaacct gcggaaa atg gta gcg atg gcg gct 235
      Met Val Ala Met Ala Ala
      -30
ggg ccg agt ggg tgt ctg gtg ccg gcg ttt ggg cta ccg ttg ttg ttg 283
Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg Leu Leu Leu
-25      -20      -15      -10
gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag ttt tca tcg 331
Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu Phe Ser Ser
      -5      1      5

```

gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt tgc agc tct	379
Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu Cys Ser Ser	
10 15 20	
tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg gat cct gat tgc	427
Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp Pro Asp Cys	
25 30 35	
aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa aag ctg tat	475
Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys Lys Leu Tyr	
40 45 50 55	
gca gga gct att ctt gaa gtt tgt gga tgaaaattgg gaaggttccc	522
Ala Gly Ala Ile Leu Glu Val Cys Gly	
60	
tcaagtccaa gcttttggtta ggagtataaa acccaaactg ttcagaggac tgcaaataca	582
gtatgtccgt ggttcagacc ctgtattaaa gcttttgtag gacaatggga acattgctga	642
agaactgagc attctcaaat ggacacagac a	673

<210> 769
 <211> 539
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 190..492

<221> sig_peptide
 <222> 190..285
 <223> Von Heijne matrix
 score 8.80000019073486
 seq VPMLLLIVGGSFG/LR

<221> misc_feature
 <222> 500..501
 <223> n=a, g, c or t
 Oligonucleotide

<400> 769	
acaagtatgt tacgatggct cgattgcttt tgccatagcgg aaaccattca ctaaggaccg	60
agcaccaaat aaccaaggaa aaggaagtga gttaaggacg tactcgtctt ggtgagagcg	120
tgagctgctg agatttgga gtctgcgcta ggcccgttg gagttctgag ccgatggaag	180
agttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac aag	231
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys	
-30 -25 -20	
act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt tct	279
Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser	
-15 -10 -5	
ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag agt	327
Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser	
1 5 10	
aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct	375
Lys Met Asp Pro Glu Leu Lys Lys Leu Lys Glu Asn Lys Ile Ser	
15 20 25 30	
tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg	423
Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp	

	35	40	45	
aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa				471
Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln				
	50	55	60	
gga aag aaa tcc aga aag cct taagacannng acaacttgac tctgctgatt				522
Gly Lys Lys Ser Arg Lys Pro				
	65			
cttttttctct ttttttt				539

<210> 770
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..468

<221> sig_peptide
 <222> 124..276
 <223> Von Heijne matrix
 score 8.10000038146973
 seq VCLCGTFCFCLG/CQ

<400> 770	
aagttacctc tccccctttca cgtarttttct atttgtggtg agattctctc ccaggccaca	60
agacatttcc tgctcggaac cttgtttact aatttccact gcttttaagg ccctgcaactg	120
aaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc	168
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val	
-50 -45 -40	
ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt	216
Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys	
-35 -30 -25	
gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc	264
Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe	
-20 -15 -10 -5	
ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg	312
Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu	
1 5 10	
tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc	360
Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly	
15 20 25	
atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct	408
Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro	
30 35 40	
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc	456
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala	
45 50 55 60	
atg cgt act ttc taaaaactga t	479
Met Arg Thr Phe	

<210> 771
 <211> 492
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 25..402

<221> sig_peptide

<222> 25..96

<223> Von Heijne matrix

score 7

seq LLCCFRALSGSLS/MR

<221> misc_feature

<222> 371

<223> n=a, g, c or t

Oligonucleotide

<400> 771

agsetggccc tccctctttc caaa atg gac aag tcc ctc ttg ctg gaa ctc 51
Met Asp Lys Ser Leu Leu Leu Glu Leu
-20

ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg 99
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met
-15 -10 -5 1

aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct 147
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro
5 10 15

gtg ata gaa att gtt cgg tgt agg atg tgc cac ctc cag ttc cca gga 195
Val Ile Glu Ile Val Arg Cys Arg Met Cys His Leu Gln Phe Pro Gly
20 25 30

gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag 243
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu
35 40 45

gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta 291
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu
50 55 60 65

acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg 339
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg
70 75 80

tgg agt gtc tat ttg gtg aac ttc agg tgc tnm agg agc cat gac ctg 387
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Xaa Arg Ser His Asp Leu
85 90 95

tgc aat gaa gac ctt tagaagttaa tggttcttct gtgactccaa tttctgggtg 442
Cys Asn Glu Asp Leu
100

aggttgttgc ctcagcctct tcacaatgac tttctaaaaa aatcacacac 492

<210> 772

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 7..312

<221> sig_peptide

<222> 7..54

<223> Von Heijne matrix

score 6.80000019073486

seq LWILPSLWLLLLG/GP

<400> 772

agcaag atg gat cta ctg tgg atc ctg ccc tcc ctg tgg ctt ctc ctg 48

Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu

-15

-10

-5

ctt ggg ggg cct gcc tgc ctg aag acc cag gaa cac ccc agc tgc cca 96

Leu Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro

1

5

10

gga ccc agg gaa ctg gaa gcc agc aaa gtt gtc ctc ctg ccc agt tgt 144

Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys

15

20

25

30

ccc gga gct cca gga agt cct ggg gag aag gga gcc cca ggt cct caa 192

Pro Gly Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln

35

40

45

ggg cca cct gga cca cca ggc aag atg ggc ccc aag ggt gag cca gga 240

Gly Pro Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly

50

55

60

gat cca gtg aac ctg ctc cgg tgc cag gaa ggc ccc aga aac tgc cgg 288

Asp Pro Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg

65

70

75

gag ctg ttg agc agg gcg cca cct tgagcggctg gtamcatctg tgcctacctg 342

Glu Leu Leu Ser Arg Ala Pro Pro

80

85

agggcagggc ctcccagtct tttgtgacat ggacaccgag gggggcggct ggct 396

<210> 773

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 50..229

<221> sig_peptide

<222> 50..106

<223> Von Heijne matrix

score 6.59999990463257

seq SAVVLPSTPQASA/NP

<221> misc_feature

<222> 206,354

<223> n=a, g, c or t

Oligonucleotide

<400> 773

acaggatcga tttagcggycg cagagaaaaa ccaagatttc actttcaag atg gaa agt 58

CCDS: CDS: 153..443

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                                Met Glu Ser
ccg tca grc tca gct gtg gtt tta cct agc act cct cag gcc tct gcg      106
Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln Ala Ser Ala
   -15                               -10                               -5
aat cca tca tct ccc tat aca aat agt tcc cga aaa caa cct atg agt      154
Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln Pro Met Ser
1                               5                               10                               15
gca aca ctt aga gaa aga tta agg aaa aca aga ttt tca ttt aat tcc      202
Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser Phe Asn Ser
                20                               25                               30
tct nac aat gtg gtg aac gtc tta aag tagagagtga agaaaatgat      249
Ser Xaa Asn Val Val Asn Val Leu Lys
        35                               40
cagacctttt cagagaaccc agcatcttcc acagagggraa actgtttggr attcaaagaa      309
agtttaaamc atatagrcag tgatttgaag aaaatacaaa tttgnaaaat actttgaaga      369
atctcaatgt ctgtgaatct cagtcacttg attctggatc atgcagtg      417

<210> 774
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..443

<221> sig_peptide
<222> 153..200
<223> Von Heijne matrix
      score 6.40000009536743
      seq WLWPLYFLPVSGA/LR

<221> misc_feature
<222> 359
<223> n=a, g, c or t
      Oligonucleotide

<400> 774
aggttgatcat ttcctcatcg tcaagctttg ttcctcgtgg gggctagaaa tctctttcca      60
gttcagagatt gtgaagggtt cctgagtaag cagcgtgtct ccataccccct ctctaggggc      120
tcttgatagg accttgcaat ctagaaggga ca atg gac ttc tgg ctt tgg cca      173
                                Met Asp Phe Trp Leu Trp Pro
                                -15                               -10
ctt tac ttc ctg cca gta tcr ggg gcc ctg agg atc ctc cca gaa gta      221
Leu Tyr Phe Leu Pro Val Ser Gly Ala Leu Arg Ile Leu Pro Glu Val
                -5                               1                               5
aag gta gag ggg gag ctg ggc gga tca gtt acc atc aag tgc cca ctt      269
Lys Val Glu Gly Glu Leu Gly Gly Ser Val Thr Ile Lys Cys Pro Leu
        10                               15                               20
cct gaa atg cat gtg agg ata tat ctg tgc cgg gag atg gct gga tct      317
Pro Glu Met His Val Arg Ile Tyr Leu Cys Arg Glu Met Ala Gly Ser
        25                               30                               35
gga aca tgt ggt acc gtg gta tcc acc acc aac ttc atc aan gca gaa      365
Gly Thr Cys Gly Thr Val Val Ser Thr Thr Asn Phe Ile Xaa Ala Glu

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40		45		50		55	
tac aag ggc cga gtt	act ctg aga gca	ata ccc acg caa gaa	tct gtt	413			
Tyr Lys Gly Arg Val	Thr Leu Arg Ala	Ile Pro Thr Gln Glu	Ser Val				
	60	65	70				
cct agt gga ggt aac	aca gct gac aga	aag tgacagcgga	g	454			
Pro Ser Gly Gly	Asn Thr Ala Asp	Arg Lys					
	75	80					

<210> 775
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..253

<221> sig_peptide
 <222> 8..109
 <223> Von Heijne matrix
 score 6.19999980926514
 seq MAVLAPLIALVYS/XP

<400> 775	
agtcggtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca	49
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala	
	-30 -25
gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct	97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala	
	-20 -15 -10 -5
ctc gtg tat tcg gys ccg cga ctt tca cga tgg ctc gcc caa cct tac	145
Leu Val Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr	
	1 5 10
tac ctt ctg tcg scc ctg ctc tct gmt gcc ttc cta ctc gtg agg maa	193
Tyr Leu Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa	
	15 20 25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa smc ggt aac	241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn	
	30 35 40
ccg tcr wsa ytt tgactgggtg agcctccgc gtgtagtac ccgcgcgacsk	293
Pro Ser Xaa Xaa	
45	
tgactgtscg tgcccttgca ggtgtatctg ggaaccctgg ggtttaacctc totgaggaca	353
cctgaggttc cgagcctgta gcggacttag agactattaw ktgcaggggtc cgaaccatca	413
tcgagtctaa actttgtgtt taagatggga aaacgggaaca tgtagtgcgt agcccatgca	473
caacggccca acagcttttg actgttgagt ccaggtttct ttctgtttca ccattgag	531

<210> 776
 <211> 368
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 220..363

<221> sig_peptide

<222> 220..270

<223> Von Heijne matrix

score 6

seq WLSCFLLPALVVS/VA

<221> misc_feature

<222> 201

<223> n=a, g, c or t

Oligonucleotide

<400> 776

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agaggggtgcc cacctgtgtg ccagcgctg tccggcgctt gcctgcggcc tccgtggcga      60
aggggacaca gaaataactca ctgagcctac actgggctca gcctgtgctt ggtcctgggg      120
tcacaaaggt gcatcagacg cagaccttgc cctcacatct cttctggcct ggtgggagag      180
gctcatctgc aaagagataa ngaggtcctt gcggatgtg atg gcc cag cta tgg      234
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Met Ala Gln Leu Trp

-15

```
ctg tcc tgc ttc ctc ctt cct gcc ctc gtg gtg tct gtg gca gcc aac      282
Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val Ser Val Ala Ala Asn
```

-10

-5

1

```
gtg gcc cck wag ttc cta gcc aac atg acg tca gtg atc ctg cct gag      330
Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser Val Ile Leu Pro Glu
5          10          15          20
```

```
gac tgc ctg tgg gtg ccc agg cct tct ggt tgg tagcg      368
Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp
```

25

30

<210> 777

<211> 469

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 8..322

<221> sig_peptide

<222> 8..109

<223> Von Heijne matrix

score 5.90000009536743

seq MAVLAPLIALVYS/VP

<221> misc_feature

<222> 233,352

<223> n=a, g, c or t

Oligonucleotide

<400> 777

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agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca      49
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala
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-30

-25

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gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct      97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-20          -15          -10          -5
ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac      145
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
          1          5          10
tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa      193
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
          15          20          25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gar nac ggt aac      241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn
          30          35          40
ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt      289
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
          45          50          55          60
gcc att gtg atg atg aag aac cgc aga tcc agc tgaatttgaa cttggacttc      342
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ser
          65          70
tatcccytmn gwgtctccta tttcaaagtg ccccatgaag agggacaaag aatgggatat      402
aggagtgcac agcccagcct gacctgtgac atctctgtgt ttcagtcact gtggagcaac      462
atatagg      469

<210> 778
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..340

<221> sig_peptide
<222> 77..133
<223> Von Heijne matrix
      score 5.90000009536743
      seq AFLVCLAFSLATL/VQ

<400> 778
agctcckcct cggcctcccc ttcgggcgct ctgcgcgttaa ctgtgctcct ccggggccct      60
ccgcctgctc ccagcc atg gtg gcc tgg cgc tcg gcg ttc ctt gtc tgc ctc      112
      Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu
          -15          -10
gct ttc tcc ttg gcc acc ctg gtc cag cga gga tct ggg gac ttt gat      160
Ala Phe Ser Leu Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp
          -5          1          5
gat ttt aac ctg gag gat gca gtg aaa gaa act tcc tca gta aag cag      208
Asp Phe Asn Leu Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln
          10          15          20          25
cca tgg gac cac acc acc acc aca acc aat agg cca gga acc acc      256
Pro Trp Asp His Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr
          30          35          40
aga gct ccg gca aaa cct cca ggt agt gga ttg gac ttg gct gat gct      304
Arg Ala Pro Ala Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala
          45          50          55

```

ttg gat gat caa gat gat ggc cgc aga aac cgg gta taggaggaag 350
 Leu Asp Asp Gln Asp Asp Gly Arg Arg Asn Arg Val

60 65
 agagagatgg aaccatgtaa ccaccacgac caagaggcca gtaaccacca gagctccagc 410
 aaatacttta ggaaatgatt ttgacttggc tgatgcctgg atgatcgaaa tgatcgag 468

<210> 779
 <211> 479
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 73..429

<221> sig_peptide
 <222> 73..231
 <223> Von Heijne matrix
 score 5.80000019073486
 seq ILSLQVLLTTVTS/TV

<400> 779
 gctctctcgc ggaastgggg aggaggcggg tgcggtagt ggaccgggac cggtaggggt 60
 gctgttgcca tc atg gct gac ccc gac ccc cgg tac cct cgc tcc tcg atc 111
 Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile
 -50 -45

gag gac gac ttc aac tat ggc agc agc gtg gcc tcc gcc acc gtg cac 159
 Glu Asp Asp Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His
 -40 -35 -30 -25
 atc cga atg gcc ttt ctg aga aaa gtc tac agc att ott tct ctg cag 207
 Ile Arg Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln
 -20 -15 -10

gtt ctc tta act aca gtg act tca aca gtt ttt tta tac ttt gag tct 255
 Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser
 -5 1 5

gta cgg aca ttt gta cat gag agt cct gcc tta att ttg ctg ttt gcc 303
 Val Arg Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala
 10 15 20

ctc gga tct ctg ggt ttg att ttt gcg ttg ayt tta aac aga cat aag 351
 Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys
 25 30 35 40

tat ccc ctt aac ctg tac cta ctt ttt gga ttt acg ctg ttg gaa gct 399
 Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala
 45 50 55

ctg act gtg gca gtt gtk gtt act gtt cta tgatgtatat attattctgc 449
 Leu Thr Val Ala Val Val Val Thr Val Leu
 60 65

aagctttcat actgactact acagtatttt 479

<210> 780
 <211> 504
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 <213> Homo sapiens

<220>

<221> CDS

<222> 112..423

<221> sig_peptide

<222> 112..276

<223> Von Heijne matrix

score 5.59999990463257

seq ELCCLFCCPPCPG/KI

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tcccctcattc cttttgcctg ctcccgccga ggggtggctt tgatttcggc g atg agc 117
Met Ser
-55

tcc cag aaa ggc aac gtg gct cgt tcc aga cct cag aag cac cag aat 165
Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His Gln Asn
-50 -45 -40

acg ttt agc ttc aaa aat gac aag ttc gat aaa agt gtg cag acc aag 213
Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln Thr Lys
-35 -30 -25

agc atg aat aat ctt tca ttt agt gag cta tgt tgc ctc ttc tgc tgt 261
Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys
-20 -15 -10

cca cct tgt cca ggg aag att gct tca aaa tta gcg ttt ttg cca cct 309
Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro
-5 1 5 10

gat cca act tac aca ctg atg tgt gat gaa agc gga agc gtt gga ctt 357
Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val Gly Leu
15 20 25

tac atc tgt ctg aac gag cag act ggc agt att ctt cta gag aaa aag 405
Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu Lys Lys
30 35 40

atg cta ttg agt gtt tca tgactagaac cagtaaaggc aacagaattg 453
Met Leu Leu Ser Val Ser
45

cttgtatggt tgtacgttgt tcaccaatg cgaaatacac tttactcttc t 504

<210> 781

<211> 544

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 102..479

<221> sig_peptide

<222> 102..287

<223> Von Heijne matrix

score 5.59999990463257

seq VIYLLILLTAGAGL/LV

<221> misc_feature

<222> 521

<223> n=a, g, c or t
Oligonucleotide

<400> 781

agctgcagtg gttc gatggg aaggatcttt ctccaagtgg ttctctttga ggggagcatt 60
tctgctggct ccaggacttt ggccatctat aaagcttggc a atg aga aat aag aaa 116
Met Arg Asn Lys Lys

-60

att ctc aag gag gac gag ctc ttg agt gag acc caa caa gct gct ttt 164
Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr Gln Gln Ala Ala Phe

-55

-50

-45

cac caa att gca atg gag cct ttc gaa atc aat gtt cca aag ccc aag 212
His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn Val Pro Lys Pro Lys

-40

-35

-30

agg aga aat ggg gtg aac ttc tcc cta gct gtg gtc atc tac ctg 260
Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val Val Val Ile Tyr Leu

-25

-20

-15

-10

atc ctg ctc acc gct ggc gct ggg ctg ctg gtg gtc caa gtt ctg aat 308
Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val Val Gln Val Leu Asn

-5

1

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ctg cag gcg cgg ctc cgg gtc ctg gag atg tat ttc ctc aat gac act 356
Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr Phe Leu Asn Asp Thr

10

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20

ctg gcg gct gag gac agc ccg tcc ttc tcc ttg ctg cag tca gca cac 404
Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His

25

30

35

cct gga gaa cac ctg gct cag ggt gca tcg agg ctg cag tcc tgc agg 452
Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg Leu Gln Ser Cys Arg

40

45

50

55

ccc aac tca cct ggg tcc gcg tca sca tgagcacttg ctgcagcggg 499
Pro Asn Ser Pro Gly Ser Ala Ser Xaa

60

tagacaactt cactcagaak cnacggatgt tcagaatcaa aaggt 544

<210> 782

<211> 455

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 27..428

<221> sig_peptide

<222> 27..194

<223> Von Heijne matrix
score 5.30000019073486
seq LAKLLPLPAITS/QL

<400> 782

aagagaggaa aaaaaatagc aggaag atg gcg ccc acc aag ccc agc ttt cag 53
Met Ala Pro Thr Lys Pro Ser Phe Gln
-55 -50

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cag gat cct tcc agg cga gaa cgt tta caa gca ttg aga aag gag aaa      101
Gln Asp Pro Ser Arg Arg Glu Arg Leu Gln Ala Leu Arg Lys Glu Lys
      -45                      -40                      -35

tcc cga gat gct gct cgc tcc cgc cgg gga aaa gaa aac ttt gag ttc      149
Ser Arg Asp Ala Ala Arg Ser Arg Arg Gly Lys Glu Asn Phe Glu Phe
      -30                      -25                      -20

tat gaa ttg gcc aag ttg ttg cct ctt cct gca gcc att acc agc cag      197
Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ala Ala Ile Thr Ser Gln
      -15                      -10                      -5                      1

ctc gac aag gca tcc atc att cga ctt aca att agc tat ctg aaa atg      245
Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Ile Ser Tyr Leu Lys Met
      5                      10                      15

agg gac ttt gct aac cag ggg gac cct ccg tgg aac ttg cga atg gaa      293
Arg Asp Phe Ala Asn Gln Gly Asp Pro Pro Trp Asn Leu Arg Met Glu
      20                      25                      30

ggc cct cca cct aac aca tca gta aaa gtt ata ggt gca cag cga agg      341
Gly Pro Pro Pro Asn Thr Ser Val Lys Val Ile Gly Ala Gln Arg Arg
      35                      40                      45

aga agc ccc agt gca cta gcc att gaa gta ttt gaa gca cat ttg gga      389
Arg Ser Pro Ser Ala Leu Ala Ile Glu Val Phe Glu Ala His Leu Gly
      50                      55                      60                      65

agc cac att ttg cag tcc tgg atg gct ttg tat ttg cac taaatcagga      438
Ser His Ile Leu Gln Ser Trp Met Ala Leu Tyr Leu His
      70                      75

aggaaaattt ttgtaca      455

<210> 783
<211> 453
<212> DNA
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<221> sig_peptide
<222> 85..144
<223> Von Heijne matrix
      score 5
      seq ALLSVCSTDVTTA/HA

<221> misc_feature
<222> 284
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      Oligonucleotide

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agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg      111
      Met Glu Glu Leu Gln Asp Gln Ala Leu
      -20                      -15

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg      159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr
      -10                      -5                      1                      5

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gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag	208
Val Leu Val	
aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag	268
gagtaaagtg gacacntcag ctgggtccct gggtcgtcca cccgatgtcc cccattctcc	328
ccacttggcc tccccacag gctctcgga aaggaccgtg ggaggcacct gtgacactgc	388
ccttttctg tgcagctgtt tktctcttc attctttca ctctctgtta ctctttttt	448
tttca	453

<210> 784
 <211> 587
 <212> DNA
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 score 5
 seq ALLSVCSTDVTTA/HA

<400> 784	
ccccttgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg	60
agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg	111
Met Glu Glu Leu Gln Asp Gln Ala Leu	
-20 -15	

ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg	159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr	
-10 -5 1 5	

gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag	208
Val Leu Val	
aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag	268
gagtaaagtg gacacctcag caaagccatt cgctgtgate tctgattgtg cagtgtcatg	328
tctgtcacc agagccccct cgtgtttgrk gttggccaat gccgccagca tgatctagca	388
ggccaaatcc taatctacca ttctctgaca ccagctggtc ccctgggtcg tccaccgat	448
gtcccccatc ctccccactt ggctcccccc acaggetctc ggcaaaggac cgtgggaggc	508
acctgtgaca ctgccctttt cctgtgcagc tgtttktctt cttcattctt ttcactctc	568
gttactcttt tttttttca	587

<210> 785
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 250..390

<221> sig_peptide
 <222> 250..384
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 score 4.80000019073486

seq ICCAAAAAAAAAGS/RI

<221> misc_feature

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Oligonucleotide

<400> 785

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cgtctcctcc cttgctcccc ttcttcaccc caatccctac agcctcccgc gcasctgagc     120
tctaggattg tgggttttcc atcctccgaa gacatcacct ttgctcatct cccaggagag     180
tctcgtccaa aggagggggg tgctttctgc ttcagcanga tccaccccac cctgggatcc     240
gagggagca atg gtg ggg cga gtg agg gtc tgc cgt aaa tat ccc ccg acc     291
      Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr
      -45              -40              -35
acc ctc tgg gaa ggt gct aga ggc cac agg caa att tca gtc tcc cca      339
Thr Leu Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro
      -30              -25              -20
tgg aat atc tgc tgt gct gct gct gct gct gct gct gct ggg tca agg      387
Trp Asn Ile Cys Cys Ala Ala Ala Ala Ala Ala Ala Gly Ser Arg
      -15              -10              -5              1
ata tgagcgagcc tcttcyaaa acagccggga aggagagga atccaagagg      440
Ile
aggagcaggt gggaaagaca a      461
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<210> 786

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score 3.90000009536743
seq LCCGLSMFEVILT/RI

<400> 786

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cattttctgc tctgcgactc cttttgcaga gggggagcgc ctggaggtcc gg atg aaa      58
      Met Lys
cgt ctg gaa gcc aag tat gcc ccg ctc cac ctg gtc cct ctg atc gag      106
Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu Ile Glu
      -50              -45              -40              -35
cgg ctg ggg acc cct cag caa atc gcc att gct cgc gag ggt gac ctc      154
Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly Asp Leu
      -30              -25              -20
ctg acc aag gag cgg ctg tgc tgt ggc ctg tcc atg ttc gag gtc atc      202
Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu Val Ile
      -15              -10              -5
ctg acc cgc att cgg agc tac ctg cag gac ccc atc tgg cgg ggc cca      250
Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg Gly Pro
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ccg ccc acc aat ggc gtc atg cac gtc gat gag tgt gtg gag ttc cac			298
Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu Phe His			
15	20	25	30
cgg ctg tgg agc gcc atg cag ttc gtg tac tgc atc cct gtg gga acc			346
Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val Gly Thr			
	35	40	45
aac gag ttc aca gct gag cag tgt ttc ggc gat ggc ttg aac tgg gct			394
Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn Trp Ala			
	50	55	60
ggt tck ccr kca ttg tcc tgc tsg gcc agc agc gtc gct ttg acc tgt			442
Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu Thr Cys			
	65	70	75
tcg act tct gtt acc acc tgc taaaagtgca gaggcaggac gggaag			489
Ser Thr Ser Val Thr Thr Cys			
80	85		

<210> 787
 <211> 397
 <212> DNA
 <213> Homo sapiens

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ccctcacgcc cgccctcctt gccgccagc cggccaggc ctctggcgaa c atg gcg	57
	Met Ala
	-70
ott gtc ccc tgc cag gtg ctg cgg atg gca atc ctg ctg tcy tac tgc	105
Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser Tyr Cys	
	-65 -60 -55
tct atc ctg tgt aac tac aag gcc atc gaa atg ccc tca cac cag acc	153
Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His Gln Thr	
	-50 -45 -40
tac gga ggg agc tgg aaa ttc ctg acg ttc att gat ctg gtt atc cag	201
Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val Ile Gln	
	-35 -30 -25
gct gtc ttt ttt ggc atc tgt gtg ctg amt gat ott tcc agt ctt ctg	249
Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser Leu Leu	
	-20 -15 -10
act cga gga agt ggg aac cag gar caa gag agg cag ctc aag aag ctc	297
Thr Arg Gly Ser Gly Asn Gln Glu Gln Arg Gln Leu Lys Lys Leu	
	-5 1 5 10
atc tct ctc cgg gac tgg atg tta gct gtg ttg gct ttc ctg ttg ggg	345
Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu Leu Gly	
	15 20 25

ttt ttg ttg tagcagtgtt ctgggtcatt tatgcctatg acagmgagat gat 397
Phe Leu Leu
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<210> 788
<211> 595
<212> DNA
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<221> CDS
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<221> sig_peptide
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score 3.70000004768372
seq ALTGSQLLGDTIP/RP

<400> 788
ctctctgtcc cctccccct cctgtcctt atctttccct tctgtctcc atg gcg act 58
Met Ala Thr
cac cac ctc ggc ttg cct gca tcc cag cct ctg cca ggg att ctg agc 106
His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly Ile Leu Ser
-65 -60 -55
cgg gct cca tcc ctc cct cct cgg agc cct gct acc cgc agc cgt gtc 154
Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg Ser Arg Val
-50 -45 -40 -35
tcc tcc ccc tgg ggt gag tcc agc agc agc ctc ctc ttt cct gac tgt 202
Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe Pro Asp Cys
-30 -25 -20
cac att tct ttt cca gct ctg acc ggg agt cag ctc ctc ggg gat acc 250
His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu Gly Asp Thr
-15 -10 -5
atc ccc cga cct cac ctt cca cct acc gca gcc tgc tagcctttcc 296
Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
1 5 10
gggagaaaag gcaccccttac ctctgggtga aggtctcggg gcctccccct ctgcacccgg 356
accctctccc catcccagcc tcccatgcca aggcccgct tgtcagtcac ttccttttgt 416
catcggcttg gcaaacggga gagaaaacag agcttcatgg gaaacagcgg caacagtgg 476
cccatacacc tttccccaag ttggagctag gcctggggcc ccagcccatg gygccccggg 536
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<210> 789
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<221> sig_peptide
<222> 21..125

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      -60      -55      -50
agt ctt ggg gcc cgc ttc tac cgg cag atc aaa aga cat ccg ggg atc      194
Ser Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile
      -45      -40      -35
atc ccg atg atc ggc tta atc tgc ctg ggc atg ggc agc gct gcg ctt      242
Ile Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu
      -30      -25      -20      -15
tac ttg ctg cga ctc gcc ctt cgc agc ccc gac gtc tgg ctg gga cag      290
Tyr Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln
      -10      -5      1
aaa gaa caa ccc gga gcc ctg gaa ccg cct gag ccc caa tgaccaatac      339
Lys Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln
      5      10      15
aagttccttg cagtttccac tgactataag aagctgaaga aggaccggcc agactttctaa      399
gccaggctgg gctgccagtg ccatgcaagc cacagccagc cagcccatcc acttcttcca      459
ctcctccccg caggccccaa ggcatactc cggccancct gtcccgctac tgcttacaca      519
ggccgggttc caccsanagg ggargctgct cc      551

<210> 792
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ggaaacgcgt tttgccagtt atgcgaaaac atg gct gcg gcc ggt ttg gcc ctt      54
                        Met Ala Ala Ala Gly Leu Ala Leu
                        -15      -10
ctt kgt agg aga gtt tca tcc gcc ctg aaa tct tcc cga tcg tta ata      102
Leu Xaa Arg Arg Val Ser Ser Ala Leu Lys Ser Ser Arg Ser Leu Ile
      -5      1      5
act cct cag gtc cct gcc tgc aca ggg ttt ttt ctt agt ttg ttg ctt      150
Thr Pro Gln Val Pro Ala Cys Thr Gly Phe Phe Leu Ser Leu Leu Pro
      10      15      20
aag agt aca cca aat gtg aca tcc ttt cac caa tat aga tta ctt cat      198
Lys Ser Thr Pro Asn Val Thr Ser Phe His Gln Tyr Arg Leu Leu His
      25      30      35      40
acc aca ttg tca agg aaa gga cta gaa gaa ttt ttt gat gac cca aaa      246
Thr Thr Leu Ser Arg Lys Gly Leu Glu Glu Phe Phe Asp Asp Pro Lys
      45      50      55
aac tgg ggg caa gaa aaa gta aaa tct gga gca gca tgg acc tgt cag      294
Asn Trp Gly Gln Glu Lys Val Lys Ser Gly Ala Ala Trp Thr Cys Gln
      60      65      70
caa cta agg aac aaa agt aat gaa gat tta cac aaa ctt tgg tat gtc      342
Gln Leu Arg Asn Lys Ser Asn Glu Asp Leu His Lys Leu Trp Tyr Val

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75	80	85	
tta ctg aaa gaa aga aac atg ctt cta acc cta gag cag gag gcc aag			390
Leu Leu Lys Glu Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys			
90	95	100	
cgg car aga ttg cca atg cca agt cca gag cgg tta gat agg tagta			437
Arg Gln Arg Leu Pro Met Pro Ser Pro Glu Arg Leu Asp Arg			
105	110	115	

<210> 793
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cccgcgtac agcggggccgg gaaaagtggc actgaggctc tggaacttct gccagctct	120
ccttgtaaa atg aat gaa agt aaa cct ggt gac tca cag aac ctt gct tgt	171
Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys	
1 5 10	
gtt ttc tgt cga aaa cat gat gac tgt cct aat aaa tac gga gaa aag	219
Val Phe Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys	
15 20 25 30	
aaa act aag gag aaa tgg aat ctc act gta cat tac tac tgt ttg ttg	267
Lys Thr Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu	
35 40 45	
atg tca agt gga att tgg cag aga ggc aaa gaa gaa gaa gga gtt atg	315
Met Ser Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met	
50 55 60	
gtt ttc taatagaaga tatcaggaag gaagtgaat	350
Val Phe	

<210> 794
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<220>
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 <222> 37..273

<400> 794	
gogcatgtgc agaagggaaa cgtgaagaag gtgaag atg gcg gtg gcc agg gcc	54
Met Ala Val Ala Arg Ala	
1 5	
ggg gtc ttg gga gtc cag tgg ctg caa agg gca tcc cgg aac gtg atg	102
Gly Val Leu Gly Val Gln Trp Leu Gln Arg Ala Ser Arg Asn Val Met	
10 15 20	
ccg ctg ggc gca cgg aca gcc tcc cac atg acc aag gac atg ttc ccg	150
Pro Leu Gly Ala Arg Thr Ala Ser His Met Thr Lys Asp Met Phe Pro	
25 30 35	


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ggg ccc tat cct agg acc cca gaa gaa cgg gcc gcc gcc gcc aag aag      198
Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg Ala Ala Ala Ala Lys Lys
    40                      45                      50
tat aat atg cgt gtg gaa gac tac gaa cct tac ccg gat gat ggc atg      246
Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro Tyr Pro Asp Asp Gly Met
55                      60                      65                      70
ggg tat ggc gac ctt ttc ctg twt gtc tgatttttat tatttaaaaa      293
Gly Tyr Gly Asp Leu Phe Leu Xaa Val
    75
aatggaaaaa caaaagtgc tttttcattc aataaatgtt ccaccccttat ttagttttgt      353
tgaatcaagt cactttttac aagttttgtt tgatatgtat tttcatgctg ttaacacatt      413
tttctctgtc attatatt      431

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<210> 795
 <211> 516
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 795
agagtgcatt ccggaacccg gggcgggcg cactgcgcag gcggccggac tccgctcagt      60
ttccggtgcg gcgaacacca aagtccggga acttaagcat tttcggtttc tagggttgtt      120
acgaagctgc aggagcgag atg gag gtg gac gca ccg ggt gtt gat ggt cga      172
                Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg
                1                5                10
gat ggt ctc cgg gag cgg cga ggc ttt agc gag gga ggg agg cag aac      220
Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn
                15                20                25
ttc gat gtg agg cct cag tct ggg gca aat ggg ctt ccc aaa cac tcc      268
Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser
                30                35                40
tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtg gtg gtg ttt      316
Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe
                45                50                55
ctc ttt gtg tat ttt ttg cca tgacttggtc gctgatatct aaattaagaa      367
Leu Phe Val Tyr Phe Leu Pro
60                      65
gttggttctt gagtgaattc tgaaatggct acaaacttct tgaataaaga agacaggact      427
ctcaatagaa gaatttcaca tctccaaggg accttccttt cattttacac tttgttacta      487
atttgcagaa ctctattaat tgggtagga      516

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<210> 796
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..174

<400> 796

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cctgggttttt ttgttttttg tttgggggtat ttttgggtgt atg tat gtt tat gta      54
                                Met Tyr Val Tyr Val
                                1      5
tgt gtg tgg gta tgt gtg tat aca gtg gag agc aaa ttg gaa aac agt      102
Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser Lys Leu Glu Asn Ser
                                10      15      20
tct att tat cct cct ccc tcc cca gta gaa awa aaa aaa atc ttt aca      150
Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa Lys Lys Ile Phe Thr
                                25      30      35
ttt gtt act ttt ctt ttc ccc ccg taagacacag aattaatgga aagtgagtat      204
Phe Val Thr Phe Leu Phe Pro Pro
                                40      45
cttggatttc aaatctgaag agattttttac cattagtgggt ttgatttttaa tttgcttggt      264
taactatcat atttttcata cacttctctg gattttaaata atcttgaggt attttgccac      324
tggcttcattg ctggagtaat gggtaacata tctttgggtat ggttgcttag attaaacttac      384
ctagtcatgac ccagaagaac ttcttttact agcttgcttc ctaaagtctt ttttcctc      442
  
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<210> 797
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<400> 797
acaaacggcg ggcgcggggc cggaggaaaa agctcgccac cctgaagggt cccttcccaa      60
gcccttaggg accgcagagg acttggggac cagcaagcaa cccccagggc acgagaagag      120
ctcttgctgt ctgccstgcc tcacctgcm ccacgccagg cccgggtggc cccagctgca      180
tcaagtggag gcggaggagg aggcggagga ggggtggcacc atg ggc ccg ggc ggt      235
                                Met Gly Pro Gly Gly
                                1      5
gcc ctc cat ggg ggg atg aag aca ctg ctg cca tgg aca gcc cgt gcc      283
Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro Trp Thr Ala Arg Ala
                                10      15      20
agc cgc agc ccc taagtcaggc tctccctcag ttaccagggt ctctgtcaga      335
Ser Arg Ser Pro
                                25
gcccttggag cctgagcctg gccggggccag gatgggagtg gagagttacc tgccctgtcc      395
cctgctcccc tctaccact gtcca
                                40
  
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<210> 798
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 79..372

<221> misc_feature
 <222> 364..365
 <223> n=a, g, c or t

Oligonucleotide

<400> 798

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atggggacgg ggctgttccc ggggaggctg tgatgggttg acaggtgcgt gacagtggga      60
gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc      111
                Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala
                1          5          10

gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat      159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
                15          20          25

gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta      207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
                30          35          40

tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga      255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
                45          50          55

ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct      303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
60          65          70          75

cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc      351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
                80          85          90

cat gat tac gta nnt aac ata taattttaca aagttacact gtcagttttc      402
His Asp Tyr Val Xaa Asn Ile
                95

tgtttaacca c      413

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<210> 799

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 46..195

<400> 799

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actgcagaga accagacaat accaggttgc ttataaaagg atgcc atg tgc ttg ctg      57
                Met Cys Leu Leu
                1

gag gtc cca ggt gca acc aaa ttg ctt gca gct agg agg acc ttg aag      105
Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg Arg Thr Leu Lys
5          10          15          20

aga aat ggg atc agc ccg cca aac caa gaa ggg tta gca ctt ttg cta      153
Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu Ala Leu Leu Leu
                25          30          35

gga gag ctg acc acg cac aaa cag atg aga acc aaa acc gag      195
Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys Thr Glu
                40          45          50

tgaagaggat tgaagatgaa cccacatttt aaaagttctt gtctgctgga ggtggcatta      255
cctgtgacct cgcttcactt ctccatacat ggctgttata gcagaaaatc cagctttctg      315
aagcatatatt cagcacaatat gatgagactt atgtgatgtg agacctgaga aaactatgat      375
agamagaagc aactcaagtt gcaagg      401

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<210> 800
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 96..191

<400> 800
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 ccgaggtcac tagtttcccc gtagttcagc tgcac atg aat aga aca gca atg 113
 Met Asn Arg Thr Ala Met
 1 5
 aga gcc agt cag aag gac ttt gaa aat tca atr aat caa gtg aaa ctc 161
 Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Xaa Asn Gln Val Lys Leu
 10 15 20
 ttg aaa aag gat cca gga aac gar tgm agc taaaactcta cgcgctatat 211
 Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
 25 30
 aagcaggcca ctgaaggacc ttgtaacatg cccaaaccag gtgtatttga cttgatcaac 271
 aaggccaaat gggacgcatg gaatgccctt ggcagcctgc ccaaggaagc tgccaggcag 331
 aactatgtgg atttggtgtc cagtttgagt ccttcattgg aatcctctag tcaggtggag 391
 cctggaacag acaggaaatc aactgggttt gaaactctgg tgggtgacctc cgaagatggc 451
 atcacaaaaga tcat 465

<210> 801
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 144..317

<221> misc_feature
 <222> 583..584
 <223> n=a, g, c or t
 Oligonucleotide

<400> 801
 agtccatccc ctgtgcccgg gaaccgcggc tctgccccgc aaagggcacg cggactacaa 60
 ctcccagagt ccaactgcagc ggccaagggc tactgttccc agcgaggccc gsssggcggc 120
 accgcgaagg gaggagtggc aac atg gcg tct tcg gga gct ggt gac cct ctg 173
 Met Ala Ser Ser Gly Ala Gly Asp Pro Leu
 1 5 10
 gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act 221
 Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
 15 20 25
 cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag 269
 Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
 30 35 40
 ttg ccc agt ggc aga agg tcc tac cac ggc ggc gaa ccc gga aca tcg 317
 Leu Pro Ser Gly Arg Arg Ser Tyr His Gly Gly Glu Pro Gly Thr Ser

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Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys	Pro Trp Glu Lys
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Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro			
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Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg	
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Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu	
35 40 45	
agt gcc atg ggc ttc act gcg gcg gga atc gcc tcg tcc tcc ata gca	313
Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala	
50 55 60	
gcc aag atg atg tcc gcg gcg gcc att gcc aat ggg ggt gga gtt gcc	361
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala	
65 70 75 80	
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Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu	
85 90 95	
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Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala	
100 105 110	
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Ala Val Ile Ala Arg Phe Tyr	
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Leu Gln Ser Trp Arg Ser Lys Asp Glu Phe Cys Leu Glu Glu Ser Gly
   10           15           20

aag gct tcc tgg agg agg gaa caa tgg cat gga cct tgd dga gtc aga      209
Lys Ala Ser Trp Arg Arg Glu Gln Trp His Gly Pro Xaa Xaa Val Arg
  25           30           35           40

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Ser Phe Gln Phe Ile Pro Phe Lys His Cys Ser His Val Ala Phe Lys
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His Ser Ile Val Leu Ala Val Thr Gln Ala His Ser Ala Lys Gly Ser
   60           65           70

aca tct ttc tct gcc atg agg act tat tagtgtctga agagcttttt      352
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gcygagtggc ttgaaggacg tgtttcaaca g atg gtt ggg gtt agt gtg tgt      172
                               Met Val Gly Val Ser Val Cys
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cat cac att cga gtg ggg att aag aga agg aag gct gcc ttg ctg gag      220
His His Ile Arg Val Gly Ile Lys Arg Arg Lys Ala Ala Leu Leu Glu
   10           15           20

ctg tgt ggt ctt ctc caa gtg aga gtc gca ggc aat aga act act ttg      268
Leu Cys Gly Leu Leu Gln Val Arg Val Ala Gly Asn Arg Thr Thr Leu
   25           30           35

ctt ttg gag gaa aag mgg aat tca ttt tca gca nnc acr aga aaa gca      316
Leu Leu Glu Glu Lys Arg Asn Ser Phe Ser Ala Xaa Thr Arg Lys Ala
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gtt ttt ttt tca ggg gat ctt cac ttc tct tgaacaagga actcactcag      366
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Met Pro Ser Arg Thr Ala

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cgc tat gcc cgc tac agc cca cgg cag cgg cgg cgg cgg atg ctg gct 163
 Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg Arg Arg Arg Met Leu Ala

10 15 20

gat cgc agc gtg cgt ttc cct aat gat gtc ctg ttc ttg gac cac atc 211
 Asp Arg Ser Val Arg Phe Pro Asn Asp Val Leu Phe Leu Asp His Ile

25 30 35

cgg cag ggt gac ctg gag cag gtg ggg cgc ttc atc cgg act cgg aaa 259
 Arg Gln Gly Asp Leu Glu Gln Val Gly Arg Phe Ile Arg Thr Arg Lys

40 45 50

gtc tcc ctg gcc acc atc cac ccc tca ggc ctg gcc gcc ttg cat gaa 307
 Val Ser Leu Ala Thr Ile His Pro Ser Gly Leu Ala Ala Leu His Glu

55 60 65 70

gcc gtg ctc tct gga aac ctg gaa tgc gtg aag ctg ctg gtc aaa tac 355
 Ala Val Leu Ser Gly Asn Leu Glu Cys Val Lys Leu Leu Val Lys Tyr

75 80 85

ggg gct gac att cac cag cga gat gag gcg ggc tgg aca ccc ctg cac 403
 Gly Ala Asp Ile His Gln Arg Asp Glu Ala Gly Trp Thr Pro Leu His

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Gln Gln Leu Arg Leu Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu
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cag cca gag aca gag ttt gtc ttt cct ctg tcc cat ctg cat ctc gag      326
Gln Pro Glu Thr Glu Phe Val Phe Pro Leu Ser His Leu His Leu Glu
   30           35           40

tcg cag aga ccc ccc ata ggt agt atc tca tcc atg gaa gtg aat gtg      374
Ser Gln Arg Pro Pro Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val
   45           50           55

gac aca ctg gag caa gta gaa ctt att gac ctt ggg gac ccg gat gca      422
Asp Thr Leu Glu Gln Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala
   60           65           70           75

gca gat gtg ttc ttg cct tgc gaa gat cct cca cca acc ccc cag tcg      470
Ala Asp Val Phe Leu Pro Cys Glu Asp Pro Pro Pro Thr Pro Gln Ser
   80           85           90

tct ggg gtg gac aac cat ttg gag gag ctg agc ctg ccg gnt gcc tac      518
Ser Gly Val Asp Asn His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr
   95           100           105

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atc aga cag gac cac atc taggacctcc tctctctctc cctccgactc 566
 Ile Arg Gln Asp His Ile

110

ctccaccaac ctgcataggc caaatccaag tgatgatgga gcagatacgc ccttggcaca 626
 gtcggatgaa gaggaggaaa ggggtgatgg aggggcagag cctggagcct gcagctagca 686
 gtgggcccct gcctacagac tgaccacgct ggctattctc cacatgagac cackagccca 746
 mknnagagcc tgtcgggaga agaccagact ctttacttgc agtnnracca gaggtgggaa 806
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<210> 811

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..194

<221> misc_feature

<222> 373

<223> n=a, g, c or t

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<400> 811

aagtcacatg agccaccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag 53
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
 1 5 10

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 Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
 15 20 25

gac aca aaa tat ata tca aat ggc gac att tgg aac aac agc tgg ttt 149
 Asp Thr Lys Tyr Ile Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe
 30 35 40

ctc tgg aat att ctc aaa ctt cct gtt cag acg ctg ctt caa ggt 194
 Leu Trp Asn Ile Leu Lys Leu Pro Val Gln Thr Leu Leu Gln Gly
 45 50 55

taaacatgat gctttgaaga catatgcac attggctaca cttccatttt tgtctactgt 254
 tgttactgac aagctttttg taattgatgc tttgtattca gataatataa gcaaggaaaa 314
 ctgtgttttc agaagctcac tgattggcat agtttgtggw gttttctatc ccagttctnt 374
 ggcttttact a 385

<210> 812

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 812

Met Leu Leu Pro Leu Leu Leu Leu Leu Pro Met Cys Trp Ala Val Glu
 -10 -5 1
 Val Lys Arg Pro Arg Gly Val Ser Leu Thr Asn His His Phe Tyr Asp

	5					10				15							
Glu	Ser	Lys	Pro	Phe	Thr	Cys	Leu	Asp	Gly	Ser	Ala	Thr	Ile	Pro	Phe		
	20					25					30						
Asp	Gln	Val	Asn	Asp	Asp	Tyr	Cys	Asp	Cys	Lys	Asp	Gly	Ser	Asp	Glu		
35					40					45					50		
Pro	Gly	Thr	Ala	Ala	Cys	Pro	Asn	Gly	Ser	Phe	His	Cys	Thr	Asn	Thr		
				55					60						65		
Gly	Tyr	Lys	Pro	Leu	Tyr	Ile	Pro	Ser	Asn								
			70					75									

<210> 813
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

Met	Arg	Leu	Ser	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Trp	Ala			
	-15					-10				-5							
Ile	Pro	Gly	Gly	Leu	Gly	Asp	Arg	Ala	Pro	Leu	Thr	Ala	Thr	Ala	Pro		
1				5					10					15			
Gln	Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu		
			20					25				30					
Arg	Cys	Asp	Ala	Cys	Arg	Ala	Val	Ala	Tyr	Gln	Val	Ser	Pro	Ser	Pro		
		35				40						45					
Leu	Ser	Pro	Ala	Leu	Leu	Thr	Pro	Leu	Leu	Lys	Pro	Ala	Pro	Thr	Gly		
	50					55					60						

<210> 814
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp		
	-20						-15				-10						
Leu	Arg	Gly	Ala	Arg	Cys	Gly	Val	Gln	Met	Thr	Gln	Phe	Pro	Leu	Ser		
	-5					1				5					10		
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser		
				15					20					25			
His	Ile	Ile	Asn	Ile	Phe	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys		
			30					35					40				
Ala	Pro	Trp															

<210> 815
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<212> PRT
<213> Homo sapiens

<220>
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<222> -23..-1

<400> 815
Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu Leu
 -20 -15 -10
Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala Ala Glu
 -5 1 5
Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Xaa Arg Phe Lys Ile Glu
10 15 20 25
Gly Leu

<210> 816
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 816
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 -20 -15 -10
Leu Xaa Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Val Leu
 -5 1 5 10
Pro Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
 15 20 25
Ser Ile Gly Ser Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly His Ala
 30 35 40
Pro Arg Leu Leu Ile Tyr Ala Ala Thr Thr Leu Ser Arg Gly Gly Pro
 45 50 55
Ala Arg Phe Ser
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<210> 817
<211> 72
<212> PRT
<213> Homo sapiens

<220>
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<222> -32..-1

<400> 817
Met Ala Ala Ser Arg Trp Ala Arg Lys Ala Val Val Leu Leu Cys Ala
 -30 -25 -20
Ser Asp Leu Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Gly Ser Cys
 -15 -10 -5
Ala Gly Arg Arg Ser Pro Xaa Thr Pro Asp Glu Ser Thr Pro Pro Pro

1 5 10 15
 Arg Lys Lys Lys Lys Asp Ile Arg Asp Tyr Asn Asp Ala Asp Met Ala
 20 25 30
 Arg Leu Leu Glu Gln Gly Glu Gly
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<210> 818
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -19..-1

<400> 818
 Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu Ala Leu Leu Glu Gly
 -15 -10 -5
 Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
 15 20 25
 Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Pro
 30 35 40 45
 Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly Thr Xaa Xaa Asn Ala
 50 55 60
 Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Ser
 65 70 75
 Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val Glu Asp Thr Ala Leu
 80 85 90
 Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr
 95 100 105

<210> 819
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -19..-1

<400> 819
 Met Ala Trp Thr Pro Leu Leu Leu Leu Leu Leu Ser His Cys Thr Gly
 -15 -10 -5
 Ser Leu Ser Gln Pro Val Leu Thr Gln Pro Arg Gly
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<210> 820
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<221> SIGNAL
<222> -19..-1

<400> 820

Met	Glu	Phe	Gly	Leu	Asn	Trp	Val	Phe	Leu	Val	Ala	Leu	Leu	Arg	Gly
			-15						-10					-5	
Val	Gln	Cys	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln
			1			5						10			
Pro	Gly	Thr	Ser	Leu	Thr	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Ser	Phe
	15					20				25					
Ser	Asp	Tyr	Gly	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
30					35				40						45
Glu	Trp	Val	Ala	Val	Ile	Ser	His	Asp	Gly	Asn	Asn	Lys	Tyr	Tyr	Gly
			50					55						60	
Gly	Ser	Met	Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Arg	His
			65				70					75			
Thr	Val	Ser	Leu	Gln	Met	Ser	Ser	Leu	Gly	Pro	Glu	Asp	Thr	Ala	Val
		80				85						90			
Tyr	Tyr	Cys	Ala	Lys	Asp	Arg	Thr	Gly	Gly						
	95					100									

<210> 821
<211> 93
<212> PRT
<213> Homo sapiens

<220>
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<222> -19..-1

<400> 821

Met	Lys	Leu	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Leu	Ala	Ala	Pro	Arg	Trp
			-15						-10					-5	
Val	Leu	Ser	Gln	Val	Gln	Leu	Val	Xaa	Ser	Gly	Pro	Gly	Leu	Val	Lys
			1			5						10			
Pro	Ser	Gly	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Xaa	Gly	Xaa	Xaa	Ile
	15					20				25					
Thr	Asn	Tyr	Tyr	Trp	Ser	Xaa	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu
30					35				40						45
Glu	Trp	Ile	Gly	Thr	Ile	Tyr	Tyr	Ser	Gly	Ser	Ala	Asp	His	Asn	Pro
			50					55					60		
Ser	Leu	Arg	Ser	Arg	Ala	Thr	Ile	Ser	Leu	Asp	Thr	Arg			
			65				70								

<210> 822
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 822

Met Ala Ser Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro
 -20 -15 -10 -5
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 1 5 10
 Ala Thr Xaa Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly
 15 20 25

<210> 823
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -28..-1

<400> 823
 Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
 -25 -20 -15
 Leu Leu Leu Leu Leu Leu Pro Leu Arg Gly Gln Ala Asn Thr Gly Cys
 -10 -5 1
 Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
 5 10 15 20
 Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
 25 30 35
 Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
 40 45 50
 Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
 55 60 65

<210> 824
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 824
 Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly
 -15 -10 -5
 Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
 1 5 10
 Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val
 15 20 25
 Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Met Gly Gly Phe Asp Leu Glu Ser Gly Glu Thr Ile Tyr Ala
 50 55 60
 Gln Arg Phe Gln Gly Arg Ile Thr Met Thr Glu Asp Ser Ser Ser Asp
 65 70 75
 Thr Ala Phe Met Glu Leu Ile Ser Leu Arg Pro Glu Asp Ala Ala Val
 80 85 90

Tyr Tyr Cys Ala Thr Ile Arg Leu Pro Val Val Leu Phe Phe Ala Ala
 95 100 105
 Ser Gly Ala Arg Glu Pro Trp Ser Pro Ser Pro Gln Xaa Pro Arg
 110 115 120

<210> 825
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -18..-1

<400> 825
 Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala Val
 -15 -10 -5
 Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro Asn Pro
 1 5 10
 Phe Ser Glu Glu Arg
 15

<210> 826
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -25..-1

<400> 826
 Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu
 -25 -20 -15 -10
 Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
 -5 1 5
 Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
 10 15 20
 Ala Tyr Met
 25

<210> 827
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 827
 Met Ala Trp Thr Pro Leu Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly
 -15 -10 -5
 Ser Asn Ser Gln Ala Val Xaa Thr Gln Glu Pro Leu Thr Asp Cys Val

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 830
Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu Leu Cys Leu Ala Leu Ser
-20 -15 -10
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
-5 1 5 10
Val Xaa Val Val Leu Asp Xaa Phe Leu Val Lys Asp Xaa Ala His Arg
15 20 25
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg
30 35

<210> 831
<211> 126
<212> PRT
<213> Homo sapiens

<220>
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<222> -16..-1

<400> 831
Met Ser Met Leu Val Val Phe Leu Leu Leu Trp Gly Val Thr Trp Gly
-15 -10 -5
Pro Val Thr Glu Ala Ala Ile Phe Tyr Glu Thr Gln Xaa Ser Leu Trp
1 5 10 15
Ala Glu Ser Glu His Xaa Leu Lys Thr Leu Gly Gln Cys Asp Ala Asp
20 25 30
Val Pro Gly Pro Pro Gly Asp Ser Arg Leu Pro Ala Val Gln Glu Trp
35 40 45
Gly Ala Gln Glu Pro Val His Leu Asp Ser Pro Ala Ile Lys His Gln
50 55 60
Phe Leu Leu Thr Gly Asp Thr Gln Gly Arg Tyr Arg Cys Arg Ser Gly
65 70 75 80
Leu Ser Thr Gly Trp Xaa Gln Leu Ser Lys Leu Leu Glu Leu Thr Gly
85 90 95
Pro Lys Val Leu Ala Cys Ser Leu Ala Leu Asp Gly Ala Ser
100 105 110

<210> 832
<211> 100
<212> PRT
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<220>
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<222> -19..-1

<400> 832

Met Leu Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala
 -15 -10 -5
 Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Leu Ser Val
 1 5 10
 Thr Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Xaa Ser Ile
 15 20 25
 Gly Ser Ser Leu Tyr Trp Tyr Gln Gln Lys Pro His Gln Ser Pro Lys
 30 35 40 45
 Leu Val Ile Lys Tyr Ala Ser Gln Ser Phe Ser Gly Val Ser Ser Arg
 50 55 60
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser
 65 70 75
 Leu Glu Pro Gly
 80

<210> 833
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -20..-1

<400> 833
 Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
 -20 -15 -10 -5
 Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
 1 5 10
 Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
 15 20 25
 Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
 30 35 40
 Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
 45 50 55 60
 Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
 65 70 75
 Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
 80 85 90
 Thr Thr Asp
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<210> 834
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 834
 Met Arg Pro Gly Leu Ser Phe Leu Leu Ala Leu Leu Phe Phe Leu Gly
 -20 -15 -10 -5

Gln Ala Ala Gly Asp Leu Gly Asp Val Gly Pro Pro Ile Pro Ser Pro
 1 5 10
 Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser Phe Ser Ser
 15 20 25
 Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu Gly Ser Gly Gly
 30 35 40
 Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly Ser Val Asp Asp Arg
 45 50 55 60
 Gly Thr Cys Gln Cys Ser Val Ser Leu Pro Asp Thr Thr Phe Pro Val
 65 70 75
 Asp Arg Val Glu Arg Leu Glu Phe Thr Ala His Val Leu Ser Gln Lys
 80 85 90
 Phe Glu Lys Glu Leu Ser Lys
 95

<210> 835
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -26..-1

<400> 835
 Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
 -25 -20 -15
 Leu Val Ala Ala Pro Arg Trp Val Arg Ser Gln Val Gln Leu Xaa Glu
 -10 -5 1 5
 Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Ile Cys
 10 15 20
 Gly Val Ser Gly Asp Ser Val Thr Ile Ser Gly Trp Trp Ser Trp Val
 25 30 35
 Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Ser Glu Ile Asp His
 40 45 50
 Gly Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Xaa Ile
 55 60 65 70
 Ser Leu Asp Lys Ser Lys Asn Lys Phe Ser Leu Arg Leu Thr Ser Val
 75 80 85
 Thr Ala Ala Asp Thr Ala Met Tyr Xaa Cys Ala Arg Gly Gly Ala Xaa
 90 95 100
 Ser Ser Ser Ala Phe Asp Val Trp Gly Leu Xaa Thr Met Val Ile Ile
 105 110 115
 Ser Ser Ala
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<210> 836
 <211> 139
 <212> PRT
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<220>
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<400> 836

Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
 -15 -10 -5
 Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly Pro Ala Leu Val Lys
 1 5 10
 Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
 15 20 25
 Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 30 35 40 45
 Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Asp Tyr Lys Arg Tyr
 50 55 60
 Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
 65 70 75
 Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala
 80 85 90
 Thr Tyr Trp Cys Ala Arg Leu Ser Thr Ala Ala Thr Pro Gln Phe Phe
 95 100 105
 Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
 110 115 120

<210> 837

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 837

Met Xaa His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 1 5 10
 Pro Ser Xaa Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile
 15 20 25
 Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro
 50 55 60
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
 65 70 75
 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 80 85 90
 Tyr Cys Ala Arg Xaa Leu Xaa Tyr Tyr Asp Arg Ser Gly Tyr Phe Arg
 95 100 105
 Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Trp Ser
 110 115 120

<210> 838

<211> 136

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 838

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
				-15					-10					-5	
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys
			1			5					10				
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile
	15				20					25					
Asp	Ser	Gly	Asn	Tyr	Tyr	Trp	Ser	Trp	Ile	Arg	Gln	Pro	Ala	Gly	Lys
30				35					40					45	
Gly	Leu	Glu	Trp	Ile	Gly	Arg	Ile	Tyr	Ser	Thr	Gly	Ser	Thr	Asn	Tyr
			50					55					60		
Asn	Pro	Ser	Leu	Ser	Ser	Arg	Val	Gln	Ile	Ser	Leu	Asp	Thr	Ser	Lys
			65				70					75			
Asn	Leu	Leu	Ser	Leu	Asn	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala
	80					85					90				
Val	Tyr	Phe	Cys	Ala	Arg	Thr	Phe	Pro	Phe	Tyr	Trp	Tyr	Leu	Asp	Leu
	95					100					105				
Trp	Gly	Arg	Gly	Ile	Leu	Val	Thr								
110					115										

<210> 839
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 839

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
				-15					-10					-5	
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Arg	Leu	Val	Lys
			1			5					10				
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile
	15				20					25					
Ser	Ser	Gly	Gly	Tyr	Phe	Trp	Ser	Trp	Ile	Arg	Gln	His	Pro	Gly	Arg
30				35					40					45	
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Tyr	Asn	Trp	Ser	Thr	Tyr	Tyr
			50					55					60		
Asn	Pro	Ser	Leu	Arg	Ser	Arg	Val	Thr	Met	Ser	Met	Asp	Thr	Ser	Lys
			65				70					75			
Asn	Gln	Phe	Ser	Leu	Asn	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Xaa
	80					85					90				
Met	Tyr	Tyr	Cys	Ala	Arg	Gly	Arg	Gly	Arg	Leu	Gly	Trp	Phe	Xaa	Xaa
	95					100					105				
Xaa	Gly	Xaa	Gly	Xaa	Pro	Gly	His	Arg	Leu	Ile	Ser	Arg	Pro	Gly	
110					115					120					

<210> 840
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 840
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 1 5 10
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
 15 20 25
 Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys
 30 35 40 45
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr
 50 55 60
 Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa
 65 70 75
 Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr
 80 85 90

<210> 841
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 841
 Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys
 -15 -10 -5 1
 Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu
 5 10 15
 Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys
 20 25 30
 Phe Asp Ala Pro Arg
 35

<210> 842
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 842

Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu Leu Ser
 -15 -10 -5
 Asp Pro Val Ile Pro Gly Leu
 1 5

<210> 843
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 843
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
 Val Leu Ser Gln Val Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys
 1 5 10
 Pro Ser Glu Xaa Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val
 15 20 25
 Thr Asn Phe Phe Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Leu Gly Tyr Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro
 50 55 60
 Ala Tyr Gln Ser Arg Val Ser Ile Ser Ile Asp Thr Trp
 65 70

<210> 844
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 844
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Arg Leu Val Lys
 1 5 10
 Pro Ser Glu Ala Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Ser
 15 20 25
 Ser Asn Tyr Asp Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Ile Gly Tyr Ile Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr
 50 55 60
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser
 65 70 75
 Lys Xaa Gln Leu Ser Leu Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr
 80 85 90
 Ala Val Tyr Tyr Cys Ala Arg Lys Ser Ser Met His Ser Ser Gly Trp
 95 100 105

His Asn Arg Ser Leu Tyr Trp Tyr Phe Asp Pro
 110 115 120

<210> 845
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 845
 Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp Phe Phe Leu Leu
 -25 -20 -15
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Leu Gln Glu Ser
 -10 -5 1 5
 Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Thr Cys Ala
 10 15 20
 Val Ser Gly Gly Ser Ile Ile Ser Ser Asn Trp Trp Ser Trp Val Arg
 25 30 35
 Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Tyr Glu Asp
 40 45 50
 Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser
 55 60 65 70
 Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met Arg Ser Val Thr
 75 80 85
 Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Ser Ser Val
 90 95 100
 Arg Thr Asp Tyr Trp Gly
 105

<210> 846
 <211> 144
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 846
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Ser Gly Pro Val Asp
 1 5 10
 Xaa Xaa Gln Thr Leu Xaa Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile
 15 20 25
 Ser Ser Ser Asp Asn Cys Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
 30 35 40 45
 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr
 50 55 60
 Asn Pro Thr Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg
 65 70 75

Asn	Gln	Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Xaa	Asp	Thr	Ala
		80					85					90			
Val	Tyr	Xaa	Cys	Gly	Arg	Ala	Gln	Gly	Arg	Met	Gly	Ile	Gly	Thr	Thr
	95					100					105				
Ile	Phe	Asp	Leu	Trp	Gly	Gly	Gly	Gln	Trp	Ser	Pro	Ser	Leu	Gln	Pro
110					115					120					125

<210> 847
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

Met	Asp	Trp	Thr	Trp	Arg	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Gly
				-15					-10					-5	
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			1			5					10				
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Xaa	Phe
	15				20					25					
Thr	Xaa	Xaa	Ala	Xaa	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu
30					35				40					45	
Glu	Trp	Met	Gly	Trp	Ile	Asn	Ala	Ala	Xaa	Gly	Xaa	Thr	Xaa	Tyr	Ser
			50					55						60	
Gln	Xaa	Phe	Gln	Xaa	Arg	Val	Thr	Xaa	Thr	Arg	Asp	Thr	Ser	Ala	Ser
			65				70					75			
Thr	Val	Ser	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
	80					85					90				
Tyr	Phe	Cys	Ala	Arg	Asp	Trp	Glu	Ile	Ala	Val	Val	Pro	Thr	Ala	Ile
	95					100					105				
Asn	Ser	Tyr	Gly	Phe	Asp	Pro	Gly	Ala	Arg	Glu	Pro				
110					115					120					

<210> 848
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

Met	Glu	Ala	Arg	Val	Glu	Arg	Ala	Val	Gln	Lys	Arg	Gln	Val	Leu	Phe
	-25				-20				-15						
Leu	Cys	Val	Phe	Leu	Gly	Met	Ser	Trp	Ala	Gly	Ala	Glu	Pro	Leu	Arg
-10				-5					1					5	
Tyr	Phe	Val	Ala	Glu	Glu	Thr	Glu	Arg	Gly	Thr	Xaa	Leu	Thr	Asn	Leu
			10				15						20		
Ala	Lys	Asp	Leu												
			25												

<210> 849
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 849
 Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 -15 -10 -5
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys
 1 5 10
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
 Thr Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala
 50 55 60
 Gln Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg
 65 70 75
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile
 80 85 90
 Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu
 95 100 105
 Gly Pro Gly Asn Leu Val
 110 115

<210> 850
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 850
 Met Asp Val Leu His Lys His Met Lys His Leu Trp Phe Phe Leu Leu
 -25 -20 -15
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Glu Gln Leu Arg Gln
 -10 -5 1 5
 Trp Gly Ala Xaa Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
 10 15 20
 Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr Trp Ser Trp Ile Arg
 25 30 35
 Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly Gly Ile Asn His Ser
 40 45 50
 Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser Arg Val Asp Leu Ser
 55 60 65 70
 Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg Leu Lys Leu Val Thr
 75 80 85

Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg Pro His Tyr Asp Met
 90 95 100
 Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu Trp
 105 110

<210> 851
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 851
 Met Met Leu Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser
 -15 -10 -5 1
 Gln Gly Leu Leu Trp Phe His Thr Asn Phe Lys Val Phe Val Val Ser
 5 10 15
 Ile Cys Val Lys Thr Ile Ile Gly Ile Ser Gly Gly
 20 25

<210> 852
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 852
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 -15 -10 -5
 Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys
 1 5 10
 Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 15 20 25
 Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa Leu
 30 35 40 45
 Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly
 50 55

<210> 853
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 853
 Met Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser

-35 -30 -25
 Ile Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Leu Val Leu Ser Leu
 -20 -15 -10
 Ser Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu
 -5 1 5

<210> 854
 <211> 128
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 854
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 -15 -10 -5
 Val His Ser Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 Pro Gly Thr Pro Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe
 15 20 25
 Pro Ala Phe Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu
 30 35 40 45
 Glu Trp Met Gly Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser
 50 55 60
 Gln Lys Phe Gln Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn
 65 70 75
 Ile Val Tyr Xaa Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Ala Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp
 95 100 105

<210> 855
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 855
 Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly
 -15 -10 -5
 Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala
 5 10 15
 Pro Gly Lys Thr Ala Ser Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser
 20 25 30
 Gln Val Val His Trp His Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu
 35 40 45
 Val Ile Tyr Asp Asp Thr Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe
 50 55 60
 Ser Gly Ser Asn Ser Gly His Thr Ala Thr Leu Thr Ile Ser Arg Val

65					70					75					80
Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	Ser
				85					90					95	
Ser	Gly	Gln	Gly	Ile	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg
			100					105					110		
Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu
		115					120					125			
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr								
	130					135									

<210> 856
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 856															
Met	Arg	Leu	Leu	Phe	Leu	Leu	Leu	Phe	Val	Cys	Phe	Ser	Arg	Gln	Gly
-15					-10				-5						1
Leu	Ala	Leu	Ser	Leu	Arg	Leu	Glu	Cys	Ser	Gly	Met	Ile	Met	Ala	Tyr
		5					10					15			
Cys	Ser	Ile	Ser	Leu	Pro	Gly	Ser	Ser	Ser	Pro	Leu	Thr	Ser	Ala	Ser
		20					25					30			

<210> 857
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 857															
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ser	Ala	Pro	Arg	Trp
			-15						-10				-5		
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys
		1				5					10				
Pro	Ser	Gly	Arg	Leu	Ser	Leu	Ala	Cys	Asp	Val	Val	Glu	Leu	Ser	Pro
	15					20				25					
Pro	Ala	Pro	Arg	Gly	Gly	Ser	Ala	Val	His	Leu	Arg	Asn	Leu	Ser	Ser
30				35					40					45	
Trp	Glu	Pro	His	Leu	Gln	Pro	Val	Ser	Gly						
			50					55							

<210> 858
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -32..-1

<400> 858

Met	Thr	Tyr	Phe	Pro	Leu	Gly	Arg	Tyr	Pro	Val	Met	Gly	Leu	Leu	Asp
		-30				-25					-20				
Gln	Met	Val	Val	Val	Phe	Leu	Leu	Leu	Leu	Val	Ser	Thr	Leu	Ser	Ser
	-15					-10				-5					
Val	Val	Val	Leu	Leu	Val	Cys	Ile	Pro	Thr	Ser	Ser	Val	Lys	Leu	Phe
1			5					10					15		
Pro	Phe	His	His	Ile	His	Thr	Asn	Trp							
		20				25									

<210> 859

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 859

Met	Glu	Phe	Gly	Leu	Ser	Trp	Val	Leu	Leu	Val	Ala	Met	Leu	Arg	Gly
			-15				-10			-5					
Leu	Gln	Cys	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Thr	Ala		
	1				5			10							

<210> 860

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 860

Met	Tyr	Leu	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Glu	Asn	Val	Ser	Gly	Phe
-15				-10				-5						1	
Pro	Phe	Pro	Leu	Ile	Phe	Gln	Leu	His	Ala	Ser	Pro	Gly	His	Lys	Ile
		5				10						15			
Leu	Pro	Asp	Cys	Met	Ile	Tyr	Ser	Ile	Thr	Val	Ser	Leu	Met	Phe	Pro
	20				25						30				
Val	Val	Asp	Tyr	Ile	Ser	Thr	Gln	Gly							
	35				40										

<210> 861

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 861

Met Met Arg Ala Phe Tyr Leu Ala Ile Leu Phe Cys Leu Ser Leu Ser
-25 -20 -15
Leu Trp Phe Xaa Cys Leu Leu Phe Leu Leu Phe Ala Trp Pro Gly
-10 -5 1

<210> 862

<211> 102

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 862

Met Ala Trp Thr Pro Leu Leu Phe Leu Thr Leu Leu Leu His Cys Thr
-20 -15 -10 -5
Gly Ser Leu Ala Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala
1 5 10
Ser Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gly His
15 20 25
Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro
30 35 40
Arg Phe Leu Met Lys Val Asn Ser Asp Gly Ser His Met Lys Ala Asp
45 50 55 60
Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr
65 70 75
Leu Ser Ile Ser Ser Leu
80

<210> 863

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 863

Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val Ala Leu Ala Ile Gln
-10 -5 1
Gly Gln

<210> 864

<211> 129

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 864

Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa
50 55 60
Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
65 70 75
Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr
95 100 105
Trp
110

<210> 865

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 865

Met Asp Leu Met Cys Lys Lys Met Arg His Leu Trp Phe Leu Leu Leu
-25 -20 -15
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu Gln Leu Gln Glu
-10 -5 1 5
Ser Gly Pro Gly Leu Val Lys Ala Ser Glu Thr Leu Ser Leu Ala Cys
10 15 20
Ser Val Ser Gly Asp Ser Ile Ser Ser Gly Asn Tyr Tyr Trp Gly Trp
25 30 35
Ile Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Leu Gly Ser Leu Trp
40 45 50
Asn Arg Gly Gly Pro Gln Tyr Asn Xaa Ser Leu Lys Asn Arg Val Thr
55 60 65 70
Val Ser Val Asp Thr Ser Thr Asn His Phe Phe Leu Arg Leu Asn Ser
75 80 85
Val Asn Xaa Gly His Gly Asn Leu Leu Cys Ala
90 95

<210> 866

<211> 32

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 866
 Met Arg Xaa Xaa Leu Xaa Leu Ser Val Leu Leu Gly Xaa Xaa Xaa Xaa
 -15 -10 -5
 Lys Xaa Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp
 1 5 10 15

<210> 867
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1
 <400> 867
 Met Ala Glu Ser Arg Glu Glu Gly Glu Ser Cys Val Glu Ser His Cys
 -35 -30 -25
 Val Leu Phe Phe Thr Leu Phe Phe Leu Leu Phe Phe Cys Phe Val Phe
 -20 -15 -10 -5
 Cys Leu Arg Gly Gln Gly
 1

<210> 868
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 868
 Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val Ala Phe Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Ser Tyr Ala Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ser Gly Ile Ser Ala Gly Ala Asp Asp Thr Tyr Asp Ala
 50 55 60
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Lys
 65 70 75
 Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg
 80 85 90

<210> 869
 <211> 60

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 869
Met Ala Val Ser Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 -20 -15 -10
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 -5 1 5
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
10 15 20 25
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
 30 35

<210> 870
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 870
Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
 -20 -15 -10
Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
 -5 1 5
Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
10 15 20
His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
25 30 35 40
Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
 45 50 55
Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
 60 65 70
Gln His Glu Ile Asn Leu Ile Ala Tyr Arg
75 80

<210> 871
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 871
Met Val Val Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys
 -25 -20 -15

Leu Leu Leu Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys
 -10 -5 1 5
 Asp Arg Ala Thr Cys
 10

<210> 872
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 872
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
 15 20 25
 Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala
 50 55 60
 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Xaa Ser Thr Xaa
 65 70 75
 Thr Xaa Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Xaa
 80 85 90
 Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu
 95 100 105
 Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro
 110 115 120

<210> 873
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 873
 Met Thr Tyr Ser Tyr Ser Phe Phe Arg Pro Glu Leu Ile Val Asn His
 -45 -40 -35 -30
 Leu Asn Tyr Val His Ser Glu Ala Asn Arg Arg Thr Lys Thr Lys Thr
 -25 -20 -15
 Leu Leu Ser Leu Leu Ser Phe Leu Asp Glu Thr Ser Gly Leu Ser Thr
 -10 -5 1
 His Leu Pro Cys Leu Ser Leu Ser Lys Glu Cys Gly Val Leu His Leu
 5 10 15
 Asp Ile His Gly Lys Lys Glu Asp Met Arg Asp Glu Val Leu Leu Ala
 20 25 30 35

Leu Asn Xaa Cys Thr His Arg
40

<210> 874
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 874
Met Lys Ser Phe Ser Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly
-15 -10 -5
Leu Arg Ser Lys Ala Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly
1 5 10
Phe Pro Asp Met Ala His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala
15 20 25
Ser Glu Asn Ser Lys Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr
30 35 40 45
Pro Tyr Pro Glu Pro Ser Lys Leu Pro His Thr Val Ser Leu Glu
50 55 60

<210> 875
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 875
Met Arg Val Pro Ile Phe Pro His Pro His Gln Leu Ser Leu Leu Phe
-40 -35 -30
Ile His Leu Phe Ile Tyr Leu Phe Arg Glu Arg Val Ser Leu Cys His
-25 -20 -15 -10
Leu Gly Trp Ser Ala Val Val Gln Ser Gln Pro Thr Thr Thr Leu Thr
-5 1 5
Ser Arg Ala
10

<210> 876
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 876
Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn Leu Gly Ser Ser Tyr

-35 -30 -25
 Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe Val Leu Phe Cys Phe
 -20 -15 -10
 Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser Gly
 -5 1 5

<210> 877
 <211> 26
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 877
 Met His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly
 -15 -10 -5
 Ala Val Phe Leu Thr Val Pro Ser Pro Gln
 1 5 10

<210> 878
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 878
 Met Ala Trp His Pro Thr Pro Pro Pro Leu Xaa Xaa Pro Pro Pro Leu
 -35 -30 -25
 Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp Ser Ile Ile Leu Xaa Leu
 -20 -15 -10
 Xaa Phe Pro Gly Ile Leu Gly Gln Ala His Leu Xaa Ser Glu Gln Trp
 -5 1 5
 Thr Gln Tyr Leu
 10

<210> 879
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 879
 Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile Leu Leu Ser
 -20 -15 -10
 Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu Ser Pro Leu
 -5 1 5 10

Leu Gly Leu Lys Cys
15

<210> 880
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 880
Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
-20 -15 -10 -5
Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Asp Glu Asp
1 5 10
His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
15 20 25
Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
30 35 40
Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr
45 50 55 60
Gln Asn Cys Ser His
65

<210> 881
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 881
Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala Lys
-15 -10 -5 1
Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu Lys
5 10 15
Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp
20 25 30
Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser His
35 40 45
Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln Cys
50 55 60 65
Tyr Ser Arg Val Val His Cys Ser
70

<210> 882
<211> 95
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 882

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
				-15					-10					-5	
Ala	Met	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Arg	Leu	Val	Lys
		1				5					10				
Pro	Ser	Gly	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Met
	15					20					25				
Ala	Thr	Ser	Asp	Trp	Trp	Ser	Trp	Phe	Arg	Gln	Thr	Pro	Glu	Lys	Gly
30					35					40					45
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Phe	Gln	Thr	Gly	Pro	Thr	Asn	Tyr	Asn
				50					55					60	
Pro	Ser	Leu	Lys	Ser	Arg	Val	Ser	Met	Ser	Val	Asp	Met	Ser	Lys	
			65					70						75	

<210> 883
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 883

Met	Asp	Leu	Thr	Cys	Lys	Lys	Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu
	-25					-20					-15				
Leu	Val	Ala	Ala	Pro	Arg	Trp	Ala	Leu	Ser	Gln	Leu	Gln	Leu	Gln	Glu
-10					-5					1				5	
Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys
			10					15					20		
Thr	Val	Ser	Gly	Glu	Ser	Ile	Thr	Thr	Asn	Ser	Phe	Cys	Trp	Ala	Trp
		25					30					35			
Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Thr	Val	Cys
	40					45					50				
Tyr	Gly	Gly	Thr	Thr	Tyr	Xaa	Asn	Xaa	Ser	Leu	Lys	Ser	Arg	Val	Lys
55					60					65					70
Leu	Ser	Leu	Asp	Thr	Ser	Thr	Asn	Gln	Phe	Ser	Leu	Lys	Val	Thr	Ser
				75					80					85	
Met	Thr	Ala	Gly	Asp	Ala	Ala	Val	His	Tyr	Cys	Ala	Gly	Leu	Arg	Val
			90					95					100		

Ser

<210> 884
 <211> 66
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -63..-1

<400> 884

Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr
-60 -55 -50
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys
-45 -40 -35
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala
-30 -25 -20
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala
-15 -10 -5 1
Ser Pro

<210> 885

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 885

Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-15 -10 -5
Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
15 20 25
Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
30 35 40 45
Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
50 55 60
Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg
65 70 75
Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr
95 100 105
Gln Xaa Thr Leu Trp
110

<210> 886

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 886

Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu Leu Leu Ser Ala Phe
-20 -15 -10
Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys Gly Pro Arg

-5

1

5

<210> 887
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 887
Met Lys His Leu Gly Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys
 1 5 10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
 15 20 25
Ser Ser Asp Asp Leu Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
30 35 40 45
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr
 50 55 60
Asn Pro Ser Leu Lys Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys
 65 70 75
Asn Gln Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Met Ala
 80 85 90
Val Tyr Tyr Cys Ala Thr Ser Val Met Xaa Ser Phe Gly Gly Val Leu
 95 100 105
Val Pro Asn Leu Phe Leu Thr Thr Gly Ala Arg Glu Ser Arg
110 115 120

<210> 888
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 888
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Gly Pro Arg Trp
 -15 -10 -5
Val Leu Ser Gln Val Gln Leu Xaa Glu Ser Gly Pro Arg Leu Val Lys
 1 5 10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Val
 15 20 25
Ser Ser Arg Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Leu Pro Gly Lys
30 35 40 45
Gly Leu Glu Trp Ile Gly Tyr Ile Xaa Tyr Thr Gly Ser Thr Phe Tyr
 50 55 60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys
 65 70 75
Asn Gln Phe Ser Leu Asn Leu Arg Ser Val Thr Thr Ala Asp Thr Ala

Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly Leu Leu Val
 -25 -20 -15
 Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser
 -10 -5 1

<210> 892
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 892
 Met Ser Pro Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu
 -15 -10 -5 1
 Pro Gly Ser Ala Xaa Ala Xaa Ser Ala Ser Leu Gly Gln Phe Ser Met
 5 10 15
 Cys Gly Arg Cys Pro Thr Cys Pro Gly Asn Gly Pro Leu Arg Thr Pro
 20 25 30
 Ala Ala Thr Xaa Xaa Xaa Val Pro Gly His Val Asp
 35 40 45

<210> 893
 <211> 154
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 893
 Met Ala Thr Ala Met Asp Trp Leu Pro Trp Ser Leu Leu Leu Phe Ser
 -20 -15 -10
 Leu Met Cys Glu Thr Ser Ala Phe Tyr Val Pro Gly Val Ala Pro Ile
 -5 1 5
 Asn Phe His Gln Asn Asp Pro Val Glu Ile Lys Ala Val Lys Leu Thr
 10 15 20 25
 Ser Ser Arg Thr Gln Leu Pro Tyr Glu Tyr Tyr Ser Leu Pro Phe Cys
 30 35 40
 Gln Pro Ser Lys Ile Thr Tyr Lys Ala Glu Asn Leu Gly Glu Val Leu
 45 50 55
 Arg Gly Asp Arg Ile Val Asn Thr Pro Phe Gln Val Leu Met Asn Ser
 60 65 70
 Glu Lys Lys Cys Glu Val Leu Cys Ser Gln Ser Asn Lys Pro Val Thr
 75 80 85
 Leu Thr Val Glu Gln Ser Arg Leu Val Ala Glu Arg Ile Thr Glu Asp
 90 95 100 105
 Tyr Tyr Val His Leu Ile Ala Asp Asn Leu Pro Val Ala Thr Gly Trp
 110 115 120
 Ser Ser Thr Pro Thr Glu Thr Ala Met Thr
 125 130

<210> 894
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 894
 Met Pro Ser Pro Cys Leu Ile Ser Leu Leu Gln Cys Ala His Val Ser
 -15 -10 -5
 Leu Gly Leu Gln Tyr Pro Cys Xaa Leu Leu Leu Pro
 1 5 10

<210> 895
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 895
 Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 -15 -10 -5
 Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
 1 5 10 15
 Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
 20 25 30
 Arg Ala Ala Trp Glu
 35

<210> 896
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 896
 Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Ile Phe Thr Gly
 -15 -10 -5
 Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln
 1 5 10
 Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
 15 20 25
 Gly Asp Tyr Ala Met Thr Trp Phe Arg Gln Ala Ser Gly Lys Arg Leu
 30 35 40 45
 Glu Trp Leu Gly Phe Ile Arg Asn Arg Gly Ser Gly Gly Ser Ala Glu

50
Tyr Gly Ala Ser Val
65

55

60

<210> 897
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 897
Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala Ile
-15 -10 -5
His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val Val
1 5 10 15
Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn Pro
20 25 30
Leu Asn Val

<210> 898
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 898
Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
-15 -10 -5
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly Xaa Ile Gly Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
65 70 75
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe
80 85 90
Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser Asp Thr Trp Pro Tyr
95 100 105
Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
110 115 120 125
Ser Ser Ala Ser Thr
130

<210> 899

<211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 899
 Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys Ser Leu Ala Leu Leu
 -10 -5 1
 Ala Ser Ser Pro Ile Ala Ala Xaa Pro
 5 10

<210> 900
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 900
 Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
 -15 -10 -5
 Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
 1 5 10
 Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
 15 20 25
 Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
 30 35 40 45
 Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
 50 55 60
 Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
 65 70 75
 Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
 80 85 90
 Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
 95 100 105

<210> 901
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 901
 Met Ala Gly Gln Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile
 -15 -10 -5
 Lys Ala Gln Asp Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys

1	5	10															
Pro	Pro	Pro	Phe	Leu	His	Val	Ser	Thr	Phe	Xaa	Xaa	Lys	Leu	Thr	Phe		
15					20					25					30		
Ser	Thr	Lys	Gly	Asn	Leu	Leu	His	Ser	Ile	Pro	Leu	Ser	Ser	Pro	Leu		
				35					40					45			
Ala	Cys	Val	Leu														
				50													

<210> 902
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -91..-1

<400> 902																	
Met	Lys	Glu	Ala	Val	Pro	Pro	Gly	Cys	Thr	Lys	Ser	Pro	Ser	His	Phe		
	-90					-85					-80						
Ser	Glu	Gly	Phe	Asp	Arg	Trp	Ala	Leu	Glu	Glu	Thr	Pro	Pro	Glu	Asn		
-75				-70						-65					-60		
Leu	Ile	Gly	Ala	Leu	Leu	Ala	Ile	Phe	Gly	His	Leu	Val	Val	Ser	Ile		
				-55					-50					-45			
Ala	Leu	Asn	Leu	Gln	Lys	Tyr	Cys	His	Ile	Arg	Leu	Ala	Gly	Ser	Lys		
		-40					-35						-30				
Asp	Pro	Arg	Ala	Tyr	Phe	Lys	Thr	Lys	Thr	Trp	Trp	Leu	Gly	Leu	Phe		
	-25					-20						-15					
Leu	Met	Leu	Leu	Gly	Glu	Leu	Gly	Val	Phe	Ala	Ser	Tyr	Ala	Phe	Ala		
-10					-5						1				5		
Pro	Leu	Ser	Leu	Ile	Val	Pro	Leu	Ser									
				10													

<210> 903
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 903																	
Met	Ala	Phe	Leu	Trp	Leu	Leu	Ser	Cys	Trp	Ala	Leu	Leu	Gly	Thr	Thr		
	-15						-10						-5				
Phe	Gly	Cys	Gly	Val	Pro	Ala	Ile	His	Pro	Gly	Cys	Gln	Leu	Ser	Pro		
1					5					10							
Arg	Leu	Pro	Pro	Thr	Leu	Leu	Pro	Thr	Glu	Arg	Gly						
15					20				25								

<210> 904
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 904

Met Ala Pro Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu
-20 -15 -10 -5
Gly Ser Phe Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile
1 5 10
His Phe Gly Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu
15 20 25
Met Cys Val Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr
30 35 40
Phe Phe Ser Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro
45 50 55 60
Ser Gly

<210> 905

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35..-1

<400> 905

Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu Arg Val Glu Tyr Ser
-35 -30 -25 -20
Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val Ala Phe Asn Gln Leu
-15 -10 -5
Val Phe Ala Leu Tyr Pro Ile Gln Ala Thr Xaa Cys Phe Ser Xaa Val
1 5 10
Ser Leu Pro Phe Pro Ala
15

<210> 906

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 906

Met Leu Leu Leu Leu Ala Cys Gly Val Pro Ser Leu Trp Pro Phe
-15 -10 -5 1
Ala Leu Ala Leu Leu Lys Thr
5

<210> 907

<211> 43

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 907
 Met Phe Ile Glu Asn Ile Gly Leu Lys Phe Ser Phe Leu Leu Leu His
 -20 -15 -10
 Leu Cys Gln Val Leu Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu
 -5 1 5
 Thr Ile Pro Lys Lys Leu Arg Arg Arg Asp Gly
 10 15 20

<210> 908
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 908
 Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala Leu Leu Met
 -20 -15 -10
 Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser Trp Gly Ser
 -5 1 5
 Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu Leu Leu Pro
 10 15 20
 Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser Asn Tyr Arg
 25 30 35 40
 Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu Arg Gln His
 45 50 55
 Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser Ala Ala Leu
 60 65 70
 Leu Lys Ile Met Cys Lys Gln Leu Leu
 75 80

<210> 909
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44..-1

<400> 909
 Met Lys Val Glu Gly Glu Glu Lys Leu Tyr Arg Leu Leu Arg Ser Gly
 -40 -35 -30
 Asp Leu Phe Lys Phe His Gln Pro His Phe Tyr Glu Leu Ser Gly Leu
 -25 -20 -15

Thr Cys Thr Ser Ser Leu Leu Ser Phe Ala Leu Gly Arg Ser Ile Pro
 -10 -5 1

Gly Ser Phe Pro
 5

<210> 910
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 910
 Met Glu Ser Arg Thr Leu Leu Leu Leu Phe Ser Gly Ala Val Ala Leu
 -15 -10 -5
 Ile Gln Thr Trp Ala Gly Glu Cys Gly Val Gly Arg Glu Lys Ala Ser
 1 5 10
 Ala Gly Arg Ser Glu Gly Pro Ala Arg Arg Ser Lys Ser Ala His Ile
 15 20 25
 Xaa Asn Tyr Arg Leu Gln Leu Gln Ser Arg Gln Gly
 30 35 40

<210> 911
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 911
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 -15 -10 -5
 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
 1 5 10 15
 Asp Lys Leu

<210> 912
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 912
 Met Pro Trp Thr Ile Leu Leu Phe Ala Ala Gly Ser Leu Ala Ile Pro
 -10 -5 1
 Ala Pro Ser Ile Arg Val Val Pro Pro Tyr Pro Ser Ser Gln Glu Asp
 5 10 15

Pro Ile His Ile Ala Cys Met Ala Ala Gly Asn Phe Pro Gly Ala Asn
 20 25 30
 Phe Thr Leu Tyr
 35

<210> 913
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -64..-1

<400> 913
 Met Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu
 -60 -55 -50
 Arg Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln
 -45 -40 -35
 Glu Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe
 -30 -25 -20
 Pro Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser
 -15 -10 -5
 Phe Pro Ser
 1

<210> 914
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 914
 Met Phe Cys Leu Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe
 -10 -5 1
 Pro Ser Ala Phe Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa
 5 10 15
 Thr Ala Thr Ser Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile
 20 25 30 35
 Ser Leu Trp Tyr Leu Xaa Gly Val Pro Pro Glu Val Xaa Glu Leu Pro
 40 45 50
 Phe Phe Pro Tyr Cys Ser Met
 55

<210> 915
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -17..-1

<400> 915

Met Val Asp Gly Thr Leu Leu Leu Leu Leu Ser Glu Ala Leu Ala Leu
-15 -10 -5
Thr Gln Thr Trp Ala Gly Ser His Ser Xaa Lys Tyr Phe His Thr Ser
1 5 10 15
Val Ser Arg Xaa Gly Arg Gly Glu Pro Arg Phe Ile Ser Val Gly Tyr
20 25 30
Val Asp Asp Thr Arg Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala
35 40 45
Arg Asp Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly
50 55 60
Tyr Tyr Asn Gln Ser Glu Ala Gly Ser Xaa Thr Leu Gln
65 70 75

<210> 916

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 916

Met Asn Phe Arg Gly Pro Gln Thr Phe Ser Leu Ser His Ser Leu Val
-25 -20 -15
Leu Ser Leu Ile Ser Leu Ser Ile Ala Trp Ser Met Val Glu Met Xaa
-10 -5 1 5
Thr Ser Ala Ser Tyr Lys Gln Lys Phe Ala Leu Arg Ile Leu Val Val
10 15 20
Gln Leu Pro Thr Trp Val Glu Cys Pro Val Asn His Arg Cys Ala Leu
25 30 35
Gly Arg Lys Asn Cys Ser Ile Arg Thr Gln Pro
40 45

<210> 917

<211> 25

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 917

Met Thr Gly Ile Ser Ile Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser
-20 -15 -10 -5
Leu Ile His Ser Phe Pro Pro Pro Cys
1 5

<210> 918

<211> 98

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 918
Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
-25 -20 -15
Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu Ser Gly Pro Arg
-10 -5 1 5
Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu Thr Leu Ser Leu
10 15 20
Thr Cys Thr Ile Ser Gly Asp Ser Met Ser Ser Ala Ser Tyr Tyr Trp
25 30 35
Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Phe Ile Gly Arg
40 45 50
Ala Leu Tyr Ser Gly Thr Thr Asp Tyr Asn Pro Ser Leu Ser Ser Arg
55 60 65 70
Ile Thr

<210> 919
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 919
Met Ser Ser Glu Lys Ser Gly Leu Pro Asp Ser Val Pro His Thr Ser
-45 -40 -35 -30
Pro Pro Pro Tyr Asn Ala Pro Gln Pro Pro Ala Glu Pro Pro Ala Pro
-25 -20 -15
Pro Leu Ser Leu Ser Leu Cys Leu Ser Leu Cys His Thr His Thr His
-10 -5 1
Thr His Thr His
5

<210> 920
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 920
Met Thr Pro Ala Leu Arg Cys Ala Phe Ala Leu Ala Ile Ala Gly Leu
-25 -20 -15
Val Ser Leu Leu Met Gln Pro Glu Gly Ala Leu Gly Glu Glu Ala Ala

-10 -5 1
 Ser Ala Ala Ala Gln Gly Arg Gln Leu Ala Glu Leu Arg Leu
 5 10 15

<210> 921
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38..-1

<400> 921
 Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val Asp Ile Ala
 -35 -30 -25
 Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile Phe Leu Ser
 -20 -15 -10
 Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser Tyr Thr Pro
 -5 1 5 10
 Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa Phe Pro Tyr
 15 20 25
 Leu Xaa Xaa Ser Thr Pro
 30

<210> 922
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 922
 Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile Ser Phe
 -30 -25 -20
 Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys Ala Phe
 -15 -10 -5
 Ala Phe Leu Ser Leu Leu Gly
 1 5

<210> 923
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 923
 Met Lys Phe Leu Leu Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn
 -15 -10 -5

Pro	Xaa	Pro	Ile	Xaa	Gly	Gly	Ser	Lys	Met	Cys	Glu	Xaa	His	Pro	Arg
1					5					10					15
Ile	Leu	Gln	Asp	Met	Leu	Pro	Leu	Gly	Gly	Asp	Ser	Ile	Val	His	Val
			20						25					30	
Gln	Arg	Xaa	Gln	Lys	Met	Leu	His	Gln	Leu	Leu					
			35					40							

<210> 924
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

Met	Val	Pro	Trp	Val	Arg	Thr	Met	Gly	Gln	Lys	Leu	Lys	Gln	Arg	Leu
		-40					-35					-30			
Arg	Leu	Asp	Val	Gly	Arg	Glu	Ile	Cys	Arg	Gln	Tyr	Pro	Leu	Phe	Cys
	-25					-20					-15				
Phe	Leu	Leu	Leu	Cys	Leu	Ser	Ala	Ala	Ser	Leu	Leu	Leu	Asn	Arg	Tyr
-10					-5					1				5	
Ile	His	Ile	Leu	Met	Ile	Phe	Trp	Ser	Phe	Val	Ala	Gly	Val	Val	Thr
			10					15					20		
Phe	Tyr	Cys	Ser	Leu	Gly	Pro	Asp	Ser	Leu	Leu	Pro	Asn	Ile	Phe	Phe
		25					30					35			
Thr	Ile	Lys	Tyr	Lys	Pro	Lys	Gln	Leu	Gly	Leu	Gln	Glu	Leu	Phe	Pro
	40					45					50				
Gln	Gly	His	Ser	Cys	Ala	Val	Cys	Gly							
55						60									

<210> 925
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

Met	Ala	Trp	Gly	Ser	Pro	Gly	Lys	Ile	Phe	Leu	Met	Gly	Phe	Leu	Gly
				-30					-25					-20	
Gly	Glu	Leu	Val	Phe	Leu	Leu	Cys	Leu	Phe	Xaa	Leu	Phe	Phe	Phe	Ser
			-15					-10						-5	
Phe	Leu	Lys	Arg	Ser	Phe	Ala	Leu	Glu	Cys	Asn					
	1					5									

<210> 926
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 926

Met Phe Phe Ser Ile Leu Leu Leu Leu Ala Pro Pro Leu Pro Ser Ala
-15 -10 -5
Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln
1 5 10

<210> 927

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 927

Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu Val Cys Ser Trp Leu
-20 -15 -10
Ser Ile Ser Leu His Ala His Thr Thr Ala Phe Cys Thr Tyr Ser Lys
-5 1 5 10
Lys Ile His Thr Val Met Ser Phe Phe Cys
15 20

<210> 928

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 928

Met Arg Ser Leu Leu Tyr Phe Leu Cys Val Ser Ser Tyr Val Thr Ser
-15 -10 -5
Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10

<210> 929

<211> 68

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 929

Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala Gly Thr Ser
-15 -10 -5 1

Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser Thr Met Xaa
5 10 15
Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa Val Leu Arg
20 25 30
Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa Ala Met Gly
35 40 45
Cys His Arg Trp
50

<210> 930
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 930
Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser
-15 -10 -5
Arg Ile Leu Leu Val Lys
1 5

<210> 931
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 931
Met Cys Leu Cys Pro Cys Trp Asp Val Phe Thr Val Phe Val Cys Val
-40 -35 -30
Ser Val Cys Val Ser Val Ser Val Pro Val Gly Met Tyr Leu Val Cys
-25 -20 -15
Val Cys Val Cys Val Cys Val Cys Xaa Cys Xaa Arg
-10 -5 1

<210> 932
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 932
Met Leu Ile Ala Lys Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys
-30 -25 -20
Phe Pro Leu Thr Pro Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro

-15 -10 -5
 Leu Ala Gly Gln Glu Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu
 1 5 10
 Val Ile
 15

<210> 933
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 933
 Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg Phe Arg Val Cys
 -25 -20 -15
 Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg Leu Glu Asp Ser
 -10 -5 1 5
 Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr Leu Pro Gly His
 10 15 20
 Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser Leu Gly
 25 30 35

<210> 934
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 934
 Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp Gly Ala Gln Ala Gly
 -25 -20 -15
 Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys Ser Cys Glu Arg Ser
 -10 -5 1
 Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His Ser Ser Ile Lys Gln
 5 10 15
 Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro Ala Gly His Leu Gln
 20 25 30 35
 Gly Lys Ala Thr Ala Pro Leu
 40

<210> 935
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 935

Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 -15 -10 -5
Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Val Phe
 15 20 25
Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Gln Trp Val Ala Gly Ile Gly Gly Gly
 50

<210> 936

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 936

Met Ala Leu Ala Met Leu Val Leu Val Val Ser Pro Trp Ser Ala Ala
 -15 -10 -5
Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu Leu Arg Lys Leu Pro
1 5 10 15
Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp Gly Pro Ala Leu Ala
 20 25 30
Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala Asn Asp Thr Ser Gly
 35 40 45
Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile Phe Trp Met Ala Ala
 50 55 60
Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg Cys Arg Arg Arg Asn
65 70 75 80
Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile Asp Val Cys Pro Glu
 85 90 95
Cys Gly His Leu Lys Gln Lys Xaa Val Leu Cys Ala Thr Ala Met Lys
 100 105 110

<210> 937

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 937

Met Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu
-20 -15 -10 -5
Phe Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe
 1 5 10

<210> 938
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 938
 Met Lys Gln Ser Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala
 -45 -40 -35
 Leu Gly Glu Glu Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu
 -30 -25 -20 -15
 Pro Leu Val Leu Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Gly Pro
 -10 -5 1
 Gly Glu Pro Asp Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala
 5 10 15
 Ser Thr His Xaa His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg
 20 25 30
 Pro Ala Thr Gln Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly
 35 40 45 50
 Val Arg Pro Ala Pro
 55

<210> 939
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 939
 Met Leu Leu Glu Ser Leu Cys Val Leu Ser Leu Leu Val Ser Phe Lys
 -15 -10 -5
 Ser Ala Cys Leu Thr Arg Glu Pro Ala Phe Asp Ser Gln Ala Arg Pro
 1 5 10

<210> 940
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 940
 Met Val Phe Gly Tyr Trp Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys
 -45 -40 -35
 Ser Val Lys Cys Ala Arg Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu

-30 -25 -20 -15
 Val Leu Leu Tyr Leu Ser Phe Ala Ala Leu Gly Val Val Ala Leu Arg
 -10 -5 1
 Ser Val Glu Ser Pro Leu Ala Glu Thr His Ser Cys Trp Leu Ser Leu
 5 10 15
 Gly Met Cys Val Leu Gln Cys Glu Gln Gln Trp Val Pro Thr Pro Val
 20 25 30
 Ser Phe Leu Cys Gly Leu Ser Gly Ser Ser Thr Ile Ile Val
 35 40 45

<210> 941
 <211> 66
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 941
 Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr Val Val
 -20 -15 -10
 Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys Trp Val
 -5 1 5
 Met Cys Cys Val Trp Cys Ile Cys Val Cys Val Trp Cys Val Cys Cys
 10 15 20
 Met Cys Cys Val Leu Ser Cys Val Val Ser His Gly Leu Cys Gly Val
 25 30 35 40
 Ser Trp

<210> 942
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 942
 Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Val Leu Glu Val
 -15 -10 -5
 Val Gln Cys Glu Ile Gln Leu Ile Asp Ala Gly Gly Gly His Val Gln
 1 5 10
 Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Asp Phe Leu Phe
 15 20 25
 Arg Ser Tyr Trp Met Thr Trp Val Arg His Pro
 30 35 40

<210> 943
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 943
Met Ser Ile Leu Leu Arg Val Leu Gly Ile Lys Gly Cys Trp Ile Leu
 -35 -30 -25
Ser Asn Pro Phe Ser Ala Cys Ile Glu Met Ile Leu Leu Phe Leu Phe
 -20 -15 -10
Leu Ile Leu Phe Ile Trp His Ile Arg
 -5 1

<210> 944
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 944
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25 -20 -15 -10
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
 -5 1

<210> 945
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 945
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys Leu Ala Ala
 -15 -10 -5
Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp Phe Ile Lys
 1 5 10
Pro Leu
 15

<210> 946
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 946

Met Leu Thr Ser Leu Pro Phe Leu Leu Pro Thr Ile Ser Phe Leu Leu
 -25 -20 -15
 Leu Leu Tyr Phe Phe Xaa Ile Ala Val Thr His Pro Ser Val Leu Ile
 -10 -5 1 5
 Asn Phe Ser Phe Ser Phe Pro Arg
 10

<210> 947
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 947
 Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro
 -20 -15 -10 -5
 Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro
 1 5 10
 Ala Met Tyr Tyr
 15

<210> 948
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 948
 Met Leu Phe Trp Leu Pro Ser Pro Ser Glu Thr Thr Ser Ala Trp Thr
 -25 -20 -15
 Leu Leu Ser Ile Ser Leu Ser Val Phe Trp Ser Glu Pro Phe Asn Lys
 -10 -5 1 5
 Ser Leu Gly Ser Ser Lys Leu Pro Cys His Phe Phe Ser Ile Lys Arg
 10 15 20

<210> 949
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 949
 Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe Ile Tyr Phe Cys
 -45 -40 -35
 Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala Leu Phe Gln Phe

-30 -25 -20
 Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu Cys Leu Cys Gln
 -15 -10 -5 1
 Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser Gly Val Val Cys
 5 10 15
 Gly

<210> 950
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 950
 Met Ala Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val
 -10 -5 1
 Thr Leu Leu Pro Arg
 5

<210> 951
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 951
 Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu
 -20 -15 -10 -5
 Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu
 1 5 10
 Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Arg
 15 20 25

<210> 952
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 952
 Met Val Phe Trp Glu Ile Ser Val Gln Ile Ile Leu Ile Ser Glu Leu
 -20 -15 -10
 Leu Leu Leu Arg Ser Val Thr Ser His Asn Thr Met Met Arg Ala Leu
 -5 1 5
 Ser Ser Gln Met Leu Ser Gln Ser Phe Pro Arg Pro Ser Phe Gly Phe

10 15 20
 Ile Ser Lys Ile His Pro Ser His Pro Pro
 25 30

<210> 953
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -51..-1

<400> 953
 Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val Gln Ile
 -50 -45 -40
 Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu Glu Val
 -35 -30 -25 -20
 Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu Gly Met
 -15 -10 -5
 Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile Pro Phe
 1 5 10
 Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu
 15 20

<210> 954
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 954
 Met Asn Lys His Phe Leu Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val
 -15 -10 -5
 Ala Val Thr Ser Leu Gln Cys Ile Thr Cys His Leu Arg Thr Arg Thr
 1 5 10 15
 Asp Arg Cys Arg Arg Gly Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu
 20 25 30
 Ala Cys Met Leu Leu Arg Ile His Gln Arg
 35 40

<210> 955
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 955

Met Tyr Ile Lys Met Glu Ser Val Thr Leu Ser Pro Ala Pro Val Phe
 -35 -30 -25 -20
 Pro Val Pro Ala Gln Leu Leu Leu Leu Thr Ser His Phe Leu Gly Glu
 -15 -10 -5
 Ser Leu Gly Gly Gly Thr Leu Leu Val Pro Leu Leu Pro Pro Gly
 1 5 10

<210> 956
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 956
 Met Xaa Xaa Ala Leu Leu Arg Ser Arg Met Ile Gln Gly Arg Ile Leu
 -25 -20 -15
 Leu Leu Thr Ile Cys Ala Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly
 -10 -5 1 5
 Tyr Asn Leu Ser Ile Ile Asn Asp
 10

<210> 957
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 957
 Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile Pro Pro Met Ile
 -45 -40 -35
 Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala Leu Glu Asn Phe
 -30 -25 -20
 Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa Cys Xaa Cys His
 -15 -10 -5 1
 Gly Asp Asp Asp Leu Ser
 5

<210> 958
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 958
 Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Gly Asn Ser Val

[illegible]

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<220>  
<221> SIGNAL  
<222> -14..-1
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<210> 960
<211> 48
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -19..-1
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<210> 961
<211> 28
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -22..-1
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<210> 962

<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 962
Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser
-15 -10 -5 1
Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly
5 10

<210> 963
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 963
Met Ala Ser Leu Leu Ser Gly Phe Thr Ser Phe Cys Leu Leu His Val
-25 -20 -15 -10
His Ser Phe Leu Pro Pro Val Phe Ser Thr Gln Asn
-5 1

<210> 964
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 964
Met Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe
-30 -25 -20 -15
Leu Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg
-10 -5 1
Tyr Ser Ile Pro Glu Glu Thr Glu Ser Gly
5 10

<210> 965
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 965

Met Met Leu Asp Phe Ala Leu Ser Pro Arg Leu Glu Arg Ser Gly Leu
-35 -30 -25 -20
Ile Met Ala Cys Cys Thr Leu Asp Leu Leu Gly Ser Ser Ser Pro Pro
-15 -10 -5
Thr Ser Ala Ser Gln Val Ala Gly Thr Gly His Val Pro Pro His Pro
1 5 10
Ala Ser Phe Phe Tyr Phe Xaa Val Xaa Gln Val Tyr Tyr Val Ser Gln
15 20 25
Leu Ile
30

<210> 966

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 966

Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe
-20 -15 -10
Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val
-5 1 5 10
Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
15 20 25
Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Arg
30 35 40

<210> 967

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 967

Met Pro Arg Pro Arg Ala Cys Ala Ser Trp Pro Leu Leu Ala Ala Val
-20 -15 -10
Ser Gly Leu Arg Gly Leu Glu Trp Pro Pro Ser Trp Arg Arg Val Val
-5 1 5 10
Ala Ala Val Gly Val Cys Arg Val Arg Asp Trp Gly Pro Arg
15 20 25

<210> 968

<211> 23

<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 968
Met Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp
 -15 -10 -5
Phe Trp Lys Thr His Pro Gly
 1 5

<210> 969
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 969
Met Val Phe Leu Val Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile
 -15 -10 -5
Arg Gly Ser Glu Trp Xaa Leu Pro Pro Asn Trp
 1 5

<210> 970
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 970
Met Met Thr Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser
 -15 -10 -5
Trp Ala Leu Phe Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His
 1 5 10
Leu Arg Trp Phe Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly
15 20 25 30
Gln Tyr Gly Leu Ala
 35

<210> 971
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 971

Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile
 -25 -20 -15
 Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa
 -10 -5 1
 Gly Ile Glu Xaa Pro
 5

<210> 972
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 972
 Met Ala Trp Ile Pro Leu Phe Leu Gly Val Leu Ala Tyr Cys Thr Gly
 -15 -10 -5
 Ser Val Ala Ser Tyr Glu Leu Thr His Pro Pro Ser Val Ser Val Ser
 1 5 10 15
 Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp
 20 25 30
 Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
 35 40 45
 Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
 50 55 60
 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
 65 70 75 80
 Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser
 85 90 95
 Thr Val Val Phe Gly Gly Gly Thr
 100

<210> 973
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 973
 Met Val Cys Val Ile Phe Lys Glu Leu Met Glu Phe Glu Phe Pro Gly
 -25 -20 -15
 Phe Cys Phe Xaa Leu Cys Phe Gly Arg Ser Ser Leu Cys Cys Arg Xaa
 -10 -5 1

<210> 974
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 974

Met	Glu	Ser	Ser	Gly	Thr	Pro	Ser	Val	Thr	Leu	Ile	Val	Gly	Ser	Gly
-30					-25					-20					-15
Leu	Ser	Cys	Leu	Ala	Leu	Xaa	Thr	Leu	Ala	Val	Val	Tyr	Ala	Ala	Leu
				-10					-5					1	
Trp	Arg	Tyr	Ile	Arg	Ser	Glu	Arg	Ser	Ile	Ile	Leu	Ile	Asn	Phe	Cys
	5					10					15				
Leu	Ser	Ile	Ile	Ser	Ser	Asn	Ile	Leu	Ile	Leu	Val	Gly	Gln	Thr	Gln
20						25					30				
Thr	His	Asn	Lys	Glu	Tyr	Leu	His	Asn	His	His	Cys	Ile	Phe		
35						40				45					

<210> 975
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 975

Met	Gly	Val	Cys	Cys	Ala	Gln	Asn	Cys	Ser	Val	Ser	Gly	Xaa	Xaa	Arg
-30						-25					-20				
Asn	Ala	Leu	Xaa	Phe	Leu	Ala	Ser	Ser	Phe	Cys	Phe	Gly	Glu	Ala	Asp
-15					-10					-5				1	
Ser	Gly	Ser	Arg	Cys	Cys	Leu	Lys	Ile	Ile	Leu	Gly	Phe	Tyr	Leu	Ile
		5					10					15			
Arg	Tyr	Ser	Leu	Ile	Thr	Tyr	Gln	Val	Arg						
20						25									

<210> 976
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 976

Met	Lys	Ile	Leu	Tyr	Leu	Phe	Phe	Phe	Leu	Lys	Trp	Ser	His	Pro	Gly
			-15					-10					-5		
Trp	Ser	Ala	Thr	Xaa	Trp	Ser	Trp	His	Thr	Ala	Thr	Ser	Ala	Ser	Leu
	1					5					10				
Ile	Gln	Val	Ile	Leu	Pro	Pro	Trp								
15					20										

<210> 977
 <211> 34

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 977
 Met Thr Pro Cys Phe Leu Gln Met Asp Asn Leu Thr Pro Leu Phe Leu
 -25 -20 -15
 Ser Gly Cys Phe Leu Phe Leu Ser Xaa Cys Xaa Ile Tyr Leu Ala Arg
 -10 -5 1 5
 Ile Leu

<210> 978
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 978
 Met Gly Ser Ala Gly Arg Leu His Tyr Leu Xaa Met Thr Ala Glu Asn
 -40 -35 -30 -25
 Pro Thr Pro Gly Asp Leu Ala Pro Xaa Pro Leu Ile Thr Cys Lys Leu
 -20 -15 -10
 Cys Leu Cys Glu Gln Ser Xaa Gly Gln Asp Asp His Thr Pro Gly Met
 -5 1 5

<210> 979
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 979
 Met Asn His Leu Pro Pro Asn His Tyr Arg Xaa His Val Phe Thr Cys
 -45 -40 -35
 His Val Asp Gln Tyr Leu Thr Val Glu Thr Ala Gly Gly Met Glu Lys
 -30 -25 -20
 Glu Ala Val Ser Val Thr Val Leu Ser Ala Ala Pro Cys Leu Leu
 -15 -10 -5
 Ser Cys Phe Leu Gly Ser Ser Val Ser Gly Leu Ala Phe Trp Val Ser
 1 5 10 15
 Gln Gln Lys Thr Lys Gly Pro Glu Arg Cys Lys Asn Thr His His Xaa
 20 25 30
 Ala Xaa Asn Asn Phe Pro Ala Arg
 35

<210> 980
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 980
 Met Asn Lys Ile Lys Glu Asn Thr His Thr His Thr His Thr
 -40 -35 -30 -25
 His Lys Asn Asn Thr Lys Leu Val Ser Asn Leu Phe Leu Phe Met Leu
 -20 -15 -10
 Pro Leu Trp Cys Ser Ile Gly Thr Cys Thr
 -5 1

<210> 981
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 981
 Met His Asp Ser Ser Gly Lys Asn Asn Phe Arg Lys Ile Pro Val Val
 -40 -35 -30
 Asn Leu Ile Tyr Leu Tyr Val Asp Ile His Ile His Lys Leu Phe Leu
 -25 -20 -15
 Tyr Ser Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu
 -10 -5 1 5
 Arg Arg Leu

<210> 982
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 982
 Met Gly Arg Leu His Arg Pro Arg Ser Ser Thr Ser Tyr Arg Asn Leu
 -30 -25 -20
 Pro His Leu Phe Leu Phe Phe Leu Phe Val Gly Pro Phe Ser Cys Leu
 -15 -10 -5
 Gly Ser Tyr Ser Arg
 1

<210> 983
 <211> 44

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 983
Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro Gly Xaa Ser Arg Leu
-25 -20 -15
Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro Pro Xaa Leu Arg
-10 -5 1 5
Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala Gly
10 15

<210> 984
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 984
Met Arg Leu Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu
-15 -10 -5 1
Gly Ser Gln Gln Ala Thr Asp Trp Trp
5 10

<210> 985
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 985
Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe
-25 -20 -15 -10
Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe
-5 1 5

<210> 986
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 986

Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu
-20 -15 -10
Phe Phe Ser Val Phe Cys Phe Phe Phe
-5 1

<210> 987

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 987

Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
-20 -15 -10
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
-5 1 5 10
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
15 20 25
Val Asn Ser Gly Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg
30 35 40
Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
45 50 55
Leu Gly Thr Val Asp Val Leu Lys Gln His Arg
60 65 70

<210> 988

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 988

Met Ala His Cys Ser Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile
-15 -10 -5
Ser Ala Ser Gln Ser Thr Gly Ile Thr Ser Val Ser
1 5 10

<210> 989

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 989

Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser Leu Phe Leu Phe Phe
 -15 -10 -5
 Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu Glu Cys Ser Cys Val
 1 5 10 15
 Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala Arg
 20 25

<210> 990
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 990
 Met Tyr Thr Asn Lys Tyr Thr Leu Ile Tyr Asn Ile Leu Ile Tyr Asn
 -45 -40 -35
 Ile Cys Xaa Xaa Tyr Met Trp Leu Ile Leu Ile Tyr Met Tyr Leu His
 -30 -25 -20 -15
 Ile Cys Leu Phe Cys Cys Xaa Phe Ile Ser Ser Cys Asn Ser Val Phe
 -10 -5 1
 Pro Cys Val Ile Xaa Phe Leu Leu Pro Glu Glu Leu Leu Xaa Val Xaa
 5 10 15
 Leu Xaa Xaa Xaa Phe Xaa Val Arg Trp Ser Leu Xaa Xaa Ser Ser Arg
 20 25 30
 Leu Glu Cys
 35

<210> 991
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 991
 Met Leu Leu Thr His Asn Glu Asp Tyr Met Pro Gly Asn Xaa Xaa Xaa
 -30 -25 -20
 Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val His Ile Cys Leu Gly Arg
 -15 -10 -5 1
 Lys Lys Lys

<210> 992
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 992

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
 -15 -10 -5
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala Xaa Gly Lys Gly Leu
30 35 40 45
Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn Thr Ala Xaa Tyr Ala
 50 55 60
Xaa Ser Val Lys Xaa Arg Phe Thr Ile
 65 70

<210> 993

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 993

Met Lys Arg Phe Phe Leu Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys
 -15 -10 -5
Ser Val Thr Arg Leu Gly Cys Cys Gly Ala Ile Ser Ala His Cys Xaa
1 5 10 15
Leu Arg Leu Pro Gly Ser Ser Xaa Xaa Pro Ala Ser Thr Ser Arg Val
 20 25 30
Xaa Gly Ile Thr Gly Met Arg
 35

<210> 994

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -38..-1

<400> 994

Met Ser Cys His Ser Leu Leu Ala Cys Lys Val Phe Thr Glu Lys Ser
 -35 -30 -25
Pro Thr Lys His Ile Arg Glu His His Cys Met Leu Phe Val Ser Phe
 -20 -15 -10
Leu Leu Leu Leu Gly Ser Arg
 -5 1

<210> 995

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 995

Met Thr Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser
-25 -20 -15
Met Leu Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu
-10 -5 1 5
Gly Thr Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala
10 15 20
Thr Gln

<210> 996

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 996

Met Val Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr
-15 -10 -5
Val Gln Thr Ala Thr Tyr Thr
1

<210> 997

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 997

Met Glu Lys Thr Ala Leu Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys
-15 -10 -5
Cys Ala Pro Arg Thr Tyr Val Val Ser Ala Thr Thr Leu Ser Ala Val
1 5 10 15
Gln Gly His Cys Pro Leu Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu
20 25 30
Trp Pro Phe Gly
35

<210> 998

<211> 50

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 998
 Met Ile Phe Thr Phe Gln Gln Ile Gly Gly Lys Leu Leu Leu Ser Gly
 -20 -15 -10
 Leu Thr Gln Glu Cys Leu Gly Ala Leu Pro Glu Ala Asn Val Phe Cys
 -5 1 5
 Arg Gly Gly Cys Thr Ala Thr Val Leu Lys His Gly Lys Ala Ser Pro
 10 15 20 25
 Glu Ser

<210> 999
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 999
 Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr
 -30 -25 -20
 Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu
 -15 -10 -5 1
 Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met
 5 10 15

<210> 1000
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 1000
 Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr Arg Asn Ala Cys
 -40 -35 -30 -25
 Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu Leu Lys Leu Leu
 -20 -15 -10
 Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly
 -5 1

<210> 1001
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -25..-1

<400> 1001

Met Phe Ser Ser Pro Gly Leu Arg Thr Leu Phe Val Leu Val Gly Ser
-25 -20 -15 -10
Leu His Leu Phe Leu Ser Val Leu Ala Ser Lys Ser Arg Asn Ser Lys
-5 1 5
Lys Gln Arg Leu Phe Leu Leu Val Pro Leu Tyr
10 15

<210> 1002

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1002

Met Leu Thr Asp Gly Ile Leu Met Arg Val Asn Val Cys Ser Leu Pro
-20 -15 -10
Ala Pro Gly Leu Cys Ser Gly Gln Pro Gly Val Arg Ala Trp Pro Gly
-5 1 5
Val Thr Gln Leu Thr Gln Xaa Glu Glu Cys Pro Trp Phe Ser Ala Leu
10 15 20 25
Glu Gly Leu

<210> 1003

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -33..-1

<400> 1003

Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly Xaa Ala
-30 -25 -20
Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro Cys Ile
-15 -10 -5
Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser Gly Lys
1 5 10 15
Arg

<210> 1004

<211> 102

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 1004

Met Ala Gly Ser Arg Gln Arg Gly Leu Arg Ala Arg Val Arg Pro Leu
-25 -20 -15
Phe Cys Ala Leu Leu Leu Ser Leu Xaa Xaa Xaa Xaa Pro Xaa Xaa Arg
-10 -5 1
Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala Thr Ser Pro Phe Arg Val
5 10 15
Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly Ala Glu Arg Arg Asp Arg
20 25 30 35
Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr Ser Lys Phe Arg Ser Asn
40 45 50
Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys Arg Leu Ser Val Xaa Xaa
55 60 65
Asp Xaa Ser Gly Pro Gly
70

<210> 1005

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 1005

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
-15 -10 -5
Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Leu
15 20 25
Ser Asn Asp Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Val Trp Val Ser His Ile Asp Ser Ser Xaa Thr Ile Thr Asn Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Trp
65 70 75

<210> 1006

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1006

Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val Ala Tyr Gln Cys
-15 -10 -5 1
His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr Leu Lys Ser Glu
5 10 15

Thr Leu Met Pro Ala Ala
20

<210> 1007
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 1007
Met Trp Glu Asp Ser Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser
 -45 -40 -35
Leu Ala Lys Gln Gln Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu
 -30 -25 -20
Thr Phe Ser Val Phe Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr
 -15 -10 -5
Gly Ile Leu Ala Phe Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn
1 5 10 15
Leu Phe Ile Asn Asn Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu
 20 25 30
Gln Xaa Leu Ile Asp Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa
 35 40 45
Glu Ala Pro Ile Xaa Gly Thr Gly
 50 55

<210> 1008
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1008
Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr Ala Met Ile
 -10 -5 1
Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe Leu Val Val
5 10 15
Phe Asn
20

<210> 1009
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1009

Met Tyr Ile Val Met Asp Leu Pro Leu Trp Leu Ser His Glu Val Gln
-30 -25 -20
Ser Tyr Ile Pro Ser Phe Phe Leu Phe Phe Cys Phe Glu Thr Gly Ser
-15 -10 -5
His Ser Val Thr His Gly
1

<210> 1010

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 1010

Met Val Ala His Asp Tyr Gln Asn Ile Ile Ser Leu Phe Phe Leu Ala
-25 -20 -15
Phe Ser Phe Ser Phe Phe Pro Ser Ser Phe Ser Ser Phe Phe Leu Xaa
-10 -5 1 5
Phe Leu Ser Phe Phe Ser Ser Phe Phe Leu Ser Leu Leu Ser Phe Pro
10 15 20
Ser Phe Leu Pro Pro Gly
25

<210> 1011

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1011

Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
-15 -10 -5 1
Val Leu Arg Xaa Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
5 10 15
Gly Val Arg Gln Trp Gln Pro Asp Val Glu Trp Ala Gln Gln Phe Gly
20 25 30
Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
35 40 45
Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
50 55 60 65
Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
70 75 80
Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
85 90 95
Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Xaa
100 105 110
Tyr Leu Gln Ala Leu Pro Tyr Phe

115

120

<210> 1012
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1012

Met	Leu	Ile	Trp	Ser	Ser	Ser	Ser	Phe	Pro	Ala	Pro	Pro	Leu	Phe	Leu
			-25					-20					-15		
Val	Phe	Leu	His	Leu	Phe	Leu	Xaa	Val	Tyr	Leu	Gly	Leu	Val	Met	Pro
		-10					-5					1			
Thr	Gln	Gln	Tyr	Leu	Leu	Leu	Gln	Ser	Pro	Leu	Met	Phe	Thr	Asp	Lys
5					10					15					20
Ala	Gln														

<210> 1013
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 1013

Met	Cys	Arg	Met	Cys	Arg	Phe	Val	Thr	Trp	Ile	Asn	Val	Cys	His	Gly
	-45					-40					-35				
Asp	Leu	Leu	His	Arg	Ser	Ser	Arg	Arg	Leu	Gly	Val	Lys	Pro	Ser	Thr
-30				-25					-20					-15	
His	Trp	Leu	Phe	Phe	Leu	Met	Leu	Ser	Leu	Cys	Thr	Pro	Pro	Asp	Arg
			-10					-5						1	
Pro	Trp	Cys	Val	Leu	Phe	Pro	Pro	Leu							
	5					10									

<210> 1014
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1014

Met	Xaa	Thr	Gln	Glu	Ala	Gly	Leu	Ile	Phe	Phe	Ser	Pro	Pro	Phe	Ser
	-30					-25					-20				
Leu	Ser	Leu	Ser	Leu	Ser	Leu	Pro	Leu	Ser	Leu	Xaa	Leu	Leu	Xaa	Xaa
-15				-10				-5						1	
Pro	His	Ser	Arg	Thr	Pro	Gln	Arg								

5

<210> 1015
 <211> 43
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 1015
 Met Glu Phe Leu Leu Leu Trp Ser Leu Xaa Ser Asn Gly Lys Arg Gly
 -10 -5 1
 Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val Trp Glu Pro Glu
 5 10 15
 Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg
 20 25 30

<210> 1016
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 1016
 Met Met Val Thr Tyr Arg Trp Gly Phe Gly Val Asp Val Xaa Phe Val
 -35 -30 -25
 Ala Val Asp Ala Ile Pro Phe Cys Leu Leu Val Phe Phe Leu Ile Val
 -20 -15 -10
 Arg Thr Leu Ser Cys Arg Ser Val Gly Val Cys Trp Arg Ser Thr Pro
 -5 1 5 10
 Asp Pro Val Cys Leu Gly Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile
 15 20 25
 Leu Gln Asn Ser Lys Cys Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser
 30 35 40
 Ser Gln Arg Gly Thr Glu Cys Met
 45 50

<210> 1017
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1017
 Met Leu Tyr Pro Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro
 -15 -10 -5

Ala Asn Ala Gln Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys
 1 5 10

Pro Gly
 15

<210> 1018
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1018
 Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val Arg Arg Arg Leu
 -25 -20 -15
 Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr Ser Leu Leu Lys
 -10 -5 1 5
 Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr Leu Thr Ser Ser
 10 15 20

<210> 1019
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1019
 Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser Val Leu Ile
 -20 -15 -10
 Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr Ile Xaa Arg
 -5 1 5
 Gly

<210> 1020
 <211> 117
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1020
 Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu Arg Ser
 -15 -10 -5
 Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln Pro Trp
 1 5 10 15
 His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met Gly Leu
 20 25 30

Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser Pro Glu
35 40 45
Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile Leu Thr
50 55 60
Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala Ile Gln
65 70 75 80
Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln Leu Glu
85 90 95
Glu Ala Thr Arg Gln
100

<210> 1021
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1021
Met Leu Leu Thr Phe Ser Ser Ser Ser Arg His Arg Arg Leu Tyr Arg
-30 -25 -20
Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro Pro
-15 -10 -5
Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Xaa Val Leu Xaa Xaa
1 5 10
Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu Phe
15 20 25 30
Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa Cys
35 40 45
Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala Ser
50 55 60
Arg Xaa Arg
65

<210> 1022
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1022
Met Leu Leu Leu Leu Gln Leu Asn Leu Lys Thr Leu Ser Ser Ser Thr
-10 -5 1
Ile Ala Leu Lys Lys Ile Ser Gly Glu Leu Leu Arg Lys Arg Lys Arg
5 10 15

<210> 1023
<211> 18
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1023

Met Ser Leu Phe Val Leu Leu Ile Ile Thr Gln Leu Leu Tyr Gly Gly
-15 -10 -5 1
Ile Leu

<210> 1024

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 1024

Met Asn Cys Phe Cys Asn Phe Val Lys Thr Ser Glu Ala Tyr Met Ile
-25 -20 -15
Leu Phe Leu Gly Val Leu Leu Ser Ala Ser Asp Leu Cys Val Tyr Pro
-10 -5 1
Ile Gly
5

<210> 1025

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1025

Met Ser Val Ile Leu Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Pro
-10 -5 1
Glu Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val
5 10 15
Gln

<210> 1026

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 1026

Met	Tyr	Gly	Glu	Ser	Thr	Leu	Phe	Ile	His	Ser	Ser	Val	His	Gly	His
				-25					-20					-15	
Leu	Gly	Cys	Leu	Leu	Leu	Ala	Val	Arg	Ser	Ser	Ala	Thr	Val	Asn	Ile
		-10						-5					1		
Thr	Tyr	Xaa	Xaa	Val	Cys	Val	Asp	Ile	Xaa	Xaa	His	Phe	His	Met	Leu
	5					10					15				
Met	Ser	Gly	Ile	Thr	Gly	Ser	Tyr	Gly	Asn	Ser	Leu	Ser			
20					25					30					

<210> 1027
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -51..-1

Met	Ala	Ala	Ser	Val	Leu	Asn	Thr	Val	Leu	Arg	Arg	Leu	Pro	Met	Leu
	-50					-45				-40					
Ser	Leu	Phe	Arg	Gly	Ser	His	Arg	Val	Gln	Val	Thr	Leu	Arg	Lys	Thr
-35					-30				-25					-20	
Phe	Cys	Thr	Thr	Ser	Ser	Trp	Leu	Tyr	Leu	Leu	Glu	Val	Val	Ala	Pro
				-15					-10					-5	
Leu	Ser	Gly	Ile	His	Glu	Trp	Arg	Pro	Ser	His	Val	Cys	Leu	Ser	Cys
			1			5						10			
Leu	Gly	Ser	Thr	Ser	Cys	Asn	Pro	Pro	Glu						
	15					20									

<210> 1028
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -65..-1

Met	Leu	Arg	Ser	Ala	Cys	Val	Ser	Gln	His	Ala	Gly	Gly	Ile	Trp	Val
-65					-60					-55					-50
Asp	Arg	Gly	Gly	Pro	Gln	Cys	Gln	Arg	Val	Phe	Thr	Phe	Cys	Arg	Gly
			-45					-40					-35		
Leu	Ser	Pro	Asn	Phe	Gly	Arg	Ser	Glu	Thr	Gln	Arg	Glu	Arg	Trp	Ile
		-30					-25					-20			
Arg	Pro	Gly	Gln	Leu	Met	Val	Val	Ala	Glu	Thr	Ser	Gln	Gly	Ser	Trp
	-15					-10					-5				
Ser	Ala	Pro	Thr	Ser	Pro	Xaa	Thr	Ser	Cys	Pro	Pro	Pro	Asn	Thr	Xaa
	1				5					10					15
Thr	Thr	Pro	Xaa												

<210> 1029
 <211> 94

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 1029
 Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys Met
 -45 -40 -35 -30
 Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met Pro
 -25 -20 -15
 Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val Ala
 -10 -5 1
 Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro Arg
 5 10 15
 Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa Leu
 20 25 30 35
 Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe
 40 45

<210> 1030
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1030
 Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser Leu Ile
 -20 -15 -10
 Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val Gly Pro
 -5 1 5 10
 Ser Glu Pro Arg Arg Gly
 15

<210> 1031
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1031
 Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala
 -20 -15 -10 -5
 Pro Ser Thr Gly Leu Gly
 1

<210> 1032

<211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 1032
 Met Lys Leu Gln Phe Ala Phe Cys Tyr Phe Leu Tyr Leu Asp Thr Phe
 -25 -20 -15
 Phe Leu Phe Leu Phe Phe Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Gly
 -10 -5 1
 Arg Ser Ala Val Ala Xaa Pro Gln Leu Xaa Ala Ala Ser Thr Phe Xaa
 5 10 15 20
 Phe Gln Ala Ile Phe Leu Pro Gln Xaa
 25

<210> 1033
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 1033
 Met Ala Ala Gly Glu Leu Glu Gly Gly Lys Pro Leu Ser Gly Leu Leu
 -65 -60 -55
 Asn Ala Leu Ala Gln Asp Thr Phe His Gly Tyr Pro Gly Ile Thr Glu
 -50 -45 -40
 Glu Leu Leu Arg Ser Gln Leu Tyr Pro Glu Val Pro Pro Glu Glu Phe
 -35 -30 -25
 His Pro Phe Leu Ala Lys Met Arg Gly Ile Leu Lys Val Leu Leu Phe
 -20 -15 -10
 Ser Val Val Ser Gly Leu Glu Gln Asn Pro Leu Ala Ala Gly Phe Arg
 -5 1 5 10
 Leu Ser His Pro
 15

<210> 1034
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 1034
 Met Met Met Ser Asn Val Met Leu Met Leu Gln Leu Gln Pro Leu Leu
 -30 -25 -20
 Ala Xaa Ser Leu Ile Leu Ser Pro Ser Pro Arg Pro Val Leu Gly Phe

<220>

<221> SIGNAL

<222> -14..-1

<400> 1038

Met Gly Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr
 -10 -5 1
Arg Val Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser
 5 10 15

<210> 1039

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 1039

Met Met Leu Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr
 -40 -35 -30
Asp Gly Phe Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val
 -25 -20 -15
Leu Ser Leu Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro
 -10 -5 1 5
Tyr Tyr Ile Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala
 10 15 20
Arg

<210> 1040

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<400> 1040

Met Tyr Val Cys Ile Tyr Ile Xaa Leu Xaa Asp Leu Tyr Asp Phe Phe
 -35 -30 -25
Leu Leu Gly Thr Tyr Phe Phe Glu Arg Lys Cys Phe Val Cys Xaa Leu
 -20 -15 -10
Phe Val Phe Leu Leu Ser Gly Leu Asn Tyr Phe Ser Ile Leu Ser Phe
 -5 1 5
Tyr Pro Arg
10

<210> 1041

<211> 50

<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1041
Met Cys Ile Phe Cys Leu Phe His Leu Leu Tyr His Lys Leu Leu Ser
-40 -35 -30 -25
Arg Ser Leu Phe Phe Cys Cys Ile Phe Ser Gly Phe Ile Thr Phe Ile
-20 -15 -10
Phe Ser Phe Ser Phe Cys Glu Cys Ile Val Gly Met Tyr Ile Tyr Gly
-5 1 5
Ala Arg
10

<210> 1042
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1042
Met Xaa Ile Cys Tyr Asn Ile Phe Gln Asn Ile Leu Gly Leu Leu Leu
-25 -20 -15
Ile Phe Leu Tyr Leu Ser Leu Asn Leu Phe Cys Ile Phe Phe Ser Val
-10 -5 1 5
Pro Ala Leu Gln Pro Arg Arg Leu
10

<210> 1043
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1043
Met Ala Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr
-25 -20 -15
Leu Leu Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser
-10 -5 1

<210> 1044
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -20..-1

<400> 1044

Met Gly Arg Ser Lys Arg Gln Leu Leu Ser Leu Pro Gly Ser Phe Ile
-20 -15 -10 -5
Pro Gly Asn Cys Arg Pro Arg Ile Leu Ser Asn Gly Glu Xaa Arg Arg
1 5 10
Lys

<210> 1045

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 1045

Met Arg Ser Asp Gly Phe Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu
-25 -20 -15 -10
Ile Phe Leu Leu Pro Pro Leu Pro Ala Met Ile Leu Arg Pro Leu Gln
-5 1 5
Pro Cys Gly Ile Ile Ser Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe
10 15 20

<210> 1046

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1046

Met Asn Thr Leu Trp Thr Ala Ser Ser Leu Pro Leu Ser Thr His Ser
-15 -10 -5
Gln Arg Thr Met Ile His Trp Asn Val Phe Leu Trp Asn Ser Phe Tyr
1 5 10 15
Ser Cys Ile Lys Ile Phe Pro
20

<210> 1047

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31..-1

<400> 1047

Met Thr Trp Thr Lys Cys Pro Leu Pro Leu Gly Pro Ala Phe Phe Thr

-30 -25 -20
 Gln Cys Cys Leu Ile Gly Leu Leu Val Pro Leu Leu Gly Trp Gly Asn
 -15 -10 -5 1
 Gln Asn Thr Gln Trp Tyr Pro Thr Ser Lys Met Pro Asp Gly
 5 10 15

<210> 1048
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 1048
 Met Gly Arg Ser Asn Asp Phe Arg Phe Ala Phe Leu Thr Cys Phe Leu
 -30 -25 -20
 Gly Trp Glu Ile Val Tyr Phe Leu Val Leu Leu Arg Val Leu Tyr Thr
 -15 -10 -5
 Leu Gln Trp Gly Gly
 1 5

<210> 1049
 <211> 24
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1049
 Met Lys Thr Asp Asn Leu Thr Ser Phe Leu Thr Tyr Met Pro Leu Ile
 -15 -10 -5
 Ser Ser Ser Cys Ser Ile Ala Pro
 1 5

<210> 1050
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -79..-1

<400> 1050
 Met Arg Phe Arg Phe Cys Gly Asp Leu Asp Cys Pro Asp Trp Val Leu
 -75 -70 -65
 Ala Glu Ile Ser Thr Leu Ala Lys Met Ser Ser Val Lys Leu Arg Leu
 -60 -55 -50
 Leu Cys Ser Gln Val Leu Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr
 -45 -40 -35

Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp
 -30 -25 -20
 Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala
 -15 -10 -5 1
 Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu
 5 10 15
 Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu
 20 25 30
 Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met
 35 40 45
 Asn Arg
 50

<210> 1051
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1051
 Met Phe Leu Ala Ala Leu Phe Thr Val Ala Lys Ile Trp Lys Gln Pro
 -10 -5 1
 Lys Cys Ser Ser Thr Asn Lys Trp Thr Lys Lys Met Trp Tyr Ile Tyr
 5 10 15
 Thr Met Glu Tyr Tyr Ser Ala Ile Lys Lys Asp Asp Ile Leu Ser Phe
 20 25 30
 Ala Thr Ile Trp Met Glu Leu Glu Ser Ile Thr Leu Ser Glu Ile Ser
 35 40 45 50
 Gly Xaa Pro Lys Asp Lys Leu Leu Met Phe Ser Leu Ile Cys Gly
 55 60 65

<210> 1052
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1052
 Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe Ala His Leu Ser
 -25 -20 -15
 Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa Ser Pro
 -10 -5 1

<210> 1053
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -78..-1

<400> 1053
 Met Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala
 -75 -70 -65
 Pro Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu
 -60 -55 -50
 Cys Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu
 -45 -40 -35
 Tyr Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala
 -30 -25 -20 -15
 Gln Leu Leu Trp Phe Leu Gln Thr Phe Phe Gly Ile Ala Ser Leu
 -10 -5 1
 Xaa Ile Leu Ile
 5

<210> 1054
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1054
 Met Cys Cys Trp Ile Trp Val Ala Ser Ile Leu Leu Arg Ile Phe Ala
 -15 -10 -5
 Ser Val Leu Ile Arg Asp Ile Tyr Leu Trp Phe Ser Phe Phe Phe
 1 5 10 15

<210> 1055
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1055
 Met Ile Ser Ser His Leu Tyr Asn Phe Ser Leu Leu Phe Phe Xaa Leu
 -20 -15 -10
 Trp Leu Arg Tyr Lys Glu Ser Gly Arg Glu Gly Asn Cys Glu Glu Gly
 -5 1 5
 Ala Phe Ser Arg Trp
 10

<210> 1056
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1056

Met	Gly	Trp	Gln	Arg	Leu	Leu	Leu	Leu	Pro	Arg	Pro	Pro	Ala	Ser	Thr
		-15					-10				-5				
Gly	Ala	Ser	Asn	Ala	Thr	Arg	Xaa	Pro	Lys	Xaa	Leu	Tyr	Arg	Xaa	Tyr
1					5				10						15
Asn	His	Gly	Val	Leu	Lys	Ile	Thr	Ile	Cys	Lys	Ser	Cys	Gln	Lys	Pro
			20					25					30		
Val	Asp	Lys	Tyr	Ile	Glu	Tyr	Asp	Pro	Val	Ile	Ile	Leu	Xaa	Asn	Ala
		35					40					45			
Ile	Leu	Cys	Lys	Ala	Xaa	Ala	Tyr	Arg	His	Ile	Leu	Phe	Asn	Thr	Gln
	50						55				60				
Ile	Asn	Asn	Lys	Leu	Pro	Ile	Leu	Leu	Ala	Phe	Leu	Pro	Ser	Cys	Gly
	65				70					75					
Xaa	Thr	Ala	His	Asp	Gly	Lys	Lys	Lys	Pro	Asn	Phe	Ile	Leu	Leu	Leu
80					85				90						95
Lys	Xaa	Tyr	Tyr	Tyr	Leu	Ala	Thr	Glu	Asn						
				100					105						

<210> 1057
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1057

Met	Ala	Ala	Gly	Val	Ser	Leu	Leu	Ala	Leu	Val	Val	Arg	Val	Ile	Leu
			-15					-10				-5			
Ser	Thr	Ala	Ile	Leu	Cys	Pro	Ser	Gly	Ala	Ser	Arg	Arg	Gln	Arg	Ser
		1				5					10				
Ser	Glu	Val	Glu	Trp	Gly	Thr	Asp	Ser							
	15					20									

<210> 1058
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1058

Met	Asn	Pro	Leu	Phe	Trp	Leu	Ile	Leu	Cys	Ser	Gly	Leu	Leu	Cys	Asn
-15				-10				-5						1	
Lys	Ser	Phe													

<210> 1059
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1059
 Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
 -15 -10 -5
 Leu Ser Leu Phe
 1

<210> 1060
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1060
 Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu Phe Val Leu Leu
 -20 -15 -10
 Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr Leu His Pro Trp
 -5 1 5

<210> 1061
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1061
 Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
 -30 -25 -20
 Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
 -15 -10 -5
 Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
 1 5 10 15
 Gly Pro Pro Gly

<210> 1062
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -22..-1

<400> 1062
Met Gly Phe Trp Cys Glu Cys Pro Phe Cys Leu Leu Val Phe Leu Leu
 -20 -15 -10
Thr Glu Trp Thr Ser Ser Lys Leu Gln Lys Thr
 -5 1 5

<210> 1063
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1063
Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu
 -20 -15 -10
Thr Pro Ala Ser Thr Gly His Trp
 -5 1

<210> 1064
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1064
Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser Ser Ser
 -25 -20 -15
Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser Arg Asn
 -10 -5 1
Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys Gly Lys
 5 10 15
Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu
20 25

<210> 1065
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1065
Met Ser Ser Ala Trp Leu Cys Leu Pro Cys Ser Leu Cys Val Ser Gln

-15 -10 -5
 Leu Leu Pro Ser Tyr Ser Leu Leu Ile Pro Ala Pro
 1 5 10

<210> 1066
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1066
 Met Ser Pro Met Trp Ala Gly Leu Leu Ser Leu Leu Gly Pro Leu Xaa
 -20 -15 -10
 Pro Pro Met Arg Ala Cys Ser Val Cys Val Leu
 -5 1 5

<210> 1067
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1067
 Met Ser Leu Asn Glu Leu Ser Ile Ala Asp Leu Leu Pro Ser Ser Ser
 -15 -10 -5
 Phe Ala Asn Pro Lys Leu Ser Gly Pro Ile Ser Ile Ser Val Thr Ser
 1 5 10
 Ala Gly Ser Pro Pro Gly Ala
 15 20

<210> 1068
 <211> 26
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1068
 Met Lys Asp Leu Leu Gly Thr Ala Phe Leu Glu Gly Ser Leu Ala Ala
 -15 -10 -5 1
 Tyr Leu Thr Met Ala Asn Ile Thr His Val
 5 10

<210> 1069
 <211> 29
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 1069

Met	Ala	Asn	Asp	Ile	Lys	His	Leu	Phe	Met	Cys	Leu	Leu	Thr	Ile	Cys
				-15				-10						-5	
Ile	Ser	Ser	Leu	Glu	Lys	Leu	Pro	Phe	Phe	Phe	Phe	Phe			
			1				5						10		

<210> 1070

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1070

Met	Tyr	Gln	Lys	Val	Thr	Ser	Tyr	Cys	Arg	Ser	Ala	Thr	Leu	Val	Gly
				-20				-15						-10	
Phe	Thr	Val	Gly	Ser	Val	Leu	Gly	Gln	Ile	Leu	Val	Ser	Val	Ala	Gly
			-5				1				5				
Trp	Ser	Leu	Phe	Ser	Leu	Asn	Val	Ile	Ser	Leu	Thr	Cys	Val	Ser	Val
	10					15					20				
Ala	Phe	Ala	Val	Ala	Trp	Phe	Leu	Pro	Met	Pro	Gln	Lys	Ser	Leu	Phe
25				30						35				40	
Phe	His	His	Ile	Pro	Ser	Thr	Cys	Gln	Arg	Val	Asn	Gly	Ile	Lys	Val
			45					50						55	
Gln	Asn	Gly	Gly	Ile	Val	Thr	Asp	Thr	Gln	Leu	Leu	Thr	Pro	Ser	Trp
			60					65					70		
Leu	Gly														

<210> 1071

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 1071

Met	Met	Pro	Pro	Ala	Leu	Phe	Phe	Leu	Leu	Arg	Ile	Ala	Trp	Leu	Leu
				-15			-10					-5			
Gly	Leu	Phe													
	1														

<210> 1072

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 1072

Met Asn Cys Val Thr Leu Ile Gln Ala Leu Ser Leu Trp Ala Ser Val
-20 -15 -10
Ser Pro Ser Trp Met Cys Arg Pro Pro Ala Ser Phe Ile Ile Thr Thr
-5 1 5 10
Thr Thr Thr Thr Cys Gly
15

<210> 1073

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1073

Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys
-15 -10 -5
Ser Pro Arg
1

<210> 1074

<211> 255

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 1074

Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala
-30 -25 -20
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
-15 -10 -5
Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
1 5 10
Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro
15 20 25 30
Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys
35 40 45
Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
50 55 60
Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly
65 70 75
Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg

80		85		90
Leu Asp Ile Arg Met Gly	Leu Leu Tyr Ile Thr	Leu Cys Ile Val Phe		
95	100	105	110	
Leu Met Thr Cys Lys Pro	Pro Leu Tyr Met Gly	Pro Glu Tyr Ile Xaa		
	115	120	125	
Tyr Phe Asn Asp Lys Thr	Ile Asp Glu Glu Leu	Glu Arg Asp Lys Arg		
	130	135	140	
Val Thr Trp Ile Val Glu	Phe Phe Ala Xaa Trp	Ser Asn Asp Cys Gln		
	145	150	155	
Ser Phe Ala Pro Ile Tyr	Ala Asp Leu Ser Leu	Lys Tyr Asn Cys Thr		
	160	165	170	
Gly Leu Asn Phe Gly Lys	Val Asp Val Gly Arg	Tyr Thr Asp Val Ser		
175	180	185	190	
Thr Arg Tyr Lys Val Ser	Thr Ser Pro Leu Thr	Lys Gln Leu Pro Thr		
	195	200	205	
Leu Ile Leu Phe Gln Gly	Gly Lys Glu Ala Met	Arg Arg Pro Gln		
	210	215	220	

<210> 1075
 <211> 153
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1075
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
-15 -10 -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
1 5 10 15
Thr Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp
20 25 30
Pro Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu
35 40 45
Arg Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn
50 55 60
Thr Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe
65 70 75
Xaa Thr Thr Gly Val Ser Ser Val Gln Thr Pro Xaa Leu Pro Thr His
80 85 90 95
Ala Asp Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser
100 105 110
Gly Ser Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu
115 120 125
Ser Gln Met Ser Gln Glu Arg Gly Val
130 135

<210> 1076
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1076
 Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
 -15 -10 -5
 Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
 1 5 10 15
 Thr Gly Val Ser Ser Val Gln Thr Pro Gln
 20 25

<210> 1077
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1077
 Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
 -15 -10 -5
 Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
 1 5 10 15
 Thr Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His Ala Asp
 20 25 30
 Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser
 35 40 45
 Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln
 50 55 60
 Met Ser Gln Glu Arg Gly Val
 65 70

<210> 1078
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 1078
 Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr Ser
 -35 -30 -25
 Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile Trp
 -20 -15 -10 -5
 Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
 1 5

<210> 1079
 <211> 72

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64..-1

<400> 1079
Met Gly Val Leu Pro Asp Leu Val Val Glu Ile Phe Gly Val Asn Lys
 -60 -55 -50
Cys Arg Leu Ser Trp Gly Leu Val Leu Glu Ser Leu Gln Gln Pro Leu
 -45 -40 -35
Ile Asn Arg His Leu Ile Tyr Cys Leu Gly Asp Ile Ile Leu Xaa Xaa
 -30 -25 -20
Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu Leu Leu Pro Xaa Leu Xaa
 -15 -10 -5
Gln Ile Pro Gln Ala Thr Leu Arg
1 5

<210> 1080
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1080
Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp Gly Ser
-15 -10 -5 1
Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser Tyr Thr
 5 10 15
Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe
 20 25

<210> 1081
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1081
Met Lys Arg Ile Arg Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro
 -35 -30 -25
Phe Pro Ile Arg Leu Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His
 -20 -15 -10
Thr Leu Gln Val Val Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala
 -5 1 5
Phe Val Leu Cys Gly Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu
10 15 20 25

<210> 1082
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1082
 Met Leu Pro Leu Leu His Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa
 -20 -15 -10
 Val Xaa Val Xaa Xaa Ala Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln
 -5 1 5 10
 Xaa Gly Arg Ala Gln Xaa Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu
 15 20 25
 Thr Lys Xaa Gly Arg Leu Leu Glu Pro Arg Asn
 30 35

<210> 1083
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1083
 Met Val Ser Val Phe Arg Ser Glu Glu Met Cys Leu Ser Gln Leu Phe
 -20 -15 -10
 Leu Gln Val Glu Ala Ala Tyr Cys Cys Val Ala Glu Leu Gly
 -5 1 5

<210> 1084
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1084
 Met Ala Ala Leu Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp
 -25 -20 -15
 Trp Ser Val Ala Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro
 -10 -5 1
 His Ser Thr Ser Thr Arg Gly Gly Val
 5 10

<210> 1085
 <211> 47

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 1085
Met Asn Ala Leu Val Asp Gly Lys Arg Leu Xaa Xaa Cys Ile Arg Tyr
 -40 -35 -30
Phe Asp Ser Ile Ser Leu Tyr Ser Lys Ala Ser Leu Ser Cys Cys Leu
 -25 -20 -15
Val Cys Val Phe Thr Cys Ser Leu Leu Ala Phe Phe Ser Pro Cys
 -10 -5 1

<210> 1086
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1086
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
 -15 -10 -5
Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe Ala Phe
 15 20 25
Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr Thr Thr
 50 55 60
Tyr Ala Ala Trp
 65

<210> 1087
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1087
Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg Gln Ser Phe Thr Xaa Xaa
 -10 -5 1
Ala Gln Ala
 5

<210> 1088

<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1088
Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala Ser Ser Ser Leu
 -15 -10 -5
Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp Val Ser
 1 5 10

<210> 1089
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1089
Met Asn Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe
 -20 -15 -10
Leu Tyr Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile
 -5 1 5
Leu Ser Phe Met Val Val Leu Gly Xaa Thr Arg
 10 15

<210> 1090
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1090
Met Thr Met Ala Val Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His
 -20 -15 -10
Leu Leu Thr Cys Val Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His
 -5 1 5

<210> 1091
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1091

Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser Ile Leu Leu
-25 -20 -15 -10
Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr Arg Thr Ser
-5 1 5
Pro Ala

<210> 1092

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1092

Met Gly Ser Pro Tyr Val Ala His Val Gly Leu Glu Leu Leu Thr Ser
-20 -15 -10
Ser Asp Pro Pro Ser Leu Ala Ser Gln Val Leu Gly Ile His
-5 1 5

<210> 1093

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 1093

Met His Leu Tyr Thr His Val Cys Trp Leu Thr Leu Thr Leu Ala His
-15 -10 -5
Ser His Ser Leu Thr His Thr His Thr Leu Thr Pro Ser His Thr Arg
1 5 10
Thr His Ser His Thr Cys Ala Cys Leu His Ala His Lys
15 20 25

<210> 1094

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1094

Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly His
-15 -10 -5 1
Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His Cys
5 10 15

Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser Xaa
 20 25 30
 Ile Tyr Arg
 35

<210> 1095
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1095
 Met Asn Val Leu Ile Ile Val Phe Val Ala Phe Ala Phe Gly Phe Leu
 -10 -5 1
 Val Met Lys Ser Leu Leu Lys Pro Met Ser Arg Arg Val Phe Leu Met
 5 10 15
 Leu Ser Ser Arg Ile Phe Met Val Ser Gly Leu Arg Phe Lys Ser Leu
 20 25 30
 Ile His Leu Glu Leu Ile Phe Val Tyr Lys Leu Arg Asp Glu Asp Pro
 35 40 45 50
 Val Ser Phe Phe Tyr Met Trp Leu Ala Asn Tyr Pro Ser Thr Ile Cys
 55 60 65

<210> 1096
 <211> 116
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1096
 Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu
 -20 -15 -10 -5
 Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro
 1 5 10
 Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln
 15 20 25
 His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly
 30 35 40
 Ser Ser Cys Asn Thr Xaa Ala Ser Cys Gln Gln Gln Ala Arg Asn Val
 45 50 55 60
 Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn
 65 70 75
 Xaa Leu Asp Trp Arg Arg Arg Ala Arg Ile Xaa Gly Pro Trp Xaa Glu
 80 85 90
 Leu His Gly Xaa
 95

<210> 1097

<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1097
Met Val Phe Leu Phe Leu Met Ile Ser Val Phe Ala Gly Cys Gln Ile
 -10 -5 1
Pro Ser Gly
 5

<210> 1098
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1098
Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala Ser
 -20 -15 -10
Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly Met
-5 1 5 10
Ser Xaa His Thr Leu Ala
 15

<210> 1099
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1099
Met Leu Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp
 -10 -5 1
Ser Gln Asn
 5

<210> 1100
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1100

Met Thr Asn Leu Phe Met Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn
-15 -10 -5
Ala Lys Cys Leu Phe Ser Leu Phe Pro Phe Phe Ile Glu Gly
1 5 10

<210> 1101

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 1101

Met Leu Gly Tyr Ile Trp Xaa Gln Asp Lys Val Phe Ala Asn Cys Val
-25 -20 -15
Leu Phe Thr Leu Leu Val Ser Thr Arg Ser Gly Arg Ser Arg Ala Gly
-10 -5 1 5
Cys Ala Trp Arg Trp Arg Gly Arg Trp Ser Val Gly Gln Lys Gly Xaa
10 15 20

<210> 1102

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1102

Met Xaa Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15 -10 -5 1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Arg
5 10

<210> 1103

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 1103

Met Cys His Arg Arg Trp Leu His Leu Ser Thr Arg His Leu Gly Phe
-35 -30 -25
Lys Pro Arg Ile His Tyr Val Phe Val Leu Met Leu Ser Leu Pro Leu
-20 -15 -10
Pro Pro Thr Pro Gln Gln Ala Leu Gly

-5

1

<210> 1104
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1104
Met Asp His Val Val Ile Phe Val Ile Phe Pro Ala Ala Leu Leu Leu
 -15 -10 -5
Cys Trp Gly Gly Leu Ile Pro Leu Cys Ile Ile Tyr Pro Pro Ile Ala
 1 5 10
Asp Thr Val Gly
 15

<210> 1105
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1105
Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile
-25 -20 -15 -10
Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val
 -5 1 5

<210> 1106
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1106
Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln Gln Ala Pro
 -10 -5 1
Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr
 5 10

<210> 1107
<211> 79
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1107
 Met Arg Val Cys Met Arg Leu Cys Ala Cys Val Tyr Ala Cys Val Cys
 -20 -15 -10
 Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val Cys Met Xaa Val Arg
 -5 1 5 10
 Ala His Leu Cys Val Cys Met Cys Val Cys Met Cys Val His Leu Cys
 15 20 25
 Val Cys Met Cys Val Cys Val Cys Ala Ser Val Cys Val Cys Met Cys
 30 35 40
 Ala Cys Val Cys Met Cys Val Cys Val Arg Ala Ser Val Cys Val
 45 50 55

<210> 1108
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1108
 Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn Leu Val Leu Phe
 -20 -15 -10
 Ile Ser Ile Ala Ala Leu Arg
 -5 1

<210> 1109
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -51..-1

<400> 1109
 Met Glu Glu Leu Asp Arg Lys Trp Arg Glu Lys Val Leu Pro Ala Ala
 -50 -45 -40
 Lys Leu Ile Lys Arg Arg Asn Leu Phe Ser Thr Cys Thr Pro Gln Tyr
 -35 -30 -25 -20
 Gly Thr His Ala Ala Phe Leu Ser Leu His Ala Ser Leu Val Thr Lys
 -15 -10 -5
 Ala Phe Ser Ile Asn Ser Trp Glu Trp
 1 5

<210> 1110
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 1110

Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg Pro Leu Leu Leu
-25 -20 -15 -10
Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg
-5 1

<210> 1111

<211> 32

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 1111

Met Ser Cys Leu Leu Arg Ala Tyr Ile Ile Trp Ile Phe Pro Ser Phe
-25 -20 -15
Leu Pro Ser Leu Leu Ser Ser Phe Leu Leu Ser Leu Pro Pro Ser Gly
-10 -5 1 5

<210> 1112

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36..-1

<400> 1112

Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys Ile Phe
-35 -30 -25
Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe Leu Cys
-20 -15 -10 -5
Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln Phe Tyr
1 5 10
Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe Ala Gln
15 20 25
Ser Asn Trp
30

<210> 1113

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 1113

Met Ala Leu Leu Gly Lys Arg Cys Asp Val Pro Thr Asn Gly Cys Gly
 -45 -40 -35
Pro Asp Arg Xaa Xaa Xaa Gly Xaa Asn Pro Gln Xaa Arg Asp His His
 -30 -25 -20
Gln Xaa Xaa Val Cys Leu Arg Leu His Val Leu Ser Ala Val Gln Thr
 -15 -10 -5
Glu Arg Arg Gly Asp Gly
1 5

<210> 1114

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32..-1

<400> 1114

Met Arg Pro Ala Leu Arg Ser Phe Trp His Ser Ser Gly Gly Pro Pro
 -30 -25 -20
Pro Ser Ala Thr Leu Ala Leu Leu Ser Ser Asp Ser Val Ala Thr Gly
 -15 -10 -5
Ser Val Val Ser Arg
1 5

<210> 1115

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 1115

Met Leu Cys Ala Cys Lys Ala Arg Gly Val Met Leu Leu Leu Phe Ser
 -25 -20 -15
Gly Trp Leu Val Trp Trp Gly Ser Arg Ser Ser Gln Xaa Leu Arg Met
 -10 -5 1 5
Pro Glu Xaa Xaa Val Ser Gly Glu Gly Arg Ser Asp Xaa Xaa Pro His
 10 15 20
Gly

<210> 1116

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 1116

Met	Ile	Ser	Ser	Ser	Leu	Ser	Gly	Arg	Val	Pro	Val	Ile	Leu	Gly	Asn
		-40					-35					-30			
Leu	Met	Gly	Val	Gly	Ala	Ala	Val	Arg	Arg	Met	Gly	Phe	Ser	Leu	Ile
		-25				-20					-15				
Leu	Pro	Thr	Ser	Pro	Ser	Pro	Ala	His	Ser	Gly	Ser	Ala	Pro	Ser	Ala
-10					-5					1				5	
Gly	Pro	Arg													

<210> 1117

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -46..-1

<400> 1117

Met	Gly	Ile	Ile	Gln	Xaa	Ile	Leu	Ala	Thr	Ser	Arg	Asp	Cys	Tyr	Ser
	-45					-40				-35					
Phe	Lys	Lys	Lys	Pro	Ile	Pro	Lys	Lys	Pro	Thr	Met	Leu	Ala	Leu	Ala
-30				-25					-20					-15	
Lys	Ile	Leu	Leu	Ile	Ser	Thr	Leu	Phe	Tyr	Ser	Leu	Leu	Ser	Gly	Ser
				-10				-5						1	
His	Gly	Lys	Xaa	Asn	Gln	Asp	Val								
		5					10								

<210> 1118

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1118

Met	Met	Leu	Ser	Thr	Phe	Ser	Tyr	Ala	Cys	Leu	Pro	Phe	Val	Cys	Leu
		-20						-15				-10			
Leu	Leu	Arg	Asn	Val	Tyr	Ser	Asp	Leu	Leu	Pro	Asn	Arg			
		-5				1				5					

<210> 1119

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1119

Met Leu Ala Ile Leu Thr Gly Gly Arg Trp Tyr Leu Ile Val Val Leu
 -20 -15 -10
Val Cys Ile Ser Leu Val Ile Ile Asp Asp Asp Glu His Gly
 -5 1 5

<210> 1120

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1120

Met Leu Leu Pro Leu Gly Leu Lys Val Leu Gly Leu Gln Ala Arg Gly
 -10 -5 1
Thr Thr

<210> 1121

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 1121

Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys Gly Val Thr Pro
 -25 -20 -15
Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala Ser Ser Pro Ser
 -10 -5 1
Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile Ser Gln Arg Ala
5 10 15 20

<210> 1122

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -33..-1

<400> 1122

Met Gly Lys Lys Lys Ile Trp Thr Pro Ser Ser Tyr Pro Met Pro Ser
 -30 -25 -20
His Lys His Val Ser Leu Cys Leu Leu Thr Val Ala Val Leu Val Leu
 -15 -10 -5
Thr Phe Lys Ser Leu Ile His Phe Glu Xaa Ile Phe Ala Tyr Glu Ile
1 5 10 15
Gly Val Gln Gly

<210> 1123
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1123
 Met Ser Pro Val Leu Cys Phe His Arg Cys Ser Cys Pro Ser Leu Leu
 -20 -15 -10
 Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro Glu Pro Leu Leu Gly
 -5 1 5

<210> 1124
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1124
 Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile Met Phe Val Cys
 -20 -15 -10
 Met Cys Val Cys Val Cys Val Cys Val Tyr Arg Leu Phe Ser Ser Ser
 -5 1 5
 Ser Pro
 10

<210> 1125
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -91..-1

<400> 1125
 Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys Met
 -90 -85 -80
 Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe Lys
 -75 -70 -65 -60
 Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu Xaa
 -55 -50 -45
 Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly Glu
 -40 -35 -30
 Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg Val
 -25 -20 -15
 Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg Gln

-10 -5 1 5
 Ser Gln Gln Ala Thr
 10

<210> 1126
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1126
 Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe Phe Phe Phe Xaa
 -20 -15 -10 -5
 Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa Ser Gly Ala Ile
 1 5 10
 Ile Ala Asn Ser
 15

<210> 1127
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 1127
 Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
 -40 -35 -30
 Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala Arg Pro Thr Phe Arg
 -25 -20 -15
 Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly Pro
 -10 -5 1

<210> 1128
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1128
 Met Pro Ala Leu Gly Pro Ala Leu Leu Gln Gly Ser Leu Xaa Arg Val
 -10 -5 1
 Gly Pro His Pro Pro Ala Pro Ser Thr Asn Cys Ile His Ser Gln Trp
 5 10 15
 His Val Ser Ala Ala Xaa Gly Lys Gly Pro His Leu Arg His Pro Leu
 20 25 30

Xaa Gly Xaa Tyr Gln Leu Pro Val Pro Ala Glu Pro Trp Ala Ala Ala
 35 40 45 50
 Gly Gly His Ser Val His
 55

<210> 1129
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1129
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr
 1

<210> 1130
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1130
 Met Ala His Ser Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg
 -10 -5 1
 Ser Phe Leu Gly Asn Trp
 5

<210> 1131
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1131
 Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys
 -20 -15 -10 -5
 Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val Gly Gly Ala
 1 5 10

<210> 1132
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1132
 Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe Glu
 -10 -5 1

<210> 1133
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1133
 Met Trp Ala Ser Ser Pro Trp Pro Ser Ala Trp Ser Cys Cys Cys Leu
 -20 -15 -10
 Ser Ser Ser Ser Phe Ile Ala Gly Arg Arg Arg Gly Trp Thr Gln Met
 -5 1 5
 Trp Leu Thr Arg Pro Phe Ser Pro Gln Ala Ser Ser Pro Ser Ala
 10 15 20

<210> 1134
 <211> 49
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1134
 Met Thr Met Pro Ile Ser Ser Tyr Ser Gln Asn Val Leu Ser Asn Phe
 -30 -25 -20
 His Asp Gly Tyr Phe Met Leu Ile Ile Leu Ser Ala Ile Leu Leu Asn
 -15 -10 -5
 Ser Phe Ile Gly Cys Val Ser Phe Tyr His Cys Phe Ser Trp Gly Ser
 1 5 10 15
 Gly

<210> 1135
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1135

Met Leu Thr His Gly Ala Ser Leu Ser Leu Val Ile Phe Leu Leu Thr
 -20 -15 -10 -5
 Val Lys His Cys Phe Arg Tyr Arg Val Tyr Lys Thr
 1 5

<210> 1136
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1136
 Met Ser Ser Val Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile
 -20 -15 -10
 Leu Pro Leu Ser Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp
 -5 1 5 10
 Gly Met Trp

<210> 1137
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1137
 Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser Gly
 -30 -25 -20
 Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe
 -15 -10 -5
 Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys
 1 5 10 15
 Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp
 20 25 30
 Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val
 35 40 45
 Val Xaa

<210> 1138
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1138
 Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala Leu Val Phe Pro

-15 -10 -5
 Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu Cys Phe Gly Ala
 1 5 10 15
 Ser Leu Pro Pro Leu Gly Arg Ser Leu Leu Gly Gln Gly Ser Ser Phe
 20 25 30
 Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu Xaa Pro His
 35 40 45

<210> 1139
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -62..-1

<400> 1139
 Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro Ala Thr
 -60 -55 -50
 Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu Tyr Ile
 -45 -40 -35
 Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg Val Tyr
 -30 -25 -20 -15
 Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa Xaa Pro
 -10 -5 1
 Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu Phe Cys
 5 10 15

<210> 1140
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 1140
 Met Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu
 -35 -30 -25
 Phe Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val
 -20 -15 -10 -5
 Leu Ile Ser Gly Leu Gly
 1

<210> 1141
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1141

Met Asp Lys Val Glu Leu Pro Pro Pro Asp Leu Gly Pro Ser Ser Ala
 -25 -20 -15
Leu Asn Gln Thr Leu Met Leu Leu Arg Glu Val Leu Ala Ser His Asp
 -10 -5 1
Ser Ser Val Val Pro Leu Asp Ala Arg Gln Ala Asp Phe Val Gln Gly
 5 10 15

<210> 1142

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32..-1

<400> 1142

Met Gly Gly Thr Ala Gly Trp Ser Ser Gln Asn Thr His Asn Ile Xaa
 -30 -25 -20
Val His His Leu Val Trp Leu Trp Phe Val Val Pro Gln Thr Ile Thr
 -15 -10 -5
Met Ile Thr Pro Lys Ile Thr Glu His Arg Pro Xaa Ile Thr Asp Xaa
1 5 10 15
Xaa Ile Met Xaa Thr Phe Glu Xaa Leu Gly Glu Leu Pro
 20 25

<210> 1143

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 1143

Met Cys Leu Ser Val Ala Leu Tyr Leu Cys Val Cys Val Cys Val Cys
 -15 -10 -5
Leu Ile Ala Arg Val Tyr Phe Cys Ile Tyr Val Cys Val Trp
 1 5 10

<210> 1144

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1144

Met Leu His Leu Leu Phe Gly Leu Phe Pro Val Leu Trp Met Phe Leu

[illegible]

Pro Lys Thr Thr Xaa Gln
30

<210> 1148
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1148
Met Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr
-40 -35 -30
Ser Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala
-25 -20 -15
Xaa Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp
-10 -5 1 5
Val Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala
10 15 20
Gln Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa
25 30 35
Val Ser Leu Gly Val Gly Pro Ala Gly Pro Lys Xaa Gly Val Ile Ser
40 45 50
Gln Leu Glu Arg Gly Asp Glu Pro Trp Val Leu Asp Val Gln Gly Thr
55 60 65 70
Ser Gly Lys Glu His Leu Lys Lys Ser Thr Ala Gln Leu Leu Gly Pro
75 80 85
Glu Leu Lys Tyr Lys Glu Leu
90

<210> 1149
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1149
Met Ile Pro Arg Arg Thr Ser Ala Ser Arg Ala Pro Ser Val Pro Gln
-35 -30 -25
Asn Ala Gly Leu Ser Pro Leu Pro Ala Leu Ser Ser Leu Cys Val Ser
-20 -15 -10
Trp Gly Thr Ser Ser Thr Val Thr Arg Leu Arg Pro Trp Ile Ser Pro
-5 1 5 10
Thr Trp Thr Ser Arg Ala Arg
15

<210> 1150
<211> 56
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1150

```
Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe Pro Asn Pro
                    -10                    -5                    1
Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa Ile Gly Leu
      5              10              15
Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe Arg Leu Xaa
    20              25              30
Gly Leu Gly Gln Asp Ser Leu Cys
35              40
```

<210> 1151

<211> 25

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 1151

```
Met Xaa Xaa Tyr Xaa Xaa Xaa Gly Phe Cys Ser Val Thr Ser Ser Pro
-20              -15              -10              -5
Leu Ala Ser Ala Gly Arg Thr Thr Arg
              1              5
```

<210> 1152

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1152

```
Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys Pro Leu
                    -20                    -15                    -10
Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln Gln Val
      -5              1              5
Asn Leu Pro Cys Ser Ser
10              15
```

<210> 1153

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
<222> -39..-1

<400> 1153

Met	Met	Ile	Leu	Ile	Leu	Ile	Leu	Glu	His	Ile	Val	Thr	Xaa	Lys	Arg
			-35					-30						-25	
Asn	Pro	Lys	Pro	Val	Thr	Val	Pro	Ala	Phe	Leu	Xaa	Pro	Cys	Leu	Thr
			-20					-15					-10		
Ser	Phe	Ser	Cys	Xaa	Gly	Ala	Ser	Phe	Ser	Leu	Xaa	Gly	Xaa	Arg	Arg
		-5					1				5				
Gly	Trp	Gln	His	Gly	Ser	Cys	Cys	Ser	Thr	Ile	Pro	Leu	Phe	Xaa	Thr
10				15						20					25
Leu	Asn	Ser	Leu	Gly	Gln	Gly	Leu	Ile	Gly	Pro	Ala	Tyr	Ile	Gly	Ala
			30						35					40	

<210> 1154

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1154

Met	Ser	Thr	His	Ala	Ile	Ser	Ile	Leu	Leu	Cys	Ile	Gly	Ala	Ser	Ser
	-15					-10					-5				
Gln	Gly	Arg													
1															

<210> 1155

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31..-1

<400> 1155

Met	Glu	Glu	Gln	Glu	Thr	Glu	Glu	Val	Gly	Gly	Arg	Ser	Ser	Arg	Lys
	-30					-25					-20				
Asn	Ala	Ala	Thr	Val	Asn	Ala	Ala	Ser	Leu	Pro	Pro	Cys	Phe	Gly	Val
-15					-10					-5				1	
Lys	Ser	Cys	Arg	Cys	Arg	Arg	Cys	Ser	Cys	Arg	Arg	Cys	Leu	Leu	Tyr
		5					10					15			
Phe	Ser	Trp	Pro	Arg	Gly	Arg	Ile	Ser	Pro	Pro	Val	Gly	Gln	Cys	Ala
		20					25					30			
Gly	Arg	Gly													
35															

<210> 1156

<211> 145

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -33..-1

<400> 1156

```
Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser Ser Ala Xaa
      -30                      -25                      -20
Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser Gly Ala Thr
      -15                      -10                      -5
Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala Val Xaa Ser
      1                      5                      10                      15
Thr Asn Thr Ala Ser Arg Gly Arg Thr Trp Cys Arg Ala Thr Gly Pro
      20                      25                      30
Cys Pro Ser Gly Pro Thr Arg Gly Val Ser Arg Ser Arg Gly Leu Gly
      35                      40                      45
Ala Gly Phe Leu Ser Pro Phe Cys Cys Leu Phe Ala Phe His Pro Arg
      50                      55                      60
Leu Pro Trp Cys Ala Glu Val Pro Val Pro Ala Ala Ala His His Met
      65                      70                      75
Arg Cys Gly Gly Asp Leu Leu Ala Ala Pro Pro Pro Gly Pro Ser Trp
      80                      85                      90                      95
Phe Ala Arg Phe Pro Pro Leu Val Pro Glu Ser Phe Pro His His Ser
      100                      105                      110
Val
```

<210> 1157

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1157

```
Met Phe Ser Ser Arg Ser Phe Met Val Ser Gly Leu Ile Trp Val Phe
      -20                      -15                      -10
Gly Leu Val Ser Val Leu Ser Xaa Phe Leu Cys Met Val Tyr Asp Gln
      -5                      1                      5
Gly Gln
      10
```

<210> 1158

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13..-1

<400> 1158

Met Leu Leu Ala Val Ser Leu Ser Leu Val Ser Asn Cys Asn Phe Val
 -10 -5 1
 Leu Thr Asp Gln Leu Phe Pro Ala Pro Ala Ser Leu Ile Pro Glu
 5 10 15

<210> 1159
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1159
 Met Asn Gln Asp Phe Asn Pro Glu Ile Glu Ala Ser Pro Gln Val Lys
 -25 -20 -15
 Thr Gly Val Phe Leu Phe Ser Ile Ile Gly Ser Phe Gly Phe Pro Gly
 -10 -5 1
 Met Cys Asn Cys Lys Asn Pro Ala Arg
 5 10

<210> 1160
 <211> 24
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1160
 Met Pro Cys Ser Trp Ser His Ile Val Ser Ser Leu Phe Ser Trp Leu
 -20 -15 -10 -5
 Leu Ser Leu Thr Ser Val Pro Gly
 1

<210> 1161
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1161
 Met Phe Phe Phe Gly Tyr Ser Glu Asp Ile Tyr Cys Val Ser Gly Pro
 -25 -20 -15
 Val Leu Ser Cys Cys Cys Leu Thr Ala Gly Arg Ala Arg Leu Trp
 -10 -5 1

<210> 1162
 <211> 58

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1162
Met Pro Tyr Ala Ala Leu Ile Cys Pro Trp Ser Ser Gln Val Pro Ser
-15 -10 -5
Ser Pro Pro Ala Ser Leu Glu Ala Ser Ser Asn Val Tyr Leu Gln Glu
1 5 10 15
Ser Arg Ala Ala Tyr Ala Ser Val Pro Ala Gly Pro Glu Val Ala Thr
20 25 30
Gln His Thr Ser Ser Pro Val Thr Pro Met
35 40

<210> 1163
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1163
Met Gln Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile
-15 -10 -5
Lys Ala Gly Thr
1

<210> 1164
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1164
Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr Ser Ser Ala Ala
-20 -15 -10 -5
Pro Ser Arg Ala Arg Gln Gly Ala
1

<210> 1165
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -42..-1

<400> 1165

Met Leu Ala Ser Ala Pro Arg Leu Asn Ser Ala Asp Arg Pro Met Lys
-40 -35 -30
Thr Ser Val Leu Arg Gln Arg Lys Gly Ser Val Arg Lys Gln His Leu
-25 -20 -15
Leu Ser Trp Ala Xaa Gln Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu
-10 -5 1 5
Gln Ser Glu Lys Gln Thr Xaa Xaa Asp
10 15

<210> 1166

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -38..-1

<400> 1166

Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser
-35 -30 -25
Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala
-20 -15 -10
Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro
-5 1 5

<210> 1167

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1167

Met Arg Val Phe Ile Ala Ala Leu Phe Thr Ile Ala Glu Thr Trp Asn
-15 -10 -5
Gln Pro Lys Cys Pro
1 5

<210> 1168

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1168

Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser Met
 -30 -25 -20 -15
 Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp Ser
 -10 -5 1
 Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val Asn
 5 10 15
 Gly Pro Leu Tyr His Pro Arg
 20 25

<210> 1169
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1169
 Met Pro Ser Pro Gln Leu Leu Val Leu Phe Gly Ser Gln Thr Gly Thr
 -15 -10 -5
 Ala Gln Asp Val Ser Glu Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg
 1 5 10 15
 Leu Gly Cys Arg Val Gln Ala Leu Asp Ser Tyr Pro Val Val Asn Leu
 20 25 30
 Ile Asn Glu Pro Leu Val Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly
 35 40 45
 Asp Pro Pro Asp Asn Met Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys
 50 55 60
 Asn Leu Pro Ser Thr Ala Arg
 65 70

<210> 1170
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 1170
 Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu Tyr Tyr
 -40 -35 -30
 Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe Leu Phe
 -25 -20 -15 -10
 Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr Gln Ser
 -5 1 5

<210> 1171
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1171
 Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
 -25 -20 -15
 Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
 -10 -5 1
 Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val
 5 10 15 20
 Gly Val Trp

<210> 1172
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 1172
 Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln Xaa Arg
 -45 -40 -35
 Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys Ser Ser
 -30 -25 -20 -15
 Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys Val Pro
 -10 -5 1
 Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly Met Leu
 5 10 15
 Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys Asn Thr
 20 25 30
 Phe Ile Val Trp Xaa Cys Ile Phe Ser Cys Leu Gly Met Gln Leu Xaa
 35 40 45 50
 Ser Ser Xaa Val Ser Asn Val Arg Leu Leu Leu Ser His
 55 60

<210> 1173
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1173
 Met Pro His Pro Leu Ala Thr Ser Ala Phe Leu Arg Ser Ala Phe Pro
 -25 -20 -15
 Phe Val Cys Leu Thr Phe Cys Val Gly Gly Gly Pro Gly Ile Ser Gly
 -10 -5 1 5
 Val Tyr Arg Leu Leu Met Ala Asn Ala Thr Arg Arg Glu Ser Glu Val
 10 15 20

Ser Leu Arg Gly Leu Gly Arg Asp Gly Glu Gly Ala Arg Ala Thr Pro
 25 30 35

<210> 1174
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1174
 Met Thr Val Gly Leu His Ile Leu Arg Asp Ser Leu Met Val Phe Leu
 -20 -15 -10
 Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg
 -5 1

<210> 1175
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1175
 Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu Leu
 -20 -15 -10
 His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro Arg
 -5 1 5 10
 Pro Pro Leu

<210> 1176
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1176
 Met Ala Gly Ala Ala Arg Trp Val Gly Gln Xaa Ser Ser Ala Met Val
 -25 -20 -15
 Cys Phe Gly Cys Pro Gly Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg
 -10 -5 1 5
 Gly Arg Gln Ala Ser Arg Val Pro Arg Leu Glu Asn Gly Ala Gln Arg
 10 15 20
 Val Val Arg Thr Met Val His Leu Val Leu Gln Pro Lys Arg Val Thr
 25 30 35
 Leu Val His Pro Pro Arg Gly Leu Glu Pro Val Cys Thr Pro Ile Ala
 40 45 50

Xaa Met Xaa Pro Lys Ser His Gly Leu Arg Ser Ser Leu
 55 60 65

<210> 1177
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 1177
 Met Gly Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln
 -30 -25 -20
 Glu Asn Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu
 -15 -10 -5
 Tyr Gly Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp
 1 5 10

<210> 1178
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1178
 Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser Cys Xaa Arg Ser Leu
 -15 -10 -5 1
 Ser

<210> 1179
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 1179
 Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr Leu
 -35 -30 -25
 Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe Asn
 -20 -15 -10
 Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln Trp
 -5 1 5

<210> 1180
 <211> 17
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13..-1

<400> 1180

Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala Tyr Gln Leu
 -10 -5 1
Ala

<210> 1181

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1181

Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly
 -15 -10 -5
Ser Thr Phe Xaa Ala Tyr Leu
1 5

<210> 1182

<211> 35

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1182

Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val Ser Leu Ser Leu Ser
 -15 -10 -5
Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe Ser Cys Phe Leu Leu
1 5 10 15
Pro Thr Arg

<210> 1183

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1183

Met Phe Ile Ala Ala Leu Phe Thr Val Ala Lys Ile Trp Asn Gln Pro
 -10 -5 1

Lys Cys Pro Ser Thr Asp Glu Trp Ile Asn Lys Met Trp Tyr Ile Tyr
5 10 15
Thr Met Glu Tyr Tyr Pro Asp Ile Lys Lys Asn Gly Ile Leu Thr Phe
20 25 30
Lys Ala Thr Arg Met Asn Arg Lys Thr Leu
35 40

<210> 1184
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1184
Met Cys Val Cys Gly Cys Leu Cys Val Trp Met Cys Val Cys Gly Xaa
-15 -10 -5 1
Val Cys Ile Tyr Ile Xaa Val Tyr Val Cys Thr Cys Val Arg Gly
5 10 15

<210> 1185
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1185
Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val Phe Leu Ser Leu
-25 -20 -15
Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe Phe Leu Xaa
-10 -5 1 5
Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys Asp Phe Lys Ser
10 15 20
Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His Ala
25 30 35

<210> 1186
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1186
Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu Ser
-25 -20 -15
Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met Gly

-10 -5 1 5
 Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser Ile
 10 15 20
 Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly
 25 30 35

<210> 1187
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1187
 Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu Val Tyr
 -20 -15 -10
 Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr Phe Ser
 -5 1 5 10
 Ser Pro Gln Thr Gly
 15

<210> 1188
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -37..-1

<400> 1188
 Met Arg Arg Ala Trp Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro
 -35 -30 -25
 Ala Glu Arg Ala Asp Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu
 -20 -15 -10
 Arg Val Cys Cys Ser Gln Arg Ser
 -5 1

<210> 1189
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 1189
 Met Leu His Leu Ile Cys Ile Ser Leu Ile Val Asn Asp Phe Phe Ile
 -25 -20 -15 -10
 Cys Leu Leu Ala Ile Cys Val Ser Ser Phe Glu Asn Cys Leu Phe Met
 -5 1 5

Ser Leu Ala His Ser
10

<210> 1190
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 1190
Met Arg Ser Glu Arg Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser
-60 -55 -50
Gln Arg Lys Arg Lys Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu
-45 -40 -35
Cys Ser Leu Asp Ile Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu
-30 -25 -20
Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa
-15 -10 -5 1
Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg
5 10 15
Ser Glu Ser Arg Pro Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn
20 25 30

<210> 1191
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1191
Met Val Phe Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro
-20 -15 -10 -5
Ser Leu Leu Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe
1 5 10
Gln Phe Phe Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly
15 20 25

<210> 1192
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1192
Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile

-35 -30 -25
 Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
 -20 -15 -10
 Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
 -5 1 5 10
 Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu His
 15 20 25
 Gly

<210> 1193
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1193
 Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala Ile Pro
 -15 -10 -5
 Arg Xaa Thr Ser Gly Xaa Gln Asp Leu Pro Asn Trp
 1 5 10

<210> 1194
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 1194
 Met Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly
 -35 -30 -25
 Thr Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser
 -20 -15 -10
 Phe Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser
 -5 1 5
 Val Gly
 10

<210> 1195
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -62..-1

<400> 1195
 Met Met Leu Arg Gly Gly Gly Thr Phe Lys Xaa Cys Leu Ser His Glu

-60 -55 -50
 Gly Ser Ser Phe Thr Lys Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser
 -45 -40 -35
 Cys Gly Thr Arg Leu Ile Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg
 -30 -25 -20 -15
 Leu Pro Leu Ala Ala Cys Pro Leu Leu Leu Pro Ile Phe Ser His Ala
 -10 -5 1
 Arg Ser Ser
 5

<210> 1196
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 1196
 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn
 -40 -35 -30 -25
 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
 -20 -15 -10
 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
 -5 1 5
 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
 10 15 20
 Glu His Thr Thr
 25

<210> 1197
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 1197
 Met Ser Pro Ala Pro Asp Ala Ala Pro Ala Pro Ala Ser Ile Ser Leu
 -40 -35 -30
 Phe Asp Leu Ser Ala Asp Ala Pro Val Phe Gln Gly Leu Ser Leu Val
 -25 -20 -15 -10
 Ser His Ala Pro Gly Glu Ala Leu Ala Arg Ala Pro Arg Thr Ser Cys
 -5 1 5
 Ser Gly Ser Gly Glu Arg Glu Ser Pro Glu Arg Lys Leu Leu Gln Gly
 10 15 20
 Pro Met Asp Ile Ser Glu Lys Leu Phe Cys Ser Thr Cys Asp Gln Thr
 25 30 35
 Phe Gln
 40

<210> 1198
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 1198
 Met Leu Leu His Tyr Leu Lys Leu Lys Gly Asp Gln Trp Lys Leu Ser
 -35 -30 -25 -20
 Ser Val Ser Thr Leu Ile Leu Phe Ile Phe Ile Gly Ser Leu Gln Pro
 -15 -10 -5
 Val Pro Thr Arg Phe Lys Arg Phe Ser Cys Leu Xaa His Leu Ser Ser
 1 5 10
 Arg Asp His Arg Gln Ala Leu Arg
 15 20

<210> 1199
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -153..-1

<400> 1199
 Met Ala Glu Gly Asp Asn Arg Ser Thr Asn Leu Leu Ala Ala Glu Thr
 -150 -145 -140
 Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp Gly Glu Val Met Leu Met
 -135 -130 -125
 Ala Asp Lys Val Leu Arg Trp Glu Arg Ala Trp Phe Pro Pro Ala Ile
 -120 -115 -110
 Met Gly Val Val Ser Leu Val Phe Leu Ile Ile Tyr Tyr Leu Asp Pro
 -105 -100 -95 -90
 Ser Val Leu Ser Gly Val Ser Cys Phe Val Met Phe Leu Cys Leu Ala
 -85 -80 -75
 Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg Ile Phe Gly Ser Asn Lys
 -70 -65 -60
 Trp Thr Thr Glu Gln Gln Gln Arg Phe His Glu Ile Cys Ser Asn Leu
 -55 -50 -45
 Val Lys Thr Arg Arg Arg Ala Val Gly Trp Trp Lys Arg Leu Phe Thr
 -40 -35 -30
 Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe Met Thr Met Ile Val Ser
 -25 -20 -15 -10
 Leu Ala Ala Val Ala Trp Val Gly Gln Gln Val His Asn Leu Leu Leu
 -5 1 5
 Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu Pro Gly Leu Asn Gln
 10 15 20
 His Gly Ile Ile Leu Lys Tyr Ile
 25 30

<210> 1200
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1200
 Met Ala Ala Leu Lys Ala Leu Val Ser Gly Cys Gly Arg Leu Leu Arg
 -25 -20 -15
 Gly Leu Leu Ala Gly Pro Ala Ala Thr Ser Trp Ser Arg Leu Pro Ala
 -10 -5 1 5
 Arg Gly Phe Arg Glu Val Val Glu Thr Gln Glu Gly Lys Thr Thr Ile
 10 15 20
 Ile Glu Gly Arg Ile Thr Ala Thr Pro Lys Glu Ser Pro Asn Pro Pro
 25 30 35
 Asn Pro Ser Gly Gln Cys Pro Ile Cys Arg Trp Asn Leu Lys His Lys
 40 45 50
 Tyr Asn Tyr Asp Asp Val Leu Leu Leu Ser Gln Phe Ile Arg Pro His
 55 60 65 70
 Gly Gly Met Leu Pro
 75

<210> 1201
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1201
 Met Gly Ser Leu Leu Phe Ile Arg Gln Thr Leu Val Gly Phe Lys Gln
 -20 -15 -10
 Val Val Ala Trp Thr Phe Ala Ser Asp Ser His Cys Xaa Xaa Val Xaa
 -5 1 5
 Met Val Xaa Xaa Ser Gln Leu Xaa Asn Pro Pro Leu
 10 15 20

<210> 1202
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1202
 Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly
 -20 -15 -10

Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu
 -5 1 5
 Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly
 10 15 20

<210> 1203
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1203
 Met Asn Ala Ser Leu Leu Ser Phe Cys Leu Cys Ser Asp Phe Ile Ser
 -15 -10 -5
 Gln Asp Ala Leu Leu Leu Thr Val Ile Phe Pro Pro
 1 5 10

<210> 1204
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60..-1

<400> 1204
 Met Leu Asn Met Glu Pro Tyr Thr Val Ser Gly Met Ala Arg Gln Asp
 -60 -55 -50 -45
 Ser Ser Ser Glu Val Gly Glu Asn Gly Arg Ser Val Asp Gln Gly Gly
 -40 -35 -30
 Gly Gly Ser Pro Arg Lys Lys Val Ala Leu Thr Glu Asn Tyr Glu Leu
 -25 -20 -15
 Val Gly Val Ile Val His Ser Gly Gln Ala His Ala Gly His Tyr Tyr
 -10 -5 1
 Ser Phe Ile Lys Asp Arg Arg Gly Cys Gly Lys Gly Lys Trp Leu
 5 10 15

<210> 1205
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1205
 Met Xaa Xaa Ala His Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro
 -20 -15 -10 -5
 Pro Ile Leu Ala Ser Pro Val

1

<210> 1206
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1206
 Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val Leu
 -15 -10 -5
 Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe Pro
 1 5 10 15
 Ala

<210> 1207
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1207
 Met Arg Gly Cys Gln Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp
 -25 -20 -15
 Leu Leu Ser Ala Arg Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr
 -10 -5 1
 His Phe Gly Phe Glu Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu
 5 10 15
 Thr Ser Val Val Ser Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln
 20 25 30 35
 Arg Val Tyr Ala Phe Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly
 40 45 50
 Cys Ser Leu Lys
 55

<210> 1208
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -35..-1

<400> 1208
 Met Glu Asn Leu Pro Phe Pro Leu Lys Leu Leu Ser Ala Ser Ser Leu
 -35 -30 -25 -20
 Asn Thr Pro Ser Ser Thr Pro Trp Val Leu Asp Ile Phe Leu Thr Leu

Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Phe Ser Tyr
 -15 -10 -5
 1 5 10
 Leu Arg Cys Asp Asn Pro Pro
 15 20

<210> 1209
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 1209
 Met Cys Val Cys Val Phe Ala Ile Phe Gly Val Arg Cys Cys Val Cys
 -10 -5 1
 Val Arg Cys Ile
 5

<210> 1210
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44..-1

<400> 1210
 Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser Ile Ser Val Gly Cys Gly
 -40 -35 -30
 Arg Thr Ala Ala Glu Gln Val Gly Cys Lys Gln Arg Ser Phe His Xaa
 -25 -20 -15
 Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys Phe Pro Cys Pro
 -10 -5 1

<210> 1211
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1211
 Met Asn Leu Ile Cys Val Ser Leu Met Ala Ser Asp Gly Ala Ser Ser
 -15 -10 -5
 Pro Val Leu Gly Gly Ser Ser His Ser Ser Ser Xaa Xaa
 1 5 10

<210> 1212

<211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 1212
 Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu Leu Leu Leu Ser
 -45 -40 -35
 Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser Tyr Asp Cys Asp
 -30 -25 -20
 Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe Ser Ser Ser Ser
 -15 -10 -5 1
 Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala
 5 10

<210> 1213
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1213
 Met Met Ser Glu Xaa Ser Gln Asp Leu Val Val Lys Cys Ala Pro Pro
 -30 -25 -20
 Xaa Pro Phe Phe Leu Leu Phe Leu Phe Ser Ser Cys Asp Val Pro Val
 -15 -10 -5 1
 Pro Leu His Leu Leu Gln Trp Leu Gln Ser Phe Leu Arg Pro Arg
 5 10 15

<210> 1214
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1214
 Met Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu
 -25 -20 -15
 Leu Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala
 -10 -5 1 5
 Leu Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val
 10 15 20
 Val Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro
 25 30

<210> 1215
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 1215
 Met Arg Val Gly Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro
 -30 -25 -20 -15
 Arg Cys Leu Phe Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu
 -10 -5 1
 Lys Leu Leu Gln Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His
 5 10 15
 Gly Leu Ala Gly
 20

<210> 1216
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1216
 Met Tyr Phe Asp Ile Gln Ile Val Ser Asp Val Val Ser Gly Ile Pro
 -30 -25 -20
 Phe Lys Leu Leu Cys Pro Leu Thr Cys Pro His His Ser Leu Ser Thr
 -15 -10 -5 1
 Val

<210> 1217
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1217
 Met Leu Phe Ile Phe Ser Asp Ile Asp Trp Lys Met Asp Leu Cys Phe
 -30 -25 -20
 Phe Ser Phe Ser Pro Phe Leu Pro Ser Leu Pro Leu Leu Glu Ala Glu
 -15 -10 -5 1
 Arg Met Arg Val Ser Asp Gln Leu Gln Tyr Thr Thr Gly Xaa Gly
 5 10 15

<210> 1218
 <211> 61

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 1218
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala
 -35 -30 -25
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 -20 -15 -10 -5
 Thr Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg
 1 5 10
 Asp Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
 15 20 25

<210> 1219
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1219
 Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
 -15 -10 -5
 Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
 1 5 10 15
 Pro Cys Gln Xaa Gly Leu
 20

<210> 1220
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69..-1

<400> 1220
 Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
 -65 -60 -55
 Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
 -50 -45 -40
 Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
 -35 -30 -25
 Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
 -20 -15 -10
 Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
 -5 1 5 10

Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Gly
 15 20

<210> 1221
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 1221
 Met Val Asp Glu Cys Leu Thr Glu Pro Val Trp Gly Ser Lys Arg Gln
 -40 -35 -30 -25
 Gly Cys Ser Ser Gln Ala Glu Ala Ser Cys Asp Ile Val Ser Ala Ala
 -20 -15 -10
 Cys Lys Cys Gly Ser Ser Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser
 -5 1 5
 Cys Ser Glu Asp Phe Pro Val
 10 15

<210> 1222
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1222
 Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
 -10 -5 1
 Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
 5 10 15

<210> 1223
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -57..-1

<400> 1223
 Met Val Ala Lys Asp Tyr Pro Phe Tyr Leu Thr Val Lys Arg Ala Asn
 -55 -50 -45
 Cys Ser Leu Glu Leu Pro Pro Ala Ser Gly Pro Ala Lys Asp Ala Glu
 -40 -35 -30
 Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser Leu
 -25 -20 -15 -10
 Ala Asn Leu Ile Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser

1. *Phylogenetic relationships*. The phylogenetic relationships among the 10 species were determined using the maximum parsimony method. The analysis was performed using the software package PAUP 4.0 (Phylogenetic Analysis Using Parsimony, version 4.0). The analysis was based on the 1000 characters of the DNA sequence data. The results of the analysis are shown in the phylogenetic tree in Figure 1. The tree shows that the 10 species are divided into two main groups: the *Phytophthora* group and the *Phytophthora* group. The *Phytophthora* group is further divided into two subgroups: the *Phytophthora* group and the *Phytophthora* group. The *Phytophthora* group is further divided into two subgroups: the *Phytophthora* group and the *Phytophthora* group.

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<220>  
<221> SIGNAL  
<222> -28..-1
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<210> 1225
<211> 85
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -34..-1
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<210> 1226
<211> 31
<212> PRT
<213> Homo sapiens
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<220>

<221> SIGNAL

<222> -16..-1

<400> 1226

Met	Ser	Met	Ala	Cys	Phe	Phe	His	Leu	Phe	Val	Ser	Ser	Leu	Ile	Ser
	-15					-10				-5					
Phe	Glu	Gln	Cys	Phe	Xaa	Met	Leu	Arg	Lys	Leu	Leu	Lys	Ile	Ile	
1			5						10					15	

<210> 1227

<211> 79

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45..-1

<400> 1227

Met	Gly	Ser	Arg	Gly	Asp	Pro	Leu	Ile	Cys	Gly	Leu	Gln	Arg	Ser	Val
-45					-40					-35					-30
Gly	Glu	Val	Trp	Phe	Pro	Gly	Trp	Gly	His	Thr	Ile	Thr	His	Cys	Phe
				-25					-20					-15	
Pro	Trp	Leu	Glu	Val	Gly	Leu	Phe	Phe	Trp	Leu	His	Ala	Ala	Pro	Gly
			-10					-5						1	
Arg	Ala	Ile	Ala	Leu	Pro	His	Phe	Ser	Ser	Phe	Ser	Val	Gly	Gln	Xaa
5						10					15				
Val	His	Leu	Val	Ser	Pro	Leu	Xaa	Xaa	Leu	Asp	Ile	Ser	Val	Glu	
20					25					30					

<210> 1228

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 1228

Met	His	Leu	Leu	Gln	Glu	Glu	Leu	Leu	Leu	Leu	Leu	Pro	Arg	Gly	Leu
				-15					-10					-5	
Cys	Gln	Val	Cys	Pro	Arg	Leu	Cys	Leu	Gln	Arg	Xaa	Val	Gly	Glu	Leu
			1				5					10			
Gln	Xaa	Xaa	Xaa	Pro	Asp	Val	Gly	Thr	Ala	Leu	Leu	Pro	Asp	Val	Asn
15						20					25				
Arg	Thr	Ser	Cys	Thr	Thr	Trp									
30					35										

<210> 1229

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 1229

Met	Cys	Leu	Ser	Cys	Ile	Gln	Gly	Ser	Phe	Phe	Val	Glu	Ile	Leu	Gln
			-25					-20					-15		
Leu	Val	Thr	Arg	Leu	Leu	Leu	Ser	Pro	Ser	Gln	Ser	Thr	Gln	Thr	His
		-10					-5					1			
Thr	His	Thr	His	Thr	His	Thr									
5					10										

<210> 1230

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32..-1

<400> 1230

Met	Thr	Ile	Leu	Arg	Glu	Met	Xaa	Xaa	Ser	Leu	Tyr	Val	Leu	Glu	Ala
		-30					-25					-20			
Lys	Asp	Thr	Ala	Ile	Leu	Leu	Leu	Val	Xaa	Val	Ser	Asp	Lys	Asn	Glu
	-15					-10					-5				
Gln	Gln	Leu	Gly	Arg	Gly	Val									
1				5											

<210> 1231

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 1231

Met	Arg	Leu	Ser	Ser	Ser	Cys	Gly	Leu	Pro	Val	Lys	Thr	Leu	Pro	Phe
			-25						-20				-15		
Ile	Cys	Cys	Asn	Leu	Tyr	Phe	Leu	Leu	Phe	Cys	Arg	Ser	Ser	Phe	Leu
		-10						-5				1			
Tyr	Phe	Gly	Tyr	Asp	Pro	Ile	Asn	Thr	Tyr	Met	Tyr	Tyr	Asn	Val	Phe
	5					10					15				
Ser	His	Ser													
20															

<210> 1232

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -68..-1

<400> 1232

Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly Ala Xaa Arg Phe
-65 -60 -55
Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu Arg Gly Leu Cys
-50 -45 -40
Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro Pro Asp Arg Leu
-35 -30 -25
Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa Pro Leu Leu Val
-20 -15 -10 -5
Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr Leu Gly Ser Phe
1 5 10
Ser Ala Gly Pro Cys Phe Arg Thr Leu
15 20

<210> 1233

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 1233

Met His Ser Leu Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser
-25 -20 -15 -10
Leu Ser Ser Ser Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala
-5 1 5
Leu Gly Pro Leu Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp
10 15 20

<210> 1234

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44..-1

<400> 1234

Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe Ser Leu
-40 -35 -30
Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp Ile Leu
-25 -20 -15
Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val Asp Ile
-10 -5 1
Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
5 10 15

<210> 1235
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 1235
 Met Gly Gln Phe Thr Ala Ala Met Val Gly Arg Ile Ser Cys Leu Gly
 -45 -40 -35 -30
 Val Trp Lys Leu Pro Arg Val Glu Ser Cys Ser Gln Pro Ala Arg Pro
 -25 -20 -15
 Leu Leu Ser Leu Ala Gln Thr Thr Thr Lys Thr Thr Ala Thr Thr Thr
 -10 -5 1
 Thr Thr Thr Lys His Ala Thr Cys Ala Leu Ala Tyr Thr Asn Thr Pro
 5 10 15
 Thr Glu Pro Xaa Gln Ala Asp Lys Ala Ser Arg Arg Ala Ser Gly Xaa
 20 25 30 35
 Leu Xaa Xaa Ala Ala Arg His Ile Pro Trp His Gly Ala Thr Ala Ala
 40 45 50
 Gln Leu Pro Ala Pro Pro Pro Ser Val Ile Ser Ala Leu
 55 60

<210> 1236
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1236
 Met Leu Ile Phe Ile Ile Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys
 -15 -10 -5
 Phe Ala Phe Ser Cys His Val Ser Phe Phe Phe Phe
 1 5 10

<210> 1237
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1237
 Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro Phe Ala Phe Cys His
 -15 -10 -5 1
 Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys Phe Leu Leu Ser Arg

			5					10					15				
Gln	Asn	Cys	Val	Ser	Thr	Gly	Xaa	Pro	Ser	Ser	Lys	Ser	Asp	Ile	Asn		
	20						25					30					
Ser	Arg	Ser	Gly	Ser	Cys	Ser	Leu	Ala	Arg								
	35					40											

<210> 1238
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1238																	
Met	Val	Ser	Leu	Arg	Val	Gly	Ala	Ser	Pro	Phe	Arg	Phe	Pro	Leu	Ala		
	-25					-20				-15							
Pro	Leu	Xaa	Leu	Val	Phe	Ile	Ser	Leu	Leu	Pro	Ala	Pro	Phe	Phe	Pro		
	-10				-5					1					5		
Thr	Leu	Ser	Phe	Pro	Cys	Cys	Cys	Val	Ser	Trp	Leu	Phe	Ser	Leu	Ser		
				10				15						20			
Val	Xaa	Val	Ser	Leu	Arg	Leu	Ser	Leu	Xaa	Val	Ser	Cys	Leu	Ser	Leu		
		25				30						35					
Trp	Cys	Leu	Leu	Val	Leu	Phe	Leu	Ser	Pro	Thr	Leu	Tyr	Val	Ser	Asp		
	40					45					50						
Ser	Phe	Cys	Ser	Phe	Cys	Val	Leu	Pro	Ile	Ala	Leu	Cys	Pro	Xaa	Ala		
	55					60					65						
Arg	Ser																
	70																

<210> 1239
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 1239																	
Met	Ala	His	Pro	Cys	Leu	Ala	Pro	Ala	Glu	Pro	Ser	Thr	Leu	Ser	Gln		
			-50					-45					-40				
Thr	Xaa	His	Pro	Ile	Gln	Arg	Thr	Leu	Thr	Thr	Phe	Pro	Gln	Ala	Trp		
		-35					-30						-25				
Val	Leu	Thr	Ser	Ser	Phe	Ser	Ile	Gln	Pro	Gly	Leu	Ala	Phe	Leu	Ala		
	-20					-15						-10					
Ile	Leu	Thr	Val	Leu	Ala	Lys	Pro	Gly	Ser	Ser	Xaa	Trp	Ser	Pro	Gly		
	-5					1			5						10		
Gln	Phe	Thr	Pro	His	Ser	Leu	Leu										
				15													

<210> 1240
 <211> 35

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1240
Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp Ser
-30 -25 -20
Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser Thr
-15 -10 -5 1
Pro Ala Arg

<210> 1241
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1241
Met Ala Leu His Ile Leu Glu Cys Glu Arg Asn Val Cys Phe Val Ala
-35 -30 -25
Val Arg Gln Pro Ala His Glu Ser Cys Phe Val Pro Ser Leu Val Thr
-20 -15 -10 -5
Gly Ala Leu Gln Gln Ser Gln Thr Gln His Pro Pro Trp Val Cys Pro
1 5 10
Gln Val Gln Gly Ser Tyr Pro Ser Trp Lys Asn Arg Gly
15 20 25

<210> 1242
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1242
Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys Phe Ser Val His
-30 -25 -20
Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg Val Ser Phe Thr
-15 -10 -5
Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys Val Ser Ser Lys
1 5 10 15
Gly Cys Leu Phe His Leu Gly Ala Gly Arg
20 25

<210> 1243
<211> 40

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1243
Met Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu
 -15 -10 -5
Leu Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln
 1 5 10
Arg Gln Val Leu Phe Cys Asn Arg
 15 20

<210> 1244
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1244
Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu Ser Lys Ile Ser
 -15 -10 -5
Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser Ser
 1 5 10

<210> 1245
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1245
Met Leu Cys Ile Met Phe Gly Ile Glu Thr Asn Glu Ile Thr Lys Met
 -30 -25 -20
Thr Met Ser Phe Leu Leu Phe Leu Ser Ile Ser Leu Ile Thr Leu Tyr
 -15 -10 -5
Tyr Ser Ser Glu Ala Cys Gly
 1 5

<210> 1246
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -39..-1

<400> 1246

Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn Leu Arg Thr Ala
 -35 -30 -25
Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val Phe Xaa Leu Leu
 -20 -15 -10
Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn Ser Tyr Gly Thr
 -5 1 5
Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe Ser Asn Ser Asn
10 15 20 25
Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser His Val Xaa Lys
 30 35 40
Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly
 45 50

<210> 1247

<211> 99

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1247

Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln Gly Met Leu Leu
 -20 -15 -10
Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile His Ser Ala Arg
 -5 1 5
Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr Gln Asp Phe Ile
10 15 20
Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu Arg His Ala Phe
25 30 35 40
Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala Gln Val Pro Thr
 45 50 55
Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser Ile Ser Ser Ser
 60 65 70
Leu Lys Glu
 75

<210> 1248

<211> 88

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -86..-1

<400> 1248

Met Asp Met Arg Trp His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile
 -85 -80 -75
Leu Val Ala Ser Ala Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro

-70		-65		-60		-55									
Cys	Glu	Pro	Ser	Ser	Gly	Gly	Leu	Ala	Asn	Pro	Thr	Arg	Ala	Gly	Gly
				-50					-45					-40	
Arg	Glu	Pro	Tyr	Pro	Gly	Ser	Ala	Glu	Val	Ile	Arg	Glu	Ser	Ser	Ser
			-35					-30					-25		
Thr	Thr	Gly	Met	Val	Val	Gly	Ile	Val	Ala	Ala	Ala	Ala	Leu	Cys	Ile
		-20					-15						-10		
Leu	Ile	Leu	Leu	Xaa	Ala	Met	Tyr								
	-5					1									

<210> 1249
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1249
Met Ala Trp Thr Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly
-20 -15 -10 -5
Ser Val Val Ser Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala
1 5 10
Leu Gly Gln Arg Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu
15 20 25
Tyr Phe Ala Ser Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu
30 35 40
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Xaa Arg Xaa
45 50 55 60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Leu Leu Thr Ile Xaa Gly Ala
65 70 75
Gln Ala Glu Asp Xaa Ala Asp Tyr Tyr Cys Ser Xaa Arg Asp His Thr
80 85 90
Asp Asn Arg Trp Val Phe Gly Gly Gly Thr Arg Leu Thr
95 100 105

<210> 1250
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1250
Met Glu Ala Glu Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg
-20 -15 -10 -5
Asn Ser Glu Gly Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu
1 5 10
Phe Lys Asn Glu Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln
15 20 25
Asn Gln Gln Trp Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys

30 35
 Ser Ala Leu Cys Leu Ala
 45 50

40

<210> 1251
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1251
 Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
 -15 -10 -5
 Cys Ser Ile
 1

<210> 1252
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1252
 Met Ile Ser Asp Val Gln His Leu Phe Ile Tyr Leu Leu Ala Phe Cys
 -20 -15 -10
 Met Pro Ser Leu Glu Lys Cys Leu Tyr Gly Ser Leu Ala His Phe Phe
 -5 1 5 10
 Phe Phe

<210> 1253
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1253
 Met Pro Leu Phe Arg Val Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln
 -15 -10 -5 1
 Asp Phe Arg Met Gln Pro Cys Pro Pro Thr Pro Lys
 5 10

<210> 1254
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

 <400> 1254
 Met Trp Tyr Val Glu Met Trp Val Ser Phe Phe Leu Leu Phe Tyr Val
 -20 -15 -10
 Leu Leu Phe Arg Asn Leu Tyr Thr His Thr His His Thr Gly
 -5 1 5

<210> 1255
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

 <400> 1255
 Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu
 -30 -25 -20 -15
 Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa
 -10 -5 1
 Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly
 5 10 15
 His Ala Leu Gln Leu Xaa
 20

<210> 1256
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

 <400> 1256
 Met Gln Ala Arg Arg Trp Glu Ser Trp Met Trp Thr Cys Val Ala Pro
 -20 -15 -10
 Val Tyr Pro Ala Cys Ser Gly Arg Arg Ala Xaa Ala Val Xaa Gln Xaa
 -5 1 5
 Xaa Pro Arg Leu Gly Xaa Xaa Leu Pro Gly Pro Gly Xaa Glu His Leu
 10 15 20 25
 Ala His Val Cys Gly Leu Pro Ala Gly Glu Ala Gly Arg Gly Arg Gly
 30 35 40
 Val Glu Arg Pro Gln Glu Lys Arg Ala Asp Lys Ala Val Xaa Val Arg
 45 50 55
 Arg Gly Leu Gly Gly Ala Gly Leu Pro Gly Gly Asp Thr Pro Arg Gly
 60 65 70
 Pro Pro Met Ser Thr Trp Pro
 75 80

<210> 1257
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1257
 Met Phe Leu Phe Phe Phe Gly Asn Ser Pro Cys Cys Gly Ala Thr Gly
 -10 -5 1

<210> 1258
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 1258
 Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser Leu Ser Leu
 -25 -20 -15 -10
 Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser Ala Ser Pro
 -5 1 5
 Ser Leu Leu Xaa Pro Pro Xaa Arg
 10 15

<210> 1259
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1259
 Met Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg
 -20 -15 -10
 Leu Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
 -5 1 5

<210> 1260
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1260

Met Lys Phe Thr His Phe Lys Cys Thr Ile Arg Leu Leu Leu Leu Tyr
 -30 -25 -20
Leu Gln Asn Pro Val Thr Ile Thr Ile Leu Phe Leu Ile Val Ser Met
 -15 -10 -5
Ala Leu Lys Ile Asn His Ile Pro Lys Gly
 1 5

<210> 1261

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1261

Met Ser Cys Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn
 -10 -5 1
Tyr Met Leu Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr
 5 10 15
Ser Lys Leu Val Thr Ile Cys Cys Cys Phe
 20 25

<210> 1262

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1262

Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile Ser
 -10 -5 1
Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
 5 10

<210> 1263

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -53..-1

<400> 1263

Met Gly Arg Gly Pro Gly Pro Leu Gln Glu Arg Ser Leu Phe Glu Xaa
 -50 -45 -40
Lys Arg Gly Ala Pro Pro Ser Ser Asn Ile Glu Asp Phe His Gly Leu

-35 -30 -25
 Leu Pro Lys Val Ile Pro Ile Cys Ala Leu Tyr Val Ile Cys Gln Phe
 -20 -15 -10
 Ile Leu Ile Arg Ser Gly Val Asn Ile Ser Met Glu Gln Val Thr Val
 -5 1 5 10
 Val Asp Ala Ser Leu
 15

<210> 1264
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 1264
 Met Leu Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr
 -10 -5 1
 Tyr Phe Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile
 5 10 15
 His Ser Thr Ile Leu Leu Cys Val
 20 25

<210> 1265
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1265
 Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe Xaa
 -25 -20 -15
 Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
 -10 -5 1 5
 Ile His Ser Pro Met
 10

<210> 1266
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1266
 Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp Leu His Ala Ala Pro
 -10 -5 1

Pro Ser Pro Pro Arg
5

<210> 1267
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1267
Met Phe His Gly Arg Val Met Ala Met Gly Xaa Leu Thr Lys His Leu
-30 -25 -20
Asn Leu Asn Ile Ser Ile Ser Leu Leu Met Leu Xaa Xaa Tyr Trp
-15 -10 -5
Ser Cys Trp Ile Lys Ser Pro Pro Xaa Met
1 5

<210> 1268
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -128..-1

<400> 1268
Met Leu Gly Arg Ser Ser Leu Leu Xaa Trp Lys Xaa Ser Pro Gly Ser
-125 -120 -115
Lys Lys Leu Val Val Ala Thr Glu Lys Asn Val Ile Ala Ala Leu Asn
-110 -105 -100
Ser Arg Thr Gly Glu Ile Leu Trp Arg His Val Asp Lys Gly Thr Ala
-95 -90 -85
Glu Gly Ala Val Asp Ala Met Leu Leu His Gly Gln Asp Val Ile Thr
-80 -75 -70 -65
Val Ser Asn Gly Gly Arg Ile Met Arg Ser Trp Glu Thr Asn Ile Gly
-60 -55 -50
Gly Leu Asn Trp Glu Ile Thr Leu Asp Ser Gly Ser Phe Gln Ala Leu
-45 -40 -35
Gly Leu Val Gly Leu Gln Glu Ser Val Arg Tyr Ile Ala Val Leu Lys
-30 -25 -20
Lys Thr Thr Leu Ala Leu His His Leu Ser Ser Gly His Ser Ser Gly
-15 -10 -5
Trp Thr Ser Pro
1

<210> 1269
<211> 72
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL

<222> -57..-1

<400> 1269

Met	Ser	Thr	Thr	Tyr	Leu	Asn	Glu	Asp	Leu	Lys	Lys	Lys	Phe	Ser	Ala
		-55					-50					-45			
Val	Ile	Glu	Gln	Val	Leu	Phe	Ala	His	Leu	Ser	Pro	Leu	His	Val	Trp
	-40					-35				-30					
Leu	Gln	Leu	Arg	Ser	Leu	Cys	Glu	Xaa	Leu	Thr	Cys	Ile	Trp	Val	Arg
-25					-20				-15						-10
Phe	Asn	Phe	Leu	Ala	Ser	Ser	Gln	Ala	Cys	Ser	Lys	Cys	Asn	Ser	Ser
			-5						1				5		
Phe	Leu	Ile	Met	Ser	Ser	Ser	Ser								
		10					15								

<210> 1270

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<400> 1270

Met	Ala	Leu	Ile	Val	Leu	Gln	Leu	Thr	Phe	Gly	Ile	Gly	Tyr	Val	Thr
			-35					-30					-25		
Leu	Leu	Gln	Ile	His	Ser	Ile	Tyr	Ser	Gln	Leu	Ile	Ile	Leu	Asp	Leu
		-20					-15					-10			
Leu	Val	Pro	Val	Ile	Gly	Leu	Ile	Thr	Glu	Leu	Pro	Leu	His	Ile	Arg
		-5				1				5					
Glu	Thr	Leu	Leu	Phe	Thr	Ser	Ser	Leu	Ile	Leu	Thr	Leu	Asn	Thr	Val
10					15				20						25
Phe	Val	Leu	Ala	Val	Lys	Leu	Lys	Trp	Phe	Tyr	Tyr	Ser	Thr	Arg	Tyr
			30						35					40	

<210> 1271

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1271

Met	Arg	Val	Ala	Gly	Ala	Ala	Lys	Leu	Val	Val	Xaa	Val	Ala	Xaa	Phe
			-20					-15					-10		
Leu	Leu	Thr	Phe	Tyr	Val	Ile	Ser	Gln	Val	Phe	Glu	Ile	Lys	Met	Asp
		-5					1				5				
Ala	Ser	Leu	Gly	Asn	Leu	Phe	Ala	Arg	Ser	Ala	Leu	Asp	Thr	Ala	Ala
	10					15					20				
Arg	Ser	Thr	Lys	Pro	Pro										

25

30

<210> 1272

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1272

Met	His	Thr	Leu	Val	Phe	Leu	Ser	Thr	Arg	Gln	Val	Leu	Gln	Cys	Gln
-15					-10					-5					1
Pro	Ala	Ala	Cys	Gln	Ala	Leu	Pro	Leu	Leu	Pro	Arg	Glu	Leu	Phe	Pro
			5					10					15		
Leu	Leu	Phe	Lys	Val	Ala	Phe	Met	Xaa	Lys	Lys	Thr	Val	Val	Leu	Arg
			20				25					30			
Xaa	Leu	Val	His	Thr	Arg										
			35												

<210> 1273

<211> 16

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1273

Met	Thr	Val	Val	Ile	Ser	Cys	Leu	Val	Gly	Glu	Cys	Gly	Ser	Trp	Lys
				-10					-5					1	

<210> 1274

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 1274

Met	Cys	Thr	Leu	Thr	Asp	Thr	His	Thr	His	Val	Gln	Val	His	Lys	Ser
		-45					-40					-35			
Lys	Pro	Cys	Gln	Leu	Leu	Ser	Pro	Pro	Pro	Pro	Xaa	His	Gly	Pro	Leu
	-30					-25					-20				
Leu	Leu	Pro	Ile	Phe	Gly	Leu	Leu	Val	Pro	Ser	Gln	Ile	Phe	Ser	Ser
-15					-10					-5				1	
Leu	Leu	Asn	Ser	Leu	His	Leu	Gly	Leu	Pro	Ser	Phe	Pro	Lys	Met	Pro
			5					10					15		
Leu	Met	Ile	Phe	Leu	Pro	Arg	Trp								
		20					25								

<210> 1275
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -63..-1

<400> 1275
 Met Thr Leu Ile Leu Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile
 -60 -55 -50
 Phe Leu Trp Thr Lys Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp
 -45 -40 -35
 Thr Val Gln Met Lys Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro
 -30 -25 -20
 Met Lys Gln Ile Leu Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln
 -15 -10 -5 1
 Gln Arg Phe Trp Pro Arg Val Arg Val Tyr Ser Arg Ile Tyr
 5 10 15

<210> 1276
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1276
 Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu Phe Gln Lys
 -15 -10 -5
 Ile Glu Glu Glu Glu Leu Phe Pro Asn
 1 5

<210> 1277
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48..-1

<400> 1277
 Met Asp Ser Val Pro Ala Thr Val Pro Ser Ile Ala Ala Thr Pro Gly
 -45 -40 -35
 Asp Pro Glu Leu Val Gly Pro Leu Ser Val Leu Tyr Ala Ala Phe Ile
 -30 -25 -20
 Ala Lys Leu Leu Glu Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro
 -15 -10 -5
 Gly Pro Asp Phe Tyr Gly Xaa Xaa Trp Lys Leu Tyr Leu Ser Leu Pro

1		5		10		15									
Ser	Trp	Glu	Xaa	Phe	Val	Cys	His	Phe	Leu	Met	Glu	Thr	Val	Leu	Val
		20						25					30		
Val	Lys	Xaa	Arg	Val	Tyr	Xaa	Val								
		35					40								

<210> 1278
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1278
Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro Ala Ser
-15 -10 -5
Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu Arg Ile
1 5 10
Glu Ala Pro Trp Ala Arg Gly
15 20

<210> 1279
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1279
Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys Phe Gly
-25 -20 -15
Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys Cys Arg
-10 -5 1
His Gly
5

<210> 1280
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 1280
Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe Ile
-25 -20 -15 -10
Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr Gly
-5 1 5

Phe Cys Ile Phe Trp Xaa Glu Thr
 10 15

<210> 1281
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1281
 Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
 -30 -25 -20
 Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
 -15 -10 -5
 Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
 1 5 10 15
 Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
 20 25

<210> 1282
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1282
 Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
 -30 -25 -20
 Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
 -15 -10 -5 1
 Xaa Arg Leu Ala Ser Gly
 5

<210> 1283
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1283
 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
 -15 -10 -5 1
 Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly Phe Ser
 5 10 15
 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val Ile Gln

Pro Lys Gln Gly
5

<210> 1287
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -107..-1

<400> 1287

Met	Gly	Xaa	Leu	Ala	Leu	Xaa	Ala	Trp	Leu	Gln	Pro	Arg	Tyr	Arg	Lys	
		-105					-100					-95				
Asn	Ala	Tyr	Leu	Phe	Ile	Tyr	Tyr	Leu	Ile	Gln	Phe	Cys	Gly	Xaa	Ser	
		-90				-85					-80					
Trp	Ile	Phe	Ala	Asn	Met	Thr	Val	Arg	Phe	Phe	Ser	Phe	Gly	Lys	Asp	
		-75			-70					-65					-60	
Ser	Met	Val	Asp	Thr	Phe	Tyr	Ala	Ile	Gly	Leu	Val	Met	Arg	Leu	Cys	
			-55						-50					-45		
Gln	Ser	Val	Ser	Leu	Leu	Glu	Leu	Leu	His	Ile	Tyr	Val	Gly	Ile	Glu	
			-40					-35					-30			
Ser	Asn	His	Leu	Leu	Pro	Arg	Phe	Leu	Gln	Leu	Thr	Glu	Arg	Ile	Ile	
		-25					-20					-15				
Ile	Leu	Phe	Val	Val	Ile	Thr	Ser	Arg	Arg	Gly	Ser	Pro	Thr	Arg	Asn	
		-10				-5					1				5	
Met	Trp	Cys	Val	Cys	Tyr	Ser	Ser	Leu	Asp	Leu	Trp	Ile	Trp	Leu	Xaa	
			10						15					20		
Thr	Leu	Ile	Ala	Xaa	Xaa	Ser	Val	Ile	Gly	Ile	Ser	Tyr	Ala	Val	Leu	
			25					30					35			
Thr																

<210> 1288
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1288

Met	Asp	Thr	Phe	Pro	Ser	Leu	Thr	Leu	Thr	Ala	Leu	Leu	Val	Pro	Ser	
			-15					-10					-5			
Arg	Val	Gln	Pro	Gln												
			1													

<210> 1289
<211> 84
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
 <222> -20..-1

<400> 1289
 Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
 -20 -15 -10 -5
 Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
 1 5 10
 Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
 15 20 25
 Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
 30 35 40
 Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
 45 50 55 60
 Ala Val Gly Tyr

<210> 1290
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1290
 Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val
 -20 -15 -10
 Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
 -5 1

<210> 1291
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1291
 Met Ser Leu Gly Leu His Ser Asn Ser Trp Val Leu Asp Pro Ala Leu
 -20 -15 -10
 Leu Leu Thr Cys Leu Thr Phe Pro Ile Tyr Lys Leu Leu Trp Val Arg
 -5 1 5 10
 Gly Gly Thr Arg Xaa Thr Leu Xaa Ala Leu His Ser Ala Arg Thr
 15 20 25

<210> 1292
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -60..-1

<400> 1292

Met	Ala	Ala	Asn	Ser	Ser	Gly	Gln	Gly	Phe	Gln	Asn	Lys	Asn	Arg	Val
-60					-55					-50					-45
Ala	Ile	Leu	Ala	Glu	Leu	Thr	Lys	Arg	Lys	Glu	Asn	Tyr	Leu	Cys	Arg
			-40						-35					-30	
Thr	Ser	Leu	Gln	Gln	Ile	Ile	Leu	Glu	Leu	Gly	Ile	Asp	Thr	Ile	Met
			-25					-20					-15		
Trp	Val	Xaa	Cys	Xaa	Phe	Cys	Phe	Val	Leu	Phe	Cys	Phe	Glu	Thr	Glu
	-10						-5					1			
Ser	Arg	Pro	Val												
5															

<210> 1293

<211> 138

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35..-1

<400> 1293

Met	Ser	Ala	Gly	Ser	Ala	Thr	His	Pro	Gly	Ala	Gly	Gly	Arg	Arg	Ser
-35					-30					-25					-20
Lys	Trp	Asp	Gln	Pro	Ala	Pro	Ala	Pro	Leu	Leu	Phe	Leu	Pro	Pro	Ala
			-15						-10					-5	
Ala	Pro	Gly	Gly	Glu	Val	Thr	Ser	Ser	Gly	Gly	Ser	Pro	Gly	Xaa	Thr
		1				5						10			
Thr	Ala	Ala	Pro	Ser	Gly	Ala	Leu	Asp	Ala	Ala	Ala	Ala	Val	Ala	Ala
	15				20					25					
Lys	Ile	Asn	Ala	Met	Leu	Met	Ala	Lys	Gly	Lys	Leu	Lys	Pro	Thr	Gln
30				35					40						45
Xaa	Ala	Ser	Glu	Lys	Leu	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Asn
			50					55					60		
Lys	Ser	Lys	Asp	Asp	Leu	Val	Val	Ala	Glu	Val	Glu	Ile	Asn	Asp	Val
			65				70					75			
Pro	Leu	Thr	Cys	Arg	Asn	Leu	Leu	Thr	Arg	Gly	Gln	Xaa	Gln	Asp	Glu
	80					85					90				
Ile	Ser	Arg	Leu	Ser	Gly	Ala	Ala	Val	Ser						
95						100									

<210> 1294

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21..-1

<400> 1294

Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala Val Cys Leu Ser Gly
 -20 -15 -10
 Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val Arg Gly Gly Pro Asn
 -5 1 5 10
 Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile Pro Leu Cys Trp Pro
 15 20 25
 Pro Ala Val Thr Ala Gly Glu Val Lys Leu
 30 35

<210> 1295
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1295
 Met Asn Ser Phe His Phe Ile Xaa Phe Leu Pro Phe Pro Trp Ala Glu
 -15 -10 -5 1
 Xaa Ala Gln

<210> 1296
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1296
 Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro Leu
 -25 -20 -15
 Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser Thr
 -10 -5 1
 His Thr His
 5

<210> 1297
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1297
 Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg Ser Trp Thr
 -20 -15 -10
 Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro Ala Gly Thr
 -5 1 5 10

Ile Cys Thr

<210> 1298

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1298

Met Cys Ala Leu Phe Ile Leu Val Ser Ile Ser Leu Phe Tyr Ala Leu
-15 -10 -5 1
Phe Ile Ser Pro Ser Ile Gln
5

<210> 1299

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -53..-1

<400> 1299

Met Tyr Leu Val Cys Thr Thr Cys Thr Trp Cys Val Phe Ser Glu Met
-50 -45 -40
Phe Val His Gly Leu Asn Ile Thr Gln Leu Val Leu Ser Gln Leu Asp
-35 -30 -25
Tyr Phe Phe His Ser Asn Leu Thr Asn Leu Val Leu Tyr Phe Leu Val
-20 -15 -10
His Leu Leu Phe Ser Leu Ser Leu Phe Met Pro Leu Thr
-5 1 5

<210> 1300

<211> 138

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -78..-1

<400> 1300

Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly Cys Xaa
-75 -70 -65
Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa Tyr Xaa
-60 -55 -50
Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala Gly Leu
-45 -40 -35
Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu Ser Pro
-30 -25 -20 -15

Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu Ile His
 -10 -5 1
 Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe Ser Cys
 5 10 15
 Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile Glu Leu
 20 25 30
 Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly Thr Asn
 35 40 45 50
 Phe Gln Ile Met Ser His Ser His Val Ala
 55 60

<210> 1301
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1301
 Met Asn Glu Lys Lys Lys Leu Leu Gly Thr Glu Gln Lys Gln Lys Lys
 -30 -25 -20
 Arg Met Gly Asn Leu Lys Leu Leu Phe Leu Ile Leu Ile Leu Ile Ala
 -15 -10 -5
 Gly Tyr Arg
 1

<210> 1302
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1302
 Met Gly Leu Gln Ser Leu Thr Leu Pro Val Ser Cys Ser Pro Ser Ala
 -25 -20 -15
 Leu Met Leu Pro Leu Gly Cys Ala Val Arg Thr Arg Met Leu
 -10 -5 1

<210> 1303
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1303
 Met Asp Ser Asn Lys Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val

-30 -25 -20
 Trp Ile Leu Thr Thr Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu
 -15 -10 -5 1
 Gln Asp Leu Ser Ala Tyr
 5

<210> 1304
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 1304
 Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa Gly Pro Gln Asp
 -45 -40 -35
 Phe Arg Phe Cys Ser Val Phe Ser Leu Leu Leu Lys Leu Gly Asn Phe
 -30 -25 -20
 Tyr Phe Ser Phe Xaa Xaa Cys Leu Phe Leu Xaa Leu Xaa Xaa Ser Glu
 -15 -10 -5 1
 Met Glu Ser His Ser Phe Ser
 5

<210> 1305
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -65..-1

<400> 1305
 Met Glu Asp Val Glu Ala Arg Phe Ala His Leu Leu Gln Pro Ile Arg
 -65 -60 -55 -50
 Asp Leu Thr Lys Asn Trp Glu Val Asp Val Ala Ala Gln Leu Gly Glu
 -45 -40 -35
 Tyr Leu Glu Glu Leu Asp Gln Ile Cys Ile Ser Phe Asp Glu Gly Lys
 -30 -25 -20
 Thr Thr Met Asn Phe Ile Glu Ala Ala Leu Leu Ile His Gly Ser Ala
 -15 -10 -5
 Cys Val Tyr Ser Lys Lys Val Glu Tyr Leu Tyr Ser Leu Val Tyr Gln
 1 5 10 15
 Ala Leu Asp Phe Ile Ser Gly Lys Arg Arg Ala Lys Gln Leu Ser Ser
 20 25 30
 Val Gln Glu Asp Arg Ala Asn Gly Val Ala Ala Pro Gly Ser Pro Gly
 35 40 45
 Gly

<210> 1306
 <211> 20
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1306

Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr Ala
-15 -10 -5 1
Val Leu Ala Arg
5

<210> 1307

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 1307

Met Pro Glu Ala Ala Leu Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu
-25 -20 -15 -10
Tyr Phe Lys Phe Trp Gly Thr Cys Ala Glu Arg Ala Gly Leu Leu His
-5 1 5
Arg Tyr Thr Arg Ala Met Glu Val Cys Cys Thr His Gln Pro Ser Ser
10 15 20
Thr Leu Gly Ile Ser Pro Asn Ala Leu Leu Pro Leu
25 30 35

<210> 1308

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1308

Met Arg Met Gly Thr Arg Ala Ser Pro Pro Leu Cys Met His Leu Ser
-20 -15 -10
Ile His Pro Xaa Xaa Cys Ala Cys Ile Cys Pro Ser Ile Gln
-5 1 5

<210> 1309

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36..-1

<400> 1309

Met Tyr Pro Arg Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa
-35 -30 -25
Xaa Thr Arg Thr Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys
-20 -15 -10 -5
Val Cys Val Cys Val Cys
1

<210> 1310

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 1310

Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg Gly Ser Gly
-10 -5 1
Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala Tyr Arg Arg
5 10 15
Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser Ser Pro Leu
20 25 30
Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly Gln Glu Lys
35 40 45 50
Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg Val Ala Ser
55 60 65
Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu Ile Asn Ser
70 75 80
Gly Ser Arg Tyr
85

<210> 1311

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 1311

Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile Ala Lys Ala Leu Tyr Leu
-25 -20 -15 -10
Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu Tyr Tyr Met Cys Val Cys
-5 1 5
Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr Xaa Tyr Xaa Leu Ile Lys
10 15 20
Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly Leu
25 30

<210> 1312

<211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1312
 Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu Ser Glu Ala
 -25 -20 -15
 Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser Trp Leu Val
 -10 -5 1
 Gly Pro Arg Tyr
 5

<210> 1313
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1313
 Met Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val
 -30 -25 -20
 Ser Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly
 -15 -10 -5 1
 Xaa

<210> 1314
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -53..-1

<400> 1314
 Met Val Ser Gly Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg
 -50 -45 -40
 Gly Arg Arg Ala Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg
 -35 -30 -25
 Thr Ala Pro Asp Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala
 -20 -15 -10
 Ala Gly Leu Glu Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg
 -5 1 5 10
 Lys Thr Trp Pro Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu
 15 20 25
 Ile Leu Val Arg Ala Phe Pro Ala
 30 35

<210> 1315
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1315
 Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His Ser Ser Ala Leu
 -30 -25 -20
 Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro Cys Trp Cys Asp
 -15 -10 -5 1
 Gly Leu Arg Leu Arg
 5

<210> 1316
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -51..-1

<400> 1316
 Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
 -50 -45 -40
 Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp Leu Ala Ser Ser Ser Gly
 -35 -30 -25 -20
 Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu Leu Arg Ala Leu Ser Ser
 -15 -10 -5
 Glu Leu Cys Ala Pro Arg Gly Cys His Ser Pro His His Val Ser Arg
 1 5 10
 Ile Ser Trp Thr Leu Ser Val Ser Ser His Gly Pro Val Cys Gly Cys
 15 20 25
 Trp Ala Phe Arg Phe His Asn Pro His Gly Leu Leu Ser Ser Arg Ser
 30 35 40 45
 His Leu Ser Xaa Trp Leu His Ser Ala Gly
 50 55

<210> 1317
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1317
 Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr Gly Ser

-20 -15 -10
 Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly Leu Leu
 -5 1 5 10
 Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu
 15 20 25
 Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro Gly
 30 35

<210> 1318
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1318
 Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu Gly
 -20 -15 -10
 Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn Phe
 -5 1 5
 Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly Ala
 10 15 20
 Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys Asn
 25 30 35 40
 Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn Ile
 45 50 55
 Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr Gly
 60 65 70
 Cys Ser Leu Gly Leu Ala Leu
 75

<210> 1319
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1319
 Met Ser Ser Glu Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr
 -25 -20 -15
 Leu Leu Val Gly Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser
 -10 -5 1 5
 Lys Xaa Gln Ile Ser Ser Phe Val Glu
 10 15

<210> 1320
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 1320

Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg Leu Ala Ser Ala
 -15 -10 -5
Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly Ala Ala Ser Leu
 1 5 10
Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr Ser Tyr Leu Pro
15 20 25 30
Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Arg
 35 40 45

<210> 1321

<211> 24

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 1321

Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe Phe Ser Gln Tyr
 -15 -10 -5
Leu Xaa Xaa Ser Asn Pro Ala Ala
 1 5

<210> 1322

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1322

Met Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly
 -15 -10 -5
Phe Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly
1 5 10

<210> 1323

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -69..-1

<400> 1323

Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln Met Gly Ile Met Leu
-65 -60 -55
Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser Lys Lys Tyr Lys Ser
-50 -45 -40
Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys Thr Gly Glu Ser Pro
-35 -30 -25
Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg Leu Ser Cys Val Leu
-20 -15 -10
Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn Gln Lys Val Cys Tyr
-5 1 5 10
Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser Pro Thr Thr Trp Leu
15 20 25
Thr Phe Trp Val Gly
30

<210> 1324

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1324

Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser Cys Leu Trp Ser Arg
-10 -5 1
His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu Ser Pro Glu Phe Glu
5 10 15
Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
20 25

<210> 1325

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 1325

Met Pro Thr Tyr Phe Leu Phe Val Pro His Leu Ile Ser Cys Asn Trp
-15 -10 -5
Cys Glu Pro Arg Gly Asn Asn Pro Gln Ile Pro Leu Leu Ala Ile His
1 5 10 15
Thr Arg Lys Lys Asn Gln His Phe Ile Thr
20 25

<210> 1326

<211> 59

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1326
 Met Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr
 -25 -20 -15
 Ser Val Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa
 -10 -5 1 5
 Leu Ser His Trp Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa
 10 15 20
 Xaa Leu Ser His Val Thr Lys Gln Met His Leu
 25 30

<210> 1327
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1327
 Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys Val
 -10 -5 1
 Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
 5 10 15

<210> 1328
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1328
 Met Val Val Ser Phe Ala Val Gln Lys Leu Phe Ser Leu Ile Arg Ser
 -25 -20 -15
 His Leu Ser Ile Leu Ala Phe Val Ala Ile Ala Phe Gly Val Leu Asp
 -10 -5 1
 Met Lys Ser Leu Pro Thr Pro Gly
 5 10

<210> 1329
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -65..-1

<400> 1329

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Met Gly Gly Arg Lys Met Ala Thr Asp Glu Glu Asn Val Tyr Gly Leu
-65          -60          -55          -50
Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser Thr Arg Arg Leu Ile Leu
          -45          -40          -35
Val Gly Arg Thr Gly Ala Gly Lys Ser Ala Thr Gly Asn Ser Ile Leu
          -30          -25          -20
Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly Ala Thr Ser Val Xaa Arg
          -15          -10          -5
Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp Lys Cys His Val Glu Val
  1          5          10          15
Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys Cys Pro Arg Gln Ile Leu
          20          25          30
Ala Val Arg Arg Glu Val Thr Ala
          35
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<210> 1330

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31..-1

<400> 1330

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Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln Leu Ala
-30          -25          -20
Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro Gly Glu
-15          -10          -5          1
His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro Pro Ser
  5          10          15
Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp Xaa Pro
  20          25          30
Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr Arg Arg
  35          40          45
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<210> 1331

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -41..-1

<400> 1331

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Met Gly Val Tyr Thr Cys Pro Ile Phe Val His Tyr Tyr Glu Asn His
-40          -35          -30
Gly Pro Thr Pro Ser Phe Xaa Ala Phe Ile Ser Phe His Leu Phe Thr
-25          -20          -15          -10
Leu Gly Phe Leu Cys Ser Leu Cys Pro His Pro His Gly
```

-5

1

<210> 1332
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1332
Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser Leu Ser
-15 -10 -5
Lys Asp Glu Asn Ala Glu Met
1 5

<210> 1333
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1333
Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys Tyr Thr Ala Lys His
-30 -25 -20 -15
Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala Val Val Ser Ala Val
-10 -5 1
Val Met Val Gly Thr Gly Cys
5

<210> 1334
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1334
Met Pro Ser Cys Cys Tyr Leu Arg Ala Phe Leu Leu Ser Val Pro Leu
-15 -10 -5
Gly Lys Gly Ser Ala Leu Lys Asp Pro Val
1 5

<210> 1335
<211> 101
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1335
 Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser Ser
 -20 -15 -10
 Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa Lys
 -5 1 5
 Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu Arg Asn Gln
 10 15 20
 Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu
 25 30 35 40
 Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu
 45 50 55
 Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly
 60 65 70
 Leu Lys Gln Cys Glu
 75

<210> 1336
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1336
 Met His Ile Cys Leu Phe Phe Ser Phe Ser Xaa Xaa Phe Xaa Leu Phe
 -10 -5 1
 Phe Phe Phe Phe
 5

<210> 1337
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1337
 Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr
 -15 -10 -5
 Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met
 1 5 10
 Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly
 15 20 25

<210> 1338
 <211> 110

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84..-1

<400> 1338
Met Xaa Lys Leu Xaa Ser Asn Pro Ser Glu Lys Gly Thr Lys Pro Pro
 -80 -75 -70
Ser Val Glu Asp Gly Phe Gln Thr Val Pro Leu Ile Thr Pro Leu Glu
 -65 -60 -55
Val Asn His Leu Gln Leu Pro Ala Pro Glu Lys Val Ile Val Lys Thr
 -50 -45 -40
Arg Thr Glu Tyr Gln Pro Glu Gln Lys Asn Lys Gly Lys Phe Arg Val
 -35 -30 -25
Pro Lys Ile Ala Glu Phe Thr Val Thr Ile Leu Val Ser Leu Ala Leu
 -20 -15 -10 -5
Ala Phe Leu Ala Cys Ile Val Phe Leu Val Val Tyr Lys Ala Phe Thr
 1 5 10
Tyr Asp His Ser Cys Pro Glu Asp Ser Ser Xaa Ser Thr Gly
 15 20 25

<210> 1339
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1339
Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Xaa
 -20 -15 -10
Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser
 -5 1 5 10
Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe
 15 20 25
Leu Leu Met
 30

<210> 1340
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1340
Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu Ser
 -25 -20 -15

Phe Leu Ser Phe Phe Phe Phe Ser Phe Phe Leu Phe Leu Xaa Phe Phe
 -10 -5 1 5
 Phe Phe Phe

<210> 1341
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1341
 Met Phe Ile Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe
 -25 -20 -15
 Val Phe Met Ser Lys Leu Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys
 -10 -5 1
 Ala Arg Met Xaa Thr Ala Ala Pro Gly
 5 10

<210> 1342
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1342
 Met Val Thr Pro Val His Ile Leu Thr Ala Val Leu Pro Leu Val Ser
 -15 -10 -5
 His Gln Gln Asn His Leu Gly Gly Arg Phe Ala Ser Leu Gly Ser Ser
 1 5 10
 Gly Ile Arg His Gly
 15

<210> 1343
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1343
 Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn Leu Phe Ile Ser Ser
 -15 -10 -5 1
 Asn Ser Phe

<210> 1344
 <211> 27

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1344
Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser Ser Cys Phe Ala Ala
-15 -10 -5 1
Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly
5 10

<210> 1345
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1345
Met Glu Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser
-30 -25 -20
Phe Ser Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His
-15 -10 -5 1
His Pro Leu Gly
5

<210> 1346
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1346
Met Gln Phe Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro
-10 -5 1
Leu Pro Leu Xaa Gln Cys Cys Thr Leu Pro
5 10

<210> 1347
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1347

Met Val Thr Ser Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His
-50 -45 -40
Ala Gly Asn Leu Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu
-35 -30 -25
Arg Leu Phe Val Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser
-20 -15 -10
Ala Ser Ile Ser Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg
-5 1 5 10
Thr Gly Ser His Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp
15 20 25
Pro His Pro Asn
30

<210> 1348

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 1348

Met Pro Arg Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu
-25 -20 -15
Val Val Leu Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser
-10 -5 1 5
Ser Arg Leu Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp
10 15 20
Leu Pro Glu Arg Arg
25

<210> 1349

<211> 91

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -54..-1

<400> 1349

Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu Met Thr
-50 -45 -40
Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp Gly Ala
-35 -30 -25
Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu Thr Leu
-20 -15 -10
Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn Lys Gly
-5 1 5 10
Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala Ile Val
15 20 25
Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu

30

35

<210> 1350
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1350
 Met Thr Lys Ala Xaa Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu
 -15 -10 -5
 Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln
 1 5 10
 Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu
 15 20 25 30
 Cys Trp

<210> 1351
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1351
 Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly
 -20 -15 -10
 Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln
 -5 1 5
 Ile Arg Gln Trp
 10

<210> 1352
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 1352
 Met Gly Pro Val Pro Gly Ala Ala Ala Gly Val Xaa Pro Xaa Xaa Gly
 -30 -25 -20 -15
 Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser
 -10 -5 1
 Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
 5 10 15
 Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly Asp Thr Asp Tyr Asn

20		25		30	
Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn					
35		40		45	50
Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala					
	55		60		

<210> 1353
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 1353
 Met Trp Phe Gln Thr Arg Ser Cys Gly His His Asp Pro Val Gly Ile
 -35 -30 -25
 Thr Gly Val Thr Lys Val Ile Leu Pro Leu Phe Leu Cys Pro Leu Gly
 -20 -15 -10 -5
 Met Val Glu Thr Ser Phe Gly
 1

<210> 1354
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -109..-1

<400> 1354
 Met Ser Tyr Val Val Thr Lys Thr Lys Ala Ile Asn Gly Lys Tyr His
 -105 -100 -95
 Arg Phe Leu Gly Arg His Phe Pro Arg Phe Tyr Val Leu Tyr Thr Ile
 -90 -85 -80
 Phe Met Lys Gly Leu Gln Met Leu Trp Ala Asp Ala Lys Lys Ala Arg
 -75 -70 -65
 Arg Ile Lys Thr Asn Met Trp Lys His Asn Ile Lys Phe His Gln Leu
 -60 -55 -50
 Pro Tyr Arg Glu Met Glu His Leu Arg Gln Phe Arg Gln Asp Val Thr
 -45 -40 -35 -30
 Lys Cys Leu Phe Leu Gly Ile Ile Ser Ile Pro Pro Phe Ala Asn Tyr
 -25 -20 -15
 Leu Val Phe Leu Leu Met Tyr Leu Phe Pro Arg Gln Leu Leu Ile Arg
 -10 -5 1

<210> 1355
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -19..-1

<400> 1355

Met	Tyr	Asn	Tyr	Tyr	Phe	Leu	Ser	Leu	Pro	Ser	Phe	Leu	Cys	Thr	Cys
			-15						-10					-5	
Cys	Gln	Phe	Phe	Pro	His	Asp	Pro	Ile	Ser	Ser	Gln	Tyr	Ser	Ser	Pro
		1				5					10				
Gln	Gly	Lys	Pro	Cys	Gln	Val	Thr	Tyr	Lys	Phe	Leu	Phe	Ile	Leu	Leu
15					20						25				
Gly	His	Val	Tyr	Pro	Arg	Asp	Gly	Gly							
30					35										

<210> 1356
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -79..-1

<400> 1356

Met	Gln	Gly	Gly	Asn	Ser	Gly	Val	Arg	Lys	Arg	Glu	Glu	Glu	Gly	Asp
				-75					-70					-65	
Gly	Ala	Gly	Ala	Val	Ala	Ala	Pro	Pro	Ala	Ile	Asp	Phe	Pro	Ala	Glu
			-60					-55					-50		
Gly	Pro	Asp	Pro	Glu	Tyr	Asp	Glu	Ser	Asp	Val	Pro	Ala	Xaa	Ile	Gln
		-45				-40						-35			
Val	Leu	Lys	Glu	Pro	Leu	Gln	Pro	Thr	Phe	Pro	Phe	Ala	Val	Ala	
	-30					-25				-20					
Asn	Gln	Leu	Leu	Leu	Val	Ser	Leu	Leu	Glu	His	Leu	Ser	His	Val	His
-15					-10					-5					1
Glu															

<210> 1357
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1357

Met	Val	Phe	Tyr	Cys	Phe	Ala	Leu	Cys	Ile	Ile	Leu	Ile	Cys	Val	Met
		-15					-10					-5			
Ser	Cys	Arg	His	Leu											
1															

<210> 1358
<211> 65
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

<400> 1358
 Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro Val Ser Cys
 -40 -35 -30
 Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe Pro Val Leu
 -25 -20 -15
 Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro Ile Gly Pro
 -10 -5 1 5
 Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe Tyr Ser Phe
 10 15 20
 Phe

<210> 1359
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1359
 Met Thr Arg Arg Arg Thr Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg
 -20 -15 -10 -5
 Thr Ser Ser Ser Leu Ser Trp Arg Met Gly Ser Gln Ile Arg Pro Ser
 1 5 10

<210> 1360
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1360
 Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe Phe Thr Val Cys
 -15 -10 -5
 Val Cys Val Arg
 1

<210> 1361
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 1361
 Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
 -30 -25 -20
 His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
 -15 -10 -5
 Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His
 1 5 10 15
 Pro Lys Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
 20 25

<210> 1362
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1362
 Met Ser Phe Ser Ser Ser Leu Pro Pro Ser Leu Pro Pro Ser Leu Ala
 -25 -20 -15
 Ser Phe Leu Leu Leu Thr Phe Leu Pro Ser Leu Pro Arg
 -10 -5 1

<210> 1363
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -46..-1

<400> 1363
 Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala Arg Pro Leu Gln
 -45 -40 -35
 Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr Lys Arg Thr Ala
 -30 -25 -20 -15
 Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile Arg Gly Cys Pro
 -10 -5 1
 Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg Thr Arg Glu Asn
 5 10 15
 Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro Ala Ala Xaa Xaa
 20 25 30
 Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser Pro Pro Leu Pro
 35 40 45 50
 Leu Pro Leu Pro Ile Asn Ser Pro Gly
 55

<210> 1364
 <211> 52
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 1364

```
Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr Lys Thr Phe
      -35                      -30                      -25
Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu Pro Phe Gln
      -20                      -15                      -10
Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg Pro Ser His
      -5                      1                      5                      10
Pro Tyr Pro His
      15
```

<210> 1365

<211> 43

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<400> 1365

```
Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser Leu Phe Glu Arg
      -35                      -30                      -25
Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa Ser Cys Xaa Cys
      -20                      -15                      -10
Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
      -5                      1
```

<210> 1366

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28..-1

<400> 1366

```
Met Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met
      -25                      -20                      -15
Pro Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
      -10                      -5                      1
```

<210> 1367

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL
<222> -37..-1

<400> 1367

Met	Xaa	Gly	Ser	Ser	Arg	Xaa	Xaa	Gly	Leu	Gln	Ile	Thr	Ala	Ser	Arg
		-35					-30					-25			
Thr	Gly	Lys	Val	Tyr	Pro	Ala	Cys	His	Phe	Leu	Xaa	Ala	Val	Ser	Ala
	-20					-15				-10					
Ser	Ser	Ser	Xaa	Ala	Cys	Leu	Trp	Tyr	Arg	Pro	Ile	Ala	Arg	Arg	Pro
-5					1				5					10	
Ala	Gly	Pro	Gly	Gly	Ser	Leu	Ser	Ser	Ala	Gln	Val	His	Pro	Ala	
			15					20						25	

<210> 1368

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 1368

Met	Ile	Leu	Phe	Asp	His	Leu	His	Cys	Ser	Ala	Ser	Gly	Val	Thr	Phe
	-25					-20				-15					
Trp	Leu	Leu	Cys	Arg	Ile	Cys	Thr	Phe	Gly	Phe	His	Gly	Phe	Ser	Lys
-10					-5				1				5		
Tyr	Thr	Val	Ser	Arg	Gly	Thr	Gln	Gln	Gly	Ala	Gly	Xaa	Xaa	Xaa	Gly
			10					15					20		
Leu	His	Gln	Asn	Trp	Glu	Gln	Trp	Arg	Gly	Leu	Val	Gly	Lys	Ser	Ser
		25				30						35			
Ser	Ala	Ala	Val	Val	Phe	Cys	Leu	Thr	Phe	Asp	Leu	Val	Thr	Ser	Phe
	40					45				50					
Gln	Leu	Ala	Ser	Ala	Ile	Glu	Ser	Thr	His	Phe	His	Ala	Gly	Arg	Asp
55					60					65					70
Gly	Ser	His	Leu												

<210> 1369

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 1369

Met	Glu	Leu	Ser	Leu	Pro	Pro	Ser	Met	Cys	Asp	Tyr	Pro	Xaa	Phe	Cys
				-25					-20					-15	
Leu	Leu	Leu	Phe	Pro	Ala	Ser	Leu	Arg	Leu	Leu	Cys	Val	His	Pro	
			-10					-5					1		

<210> 1370

<211> 27

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1370
 Met Asp Gln Lys Pro Leu Phe Thr Val Gly Cys Ala Gly Leu Ala Gly
 -20 -15 -10 -5
 Ser Cys Arg Gly Ile Ser Phe Leu Arg Thr Arg
 1 5

<210> 1371
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1371
 Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu Leu Leu
 -20 -15 -10
 Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp His Asn
 -5 1 5
 His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
 10 15 20

<210> 1372
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45..-1

<400> 1372
 Met Ser Phe Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser
 -45 -40 -35 -30
 Val Cys Pro Val Ala Gln Ser Ser Leu Thr Cys Asp Phe Ile Asp Gly
 -25 -20 -15
 Ile Cys Leu Gly Ser Pro Leu Ala Glu Cys Leu Leu Gly Xaa Xaa Xaa
 -10 -5 1
 Xaa Ile Xaa Gly Ile Asn Xaa Xaa Cys Phe Pro Cys Gly Val Lys Cys
 5 10 15
 Ala Gly Val Val Leu Gly Leu Ser Thr Leu Trp Tyr Val Val
 20 25 30

<210> 1373
 <211> 49
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 1373

Met Lys Val Gly Lys Asp Ser Leu Glu Ser Leu Pro Ser Leu Cys Glu
-35 -30 -25
Lys His Ile Gly Pro Ser Gly Leu Phe Thr Phe Leu Ser Pro Ser Phe
-20 -15 -10
His Ser Val His Leu Ser Glu Leu Asn Glu Leu Tyr Thr Ile Ala Ala
-5 1 5 10
Gly

<210> 1374

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 1374

Met Glu Ser Lys Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln
-15 -10 -5
Leu Lys Ile Lys Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
1 5 10

<210> 1375

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1375

Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro Met Leu
-20 -15 -10
Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe Arg Phe Pro Ser Arg Leu
-5 1 5
Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile Leu Cys Pro Gln Phe Pro
10 15 20
Phe Leu Leu Ile Arg Met Ser Pro Gly Asn Ile Trp Asn Gln Lys Asn
25 30 35 40
Thr Arg Ser Asp Met Val Leu Ala Pro Ser Gly Leu Thr Thr Ala Ala
45 50 55
Thr Thr Arg Val Val Tyr Pro His Ser Gly Leu Gly Arg His Val Phe
60 65 70
Val Gly Ile Lys Leu Leu Gly Ile Pro Ala Pro Ser Val Glu Ile Thr
75 80 85

Ser Cys Met Leu Thr Leu
90

<210> 1376
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1376
Met Lys Ser Asn Leu Thr Leu Leu Thr Cys Leu Xaa Leu Xaa Gly Gly
-15 -10 -5
Glu Gly Trp Lys Gly Ala Ala Val Cys Phe Glu Thr Val Glu Gln Phe
1 5 10
Cys Ser Leu Arg Lys Trp His Val Thr Tyr Leu Xaa Lys Asp Ser Gly
15 20 25 30
Leu Cys Gln Gln Gln Glu Lys Leu Tyr Thr Lys Phe Leu Val Cys Ile
35 40 45
Lys Gly Ala Ser Asn Glu Glu Ile Lys Lys Thr Tyr
50 55

<210> 1377
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1377
Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly Ser Gly Xaa Ser Leu
-10 -5 1
Val Arg Thr Pro Trp Cys Pro Glu
5 10

<210> 1378
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1378
Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile Tyr
-15 -10 -5
Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
1 5 10
Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His

15

20

25

<210> 1379
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 1379

Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Xaa Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Xaa Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val
 10

<210> 1380
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1380

Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala Xaa Arg Arg Leu
 -15 -10 -5
 Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys Leu Tyr Pro Gly
 1 5 10
 Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys Ser His Arg Ser
 15 20 25
 Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu Met Val Arg Val
 30 35 40 45
 Arg Asp His Gly

<210> 1381
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1381

Met Thr Gly Gln Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val
 -20 -15 -10
 Pro Cys Gly Trp Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu

<211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -55..-1

<400> 1385
 Met Phe His Gly Ile Pro Ala Thr Pro Gly Ile Gly Ala Pro Gly Asn
 -55 -50 -45 -40
 Lys Pro Glu Leu Tyr Glu Val Arg Gln His Gly Arg Ala Val Cys Gly
 -35 -30 -25
 Gly Glu Asp Asn Ala Ser Pro Gly Glu Gly Leu His Gln Gly Leu Cys
 -20 -15 -10
 Leu Pro Gln Arg Val His Cys Ser Leu Leu Pro Ala Pro
 -5 1 5

<210> 1386
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1386
 Met Pro His Ser Phe Val Ser Cys Asn Leu Phe Leu Ser Val Leu Asn
 -20 -15 -10
 Phe Leu Phe Leu Leu Ser Phe Ser Thr
 -5 1

<210> 1387
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1387
 Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
 -25 -20 -15
 Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
 -10 -5 1

<210> 1388
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -26..-1

<400> 1388

Met	Ala	Asp	Ser	Glu	Ala	Leu	Pro	Ser	Leu	Ala	Gly	Asp	Pro	Val	Ala
-25						-20					-15				
Val	Glu	Ala	Leu	Leu	Arg	Ala	Val	Phe	Gly	Val	Val	Val	Asp	Glu	Ala
-10					-5				1				5		
Ile	Gln	Lys	Gly	Thr	Ser	Val	Ser	Gln	Lys	Val	Cys	Xaa	Trp	Lys	
			10					15					20		

<210> 1389

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36..-1

<400> 1389

Met	Arg	Leu	Ala	Met	Val	Gln	Leu	Val	Leu	Asn	Asn	Leu	Lys	Thr	Phe
-35						-30					-25				
Tyr	Pro	Phe	Ala	Asp	His	Asp	Leu	Ala	Glu	Leu	Pro	Val	Ser	Ser	Pro
-20					-15					-10					-5
Leu	Cys	His	Ala	Val	Leu	Lys	Thr	Leu	Gln	Cys	Trp	Glu	Gln	Val	Leu
				1				5					10		
Leu	Arg	Arg	Leu	Glu	Ile	His	Gly	Gly	Pro	Pro	Gln	Asn	Tyr	Ile	Ala
		15					20					25			
Ser	His	Thr	Ala	Xaa	Xaa	Ser	Leu	Ser	Ala	Gly	Pro	Ala	Ile	Leu	Arg
	30					35					40				
His	Lys	Ala	Leu	Leu	Glu	Pro									
45					50										

<210> 1390

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 1390

Met	Phe	Lys	Leu	Phe	Leu	Phe	Leu	Phe	Ile	Leu	Xaa	Tyr	Phe	Xaa	Xaa
-20					-15					-10					-5
Tyr	Thr	Leu	Ser	Ser	Gly	Ile	Tyr	Val	Gln	Asn	Val	Gln	Val	Cys	Tyr
				1				5					10		
Ile	Gly	Ile	His	Met	Pro	Trp	Trp	Phe	Ala	Ala	Pro	Met	Asn	Leu	Ser
		15					20					25			
Ser	Ala	Leu													
		30													

<210> 1391

<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1391
Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile
-20 -15 -10
Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr
-5 1 5

<210> 1392
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1392
Met Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr
-15 -10 -5
Gln Arg
1

<210> 1393
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1393
Met His Lys Phe Phe Arg His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe
-25 -20 -15 -10
Phe Gln Leu His Ser Cys Cys His Asp Lys Val Thr Ala Xaa Arg Ala
-5 1 5
Tyr Xaa His Tyr Ser Ser Leu Leu Thr Pro Tyr Leu Ser Gln His Pro
10 15 20
Cys Pro His Pro Gly
25

<210> 1394
<211> 121
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -26..-1

<400> 1394

Met	Ala	Ala	Leu	Gly	Ser	Pro	Ser	His	Thr	Phe	Arg	Gly	Leu	Leu	Arg
-25						-20					-15				
Glu	Leu	Arg	Tyr	Leu	Ser	Ala	Ala	Thr	Gly	His	Pro	Ile	Ala	Thr	Pro
-10					-5					1			5		
Arg	Pro	Ile	Gly	Thr	Xaa	Val	Lys	Ala	Phe	Arg	Ala	His	Arg	Val	Thr
			10				15					20			
Ser	Glu	Lys	Leu	Cys	Arg	Ala	Gln	His	Glu	Leu	His	Phe	Gln	Ala	Ala
	25					30						35			
Thr	Tyr	Leu	Cys	Leu	Leu	Arg	Xaa	Ser	Gly	Asn	Met	Trp	Pro	Tyr	Ile
40					45						50				
Arg	Asn	Phe	Met	Ala	Arg	Val	Ser	Ala	Arg	Trp	Arg	Ser	Leu	Leu	Ala
55					60					65				70	
Trp	Trp	Val	Ser	Ser	Cys	Pro	Ile	Ser	Leu	Glu	Gly	Arg	Ala	Gly	Ser
			75						80					85	
His	Glu	His	Gly	Glu	Tyr	Pro	Trp	Met							
			90					95							

<210> 1395
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1395

Met	Ile	Thr	Asp	Val	Gln	Leu	Ala	Ile	Phe	Ala	Asn	Met	Leu	Gly	Val
			-25					-20					-15		
Ser	Leu	Phe	Leu	Leu	Val	Val	Leu	Tyr	His	Tyr	Ala	Ala	Val		
		-10					-5				1				

<210> 1396
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1396

Met	Ala	Glu	Gly	Ala	Leu	Ser	Phe	Leu	Cys	Ser	Leu	Ser	Gln	Asn	Ala
			-15					-10					-5		
Leu	Asn	Ile	Ser	Leu	Ile	Ser	Arg	Lys							
	1					5									

<210> 1397
<211> 23
<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1397

Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly Thr Gln Leu
-15 -10 -5
Arg Asn Ser Ser Leu Ala Met
1 5

<210> 1398

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1398

Met Glu Ser Cys Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys
-15 -10 -5 1
Thr Ser Arg

<210> 1399

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -43..-1

<400> 1399

Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe
-40 -35 -30
Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala
-25 -20 -15
Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser
-10 -5 1 5
Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys
10 15 20
Leu Gln Arg Lys Leu Pro Val
25

<210> 1400

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1400

Met Arg Leu His Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu
 -10 -5 1
Pro Phe Leu Ser Pro Pro Leu
 5

<210> 1401

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 1401

Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys Leu Glu Arg Met Cys
 -25 -20 -15
Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg Phe
-10 -5 1

<210> 1402

<211> 35

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1402

Met Ser Ser Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala
-30 -25 -20 -15
Ser Val Gly Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His
 -10 -5 1
Pro Leu Cys
 5

<210> 1403

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 1403

Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu Ala
-20 -15 -10 -5
Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu
 1 5

<210> 1404
 <211> 26
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1404
 Met Arg Glu Lys Pro Gln Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro
 -15 -10 -5
 Ala Leu Ala Ser Gln Ile His Cys Arg Val
 1 5

<210> 1405
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1405
 Met Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val
 -25 -20 -15
 Leu Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala
 -10 -5 1 5
 Pro Leu Pro Gly Arg Met
 10

<210> 1406
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1406
 Met Lys Asn Thr Leu Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu
 -20 -15 -10
 Pro Pro His Thr Cys Thr His Thr Asp Thr His
 -5 1 5

<210> 1407
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -35..-1

<400> 1407

Met Cys Leu Asn Pro Ala Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro
-35 -30 -25 -20
Arg Leu Pro Pro Leu Phe Cys Thr Phe Leu Ser Leu Ser Leu His Pro
-15 -10 -5
Trp Gly Gly Phe Phe Leu Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp
1 5 10
Val Cys Val Xaa Ala
15

<210> 1408

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -89..-1

<400> 1408

Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro
-85 -80 -75
Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val
-70 -65 -60
Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
-55 -50 -45
Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala
-40 -35 -30
Ser Asp Phe Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val
-25 -20 -15 -10
Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
-5 1 5
Tyr Thr Ser Pro Lys
10

<210> 1409

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -18..-1

<400> 1409

Met Xaa Ser Cys Glu Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala
-15 -10 -5
Phe Ala Gln Ala Phe Pro Thr Ala Cys Asn
1 5

<210> 1410

<211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 1410
 Met Cys His Tyr Leu Trp Lys Lys Leu Tyr Ser Thr Leu Leu Tyr Ile
 -25 -20 -15 -10
 Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys Asn Leu Ile Thr Ala Val
 -5 1 5
 Ala Ser Arg Ala Gly Asn Leu Gly Val Trp Thr Glu Lys Gly
 10 15 20

<210> 1411
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 1411
 Met Xaa Ser His Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg
 -25 -20 -15
 Met Val Leu Leu Ser Ser Ala Leu Leu Ser Thr Glu Asn
 -10 -5 1

<210> 1412
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1412
 Met Arg Pro Ser His Ser Ser Ala Tyr Leu Cys Leu His Leu Cys Ala
 -20 -15 -10
 Phe Ser Thr Glu Gly Trp Met Asn Arg Leu Ser Ser Ser Leu Arg Leu
 -5 1 5 10
 Ala Pro Leu Pro Leu Tyr Pro Phe Cys Leu Pro Ser Asn Ser Pro
 15 20 25

<210> 1413
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -16..-1

<400> 1413

Met	Trp	Ser	Arg	Leu	Val	Trp	Leu	Gly	Leu	Arg	Ala	Pro	Leu	Gly	Gly
	-15					-10				-5					
Arg	Gln	Gly	Phe	Thr	Ser	Lys	Ala	Asp	Pro	Gln	Gly	Ser	Gly	Arg	Ile
1				5				10					15		
Thr	Ala	Ala	Val	Ile	Glu	His	Leu	Glu	Arg	Leu	Ala	Leu	Val	Asp	Phe
			20					25					30		
Gly	Ser	Arg	Glu	Ala	Val	Ala	Arg	Leu	Glu	Lys	Ala	Ile	Ala	Phe	Ala
		35					40					45			
Asp	Arg	Leu	Arg	Ala	Val	Asp	Thr	Asp	Gly	Val	Glu	Pro	Met	Glu	Ser
	50					55					60				
Val	Leu	Glu	Asp	Arg	Cys	Leu	Tyr	Leu	Arg	Ser	Asp	Asn	Val	Val	Glu
65					70					75				80	
Gly	Asn	Cys	Ala	Asp	Glu	Leu	Leu	Gln	Asn	Ser	His	Arg	Val	Val	Glu
				85				90						95	
Glu	Tyr	Phe	Val	Ala	Pro	Pro	Gly	Asn	Ile	Ser					
			100					105							

<210> 1414
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -81..-1

<400> 1414

Met	Ala	Pro	Pro	Val	Arg	Tyr	Cys	Ile	Pro	Gly	Glu	Arg	Leu	Cys	Asn
	-80					-75				-70					
Leu	Glu	Glu	Gly	Ser	Pro	Gly	Ser	Gly	Thr	Tyr	Thr	Arg	His	Gly	Tyr
-65					-60				-55					-50	
Ile	Phe	Ser	Ser	Leu	Xaa	Gly	Cys	Leu	Met	Lys	Ser	Ser	Glu	Asn	Gly
			-45					-40					-35		
Ala	Leu	Pro	Val	Val	Ser	Val	Val	Arg	Glu	Thr	Glu	Ser	Gln	Leu	Leu
		-30						-25				-20			
Pro	Asp	Val	Gly	Ala	Ile	Val	Thr	Cys	Lys	Ser	Leu	Ala	Ser	Ile	His
	-15						-10					-5			
Ala	Leu	Pro													
1															

<210> 1415
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -60..-1

<400> 1415

Met Val Gly Asn Gln Gly Pro Gln Pro Pro Phe Pro Met Glu Pro
 -60 -55 -50 -45
 Thr Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys
 -40 -35 -30
 Gln Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg
 -25 -20 -15
 Leu Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr
 -10 -5 1
 Glu Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser
 5 10 15 20

<210> 1416
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 1416
 Met Lys Pro Gln Thr Leu Ala Val Ser Val Thr Val Leu Lys Asp Gly
 -25 -20 -15
 Val Ala Gly Val Cys Phe Phe Arg Arg Ser Asp Ala Ser Glu Val Ser
 -10 -5 1
 Ser Phe Trp
 5

<210> 1417
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

<400> 1417
 Met Val Val Leu Ile Cys Leu Ser Leu Met Ile Ser Asn Thr Glu Leu
 -40 -35 -30
 Phe Phe Ile Arg Phe Leu Thr Ala Cys Met Pro Ser Phe Glu Lys Cys
 -25 -20 -15
 Leu Phe Leu Ser Phe Ala His Phe Leu Met Gly Arg Thr His Arg
 -10 -5 1

<210> 1418
 <211> 36
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1418

Met Ser Ser Leu Tyr Ile Leu Asp Ile Ser Leu Leu Ser Asp Ile Leu
-20 -15 -10
Phe Ala Asn Ile Phe Ser His Ser Trp Asp Val Phe Pro Leu Ser Phe
-5 1 5 10
Leu Phe Phe Ser

<210> 1419

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -84..-1

<400> 1419

Met Gly Gln Gly Ala Arg Gly Trp His Arg Glu Pro Gly Leu Gly Leu
-80 -75 -70
Arg His Ser Pro Arg Arg Leu Ser Gly Ala Leu His Leu Glu Ala Gly
-65 -60 -55
Cys Asp Arg Asn Ala Thr Thr Val Arg Pro Leu Arg Ala Lys Xaa Gly
-50 -45 -40
Asp Ala Leu Pro Glu Glu Ile Arg Glu Pro Ala Leu Arg Asp Ala Gln
-35 -30 -25
Trp Val Arg Asp Gln Leu Ala Ser Ser Leu Leu Ile Ile Leu Leu Pro
-20 -15 -10 -5
Asn Thr Gln Asp Leu Arg Ile Gln Lys Asp Pro Thr Pro Gly Pro
1 5 10

<210> 1420

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 1420

Met Arg Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu
-45 -40 -35
Cys Lys Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met
-30 -25 -20
Glu Trp Leu Asn Ser Leu Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro
-15 -10 -5
His Ser His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu
1 5 10 15
Gly Arg Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr
20 25 30
Pro Val Thr Asn Thr Thr Pro
35

<210> 1421

<211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 1421
 Met Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe
 -30 -25 -20 -15
 Leu Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro
 -10 -5 1
 Leu

<210> 1422
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 1422
 Met Ala Ala Ser Ala Ala Ala Glu Leu Gln Ala Ser Gly Gly Pro
 -30 -25 -20
 Arg His Pro Val Cys Leu Leu Val Leu Gly Met Ala Gly Ser Gly Lys
 -15 -10 -5 1
 Thr Thr Phe Val Gln Arg Leu Thr Gly His Leu His Ala Gln Gly Thr
 5 10 15
 Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Xaa
 20 25 30
 Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met
 35 40 45
 Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn
 50 55 60 65
 Leu Phe Xaa Thr Arg Phe Asp Gln Val Met Lys Leu Leu Arg Arg Pro
 70 75 80
 Arg Thr Cys Pro Asn Met Cys
 85

<210> 1423
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 1423
 Met Tyr Ala Cys Ala Met Leu Val Leu Leu Thr His Gly Leu Ile His
 -20 -15 -10 -5

Tyr Ser Phe Thr His His Leu His Tyr Val Phe Ile Leu Ile Leu Pro
1 5 10
Leu Pro Pro Pro Pro Gln
15

<210> 1424
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1424
Met Gly Phe Leu Gly Ser Pro Arg Gln Arg Asn Ser Met Cys Leu Leu
-20 -15 -10
Leu Asp Val Ser Ser Xaa Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa
-5 1 5
Leu Ile Ile Tyr Tyr Leu Ile Thr Arg Lys Gly Pro Gly
10 15 20

<210> 1425
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1425
Met Ser Cys Gln Xaa Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile
-40 -35 -30
Arg Gly Arg His Pro Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn
-25 -20 -15
Ile Phe Leu Ala Ala Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg
-10 -5 1 5
Arg Pro Gln

<210> 1426
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1426
Met Cys Pro Ala Trp Leu Pro Cys Trp Thr Ala Gln Thr Glu His Leu
-30 -25 -20
Asp Arg Tyr Arg Lys Phe His Gln Met Ala Leu Xaa Pro Gly Thr Ser
-15 -10 -5

Arg Ala Gln Ala Leu Leu Tyr Asn Glu Val Leu Glu Arg Phe Met Phe
 1 5 10
 Thr Arg Leu
 15

<210> 1427
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1427
 Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro Ser His Ser
 -15 -10 -5
 Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro Ala Thr Ser
 1 5 10
 Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
 15 20 25

<210> 1428
 <211> 162
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -121..-1

<400> 1428
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 -120 -115 -110
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
 -105 -100 -95 -90
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu
 -85 -80 -75
 Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu
 -70 -65 -60
 Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr
 -55 -50 -45
 Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys
 -40 -35 -30
 Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr
 -25 -20 -15 -10
 Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp
 -5 1 5
 Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser
 10 15 20
 Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Xaa Ala
 25 30 35
 Phe Thr
 40

<210> 1429
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38..-1

<400> 1429
 Met Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val
 -35 -30 -25
 Val Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val
 -20 -15 -10
 Thr Val Phe Val Trp Ser Cys Xaa Gln Gln Ala Glu Lys Lys His
 -5 1 5 10
 Lys Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
 15 20 25

<210> 1430
 <211> 25
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1430
 Met Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile
 -15 -10 -5 1
 Phe Phe Ser Leu Val Cys Val Leu Phe
 5 10

<210> 1431
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1431
 Met Phe Ser His Asn His Ser Tyr Thr Tyr Thr Pro Gln His Ser Pro
 -25 -20 -15
 Leu Thr His Thr His Thr Cys Thr Pro Ser Thr Ala His Pro Arg
 -10 -5 1
 Gly

<210> 1432
 <211> 22
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1432

Met Phe Xaa Met Ile Leu Leu Cys Phe Leu Ala Val Ser Asn Phe Asn
-15 -10 -5 1
Lys Leu Leu Trp Gly Xaa
5

<210> 1433

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 1433

Met Phe Leu Ile Leu Gly Lys Phe Ser Arg Val Met Gly Leu Pro Leu
-25 -20 -15
Ala Cys Phe Ser Leu Phe Gly Xaa Leu Pro Gln Gly Leu Leu Ile
-10 -5 1 5

<210> 1434

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19..-1

<400> 1434

Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro Gly Xaa Xaa His Gly
-15 -10 -5
Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile Leu Leu Cys
1 5 10

<210> 1435

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1435

Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg Asn Val Tyr Ser Asn
-15 -10 -5 1

Leu Leu Pro Ser Phe Phe
5

<210> 1436
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1436
Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
-25 -20 -15
Leu Leu Leu Pro Ala His His Gly Arg His Gly Ser Gly Leu Pro Ala
-10 -5 1 5
Pro Asp Pro Ser Pro Pro Pro Gly Pro Ala Val Pro Gly Pro Trp Pro
10 15 20
Cys Gln Asp Glu Leu Pro Ser Leu Arg Pro Ala Thr Ser His His Phe
25 30 35

<210> 1437
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1437
Met Ala Val Gly Gly Thr Ala Val Ile Thr Arg Arg Leu Leu Gly Arg
-25 -20 -15 -10
Ser Gly Phe Ser Phe Gln Val Ser Gly Trp Gly Trp Gly Glu Arg Val
-5 1 5
Asp Asp Phe Leu Phe Ser Ser Gly Ile Asp Gly
10 15

<210> 1438
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1438
Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser Leu Ala His His
-20 -15 -10
Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala Pro Ala Gln Leu
-5 1 5 10
Ser Pro

<210> 1439
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -73..-1

<400> 1439
 Met Leu Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys
 -70 -65 -60
 Asn Ser Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly
 -55 -50 -45
 Leu Thr Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu
 -40 -35 -30
 Asn Asp Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn
 -25 -20 -15 -10
 Leu Ala Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu
 -5 1 5
 Phe Leu Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser
 10 15 20
 Ile Val Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly
 25 30 35
 Gly Arg Arg
 40

<210> 1440
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 1440
 Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys Leu Ser
 -25 -20 -15 -10
 Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg Phe Leu
 -5 1 5
 Ala Pro

<210> 1441
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1441

Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln Ala Tyr Gly
 -10 -5 1

<210> 1442
 <211> 28
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1442
 Met Leu Ser Ile Phe Ser Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu
 -20 -15 -10
 Leu Arg Asn Leu Xaa Ser Tyr Ser Leu Pro Thr Thr
 -5 1

<210> 1443
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -77..-1

<400> 1443
 Met Phe Pro Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Thr Asn
 -75 -70 -65
 Lys Ser Leu Pro Arg Ser Ala Ser Thr Pro Glu Thr Arg Thr Lys Phe
 -60 -55 -50
 Thr Gln Asp Asn Leu Cys Xaa Ala Gln Arg Glu Arg Leu Asp Ser Ala
 -45 -40 -35 -30
 Asn Leu Trp Val Leu Val Asp Cys Ile Leu Arg Asp Thr Ser Glu Asp
 -25 -20 -15
 Leu Gly Leu Gln Cys Asp Ala Val Asn Leu Ala Phe Gly Arg Arg Cys
 -10 -5 1
 Glu Glu Leu Glu Asp Ala Arg His Lys Leu Gln Xaa His Leu
 5 10 15

<210> 1444
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1444
 Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser Ile Leu Tyr Ile
 -15 -10 -5 1
 Tyr His Leu Arg

5

<210> 1445
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1445
 Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe Xaa Val Phe Xaa Phe
 -20 -15 -10
 Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro Arg Leu Glu Cys Asn
 -5 1 5
 Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu Leu Ser Xaa Ser Asn
 10 15 20
 Ser Leu Ala Ser Ala Pro Arg Gly
 25 30

<210> 1446
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -90..-1

<400> 1446
 Met Glu Asp Ser Ala Ser Ala Ser Leu Ser Ser Ala Ala Ala Thr Gly
 -90 -85 -80 -75
 Thr Ser Thr Ser Thr Pro Ala Ala Pro Thr Ala Arg Lys Gln Leu Asp
 -70 -65 -60
 Lys Glu Gln Val Arg Lys Ala Val Asp Ala Leu Leu Thr His Cys Lys
 -55 -50 -45
 Ser Arg Lys Asn Asn Tyr Gly Leu Leu Leu Asn Glu Asn Glu Ser Leu
 -40 -35 -30
 Phe Leu Met Val Val Leu Trp Lys Ile Pro Ser Lys Glu Leu Arg Val
 -25 -20 -15
 Arg Leu Thr Leu Pro His Ser Ile Arg Ser Asp Ser Glu Asp Ile Cys
 -10 -5 1 5
 Xaa Phe Thr Lys Asp
 10

<210> 1447
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

<400> 1447

Met	Asn	Ala	Glu	Gly	Ala	Ser	Pro	Gly	Lys	Glu	Thr	Asn	Thr	Gly	Thr
			-25					-20						-15	
Leu	Ile	Glu	Leu	Asn	Leu	Xaa	Ser	Pro	Val	Ala	Leu	Gln	Trp	Pro	Leu
		-10				-5						1			
Ser	Ser	Pro	Ser	Cys	Leu	Arg	Ile	Leu	Ser	Asn	Lys	Val	Pro	Arg	Asn
5					10					15					
Leu	Arg	Trp	Gln	Lys	His	Tyr	Ser	Thr	His	Gln					
20					25					30					

<210> 1448

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -63..-1

<400> 1448

Met	Leu	Gly	Leu	Asp	Glu	Leu	Gly	Arg	Ser	Gly	Cys	Gly	His	Cys	Thr
		-60					-55				-50				
Gln	Ala	Asp	Leu	Arg	Phe	Gly	Asp	Ala	Ala	Gly	Xaa	Glu	Pro	Arg	Xaa
	-45				-40					-35					
Arg	Xaa	Thr	His	Arg	Asn	Thr	Ala	Ala	Ala	Arg	Val	Pro	Pro	Pro	Pro
-30				-25						-20					
Arg	Val	Met	Ala	Ala	Ala	Ala	Leu	Arg	Ala	Pro	Ala	Gln	Ser	Ser	
-15			-10					-5					1		
Val	Thr	Phe	Glu	Asp	Val	Ala	Val	Asn	Phe	Ser	Leu	Glu	Glu	Trp	Ser
		5					10					15			
Leu															

<210> 1449

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26..-1

<400> 1449

Met	Ser	Ala	Leu	Lys	Asp	Phe	Arg	Glu	Phe	Leu	Asn	Trp	Trp	Gly	Asn
-25				-20						-15					
Leu	Ser	Phe	His	Leu	Gln	Glu	Ala	His	Gly	Ser	Glu	Ile	Ala	Glu	Met
-10			-5						1				5		
Gly	Ala	Gly	Ile	Leu	Glu	Glu	Lys	Asn	Tyr	Gly	Gln	Gln	Xaa	His	Cys
		10					15					20			
Asn															

<210> 1450

<211> 36

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1450

Met Ser Leu Pro Pro Phe Phe His Pro Ser Pro Ala Pro Ser Leu Ala
-30 -25 -20 -15
Pro Pro Pro Ser Leu Phe Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro
-10 -5 1
Leu Pro Ala Arg
5

<210> 1451

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13..-1

<400> 1451

Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser Phe Phe
-10 -5 1
Phe Phe
5

<210> 1452

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 1452

Met Lys Ala Gly Pro Cys Ser Cys Gln Glu Gly Gly Arg Gln Trp Ala
-40 -35 -30
His Gly Ser Val Pro Leu Gln Pro Thr Ala Arg Leu Ala Ala Leu Gly
-25 -20 -15
Ile Phe Leu Cys Pro Gly Glu Thr Leu Ser Ala Ser Leu His Trp Asn
-10 -5 1 5
Pro Ile Gly

<210> 1453

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 1453

Met	Leu	Ser	Gln	Ser	Phe	Gln	Lys	Asn	Lys	Thr	Asn	Leu	Leu	Cys	Leu
		-20					-15					-10			
Thr	Phe	Gln	Arg	Cys	Gln	Ser	Tyr	Asn	Trp	Leu	Asn	Ile	Phe	Glu	Ala
		-5					1			5					
Thr	Tyr	Met	Thr	Thr	Leu	Phe	Ile	Ser	Val	Ile	Xaa	Thr	Asn	Phe	Leu
10					15					20					25
Lys	Arg	Tyr	Leu	Leu											
				30											

<210> 1454

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25..-1

<400> 1454

Met	Phe	Leu	Phe	Cys	Trp	Glu	Lys	Ser	Pro	Arg	Met	Gln	Leu	Leu	Gly
-25					-20				-15						-10
Cys	Met	Val	Leu	Tyr	Asp	Cys	Phe	Ser	Phe	Lys	Lys	Leu	Pro	Gly	
			-5					1				5			

<210> 1455

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1455

Met	Ser	Phe	Ile	Ser	Val	Ile	Phe	Pro	Leu	Ile	Leu	Leu	Asn	Arg	Phe
-30					-25				-20					-15	
Ser	Phe	Val	Cys	Phe	Phe	His	Val	Phe	Tyr	Cys	Val	Phe	Cys	Asn	Val
			-10					-5					1		
Ser	Ser	Leu	Phe	Ser	Tyr	Gln	Phe	Leu	Leu	His	Phe	Cys	Asp	Asp	
	5					10						15			

<210> 1456

<211> 35

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31..-1

<400> 1456

Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe Asn Ser Pro Asn
 -30 -25 -20
 Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly Val Lys Ser Trp
 -15 -10 -5 1
 Ile Gly Gly

<210> 1457
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 1457
 Met Ala Ser Xaa Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
 -35 -30 -25
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser
 -20 -15 -10 -5
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys
 1 5 10
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu
 15 20 25
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys
 30 35 40
 His Glu Ser
 45

<210> 1458
 <211> 24
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1458
 Met Val Ile Ser Ala Gly Ala Leu Leu Trp Met Ala Trp Asp Gly Gln
 -15 -10 -5
 Leu Ser Arg Pro Glu Gly Ala Arg
 1 5

<210> 1459
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1459

Met Val His Cys Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile
 -15 -10 -5
 Ser Ala Ser Pro Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val
 1 5 10

<210> 1460
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -88..-1

<400> 1460
 Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg
 -85 -80 -75
 Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu
 -70 -65 -60
 Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys
 -55 -50 -45
 Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr
 -40 -35 -30 -25
 Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu
 -20 -15 -10
 Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu
 -5 1 5
 Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser
 10 15 20
 Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser
 25 30 35

<210> 1461
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43..-1

<400> 1461
 Met Arg Gly Trp Xaa Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg
 -40 -35 -30
 Leu Pro Met Gly Ser Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp
 -25 -20 -15
 Cys Leu Xaa Leu Lys Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr
 -10 -5 1 5
 Leu Gly Ile Gln Gly Phe
 10

<210> 1462
 <211> 49
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 1462

Met Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu
 -30 -25 -20
Gln Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr
 -15 -10 -5
Trp Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr
 1 5 10
Arg
15

<210> 1463

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<400> 1463

Met Ser Ser Asn Ile Gln Arg Leu Gly Phe Pro Leu Leu Phe Leu Phe
 -20 -15 -10
Phe Leu Phe Leu Phe Phe Phe Phe Phe
 -5 1

<210> 1464

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -67..-1

<400> 1464

Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser Glu Asn
 -65 -60 -55
Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr Arg Lys
 -50 -45 -40
Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn Gly Asp
 -35 -30 -25 -20
Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu Pro Thr
 -15 -10 -5
Ser Asn Arg Lys Arg
 1

<210> 1465

<211> 35

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 1465
 Met Phe Leu Tyr Arg Ser Phe Gly Gly Gln Leu Leu Ser Phe Leu Leu
 -20 -15 -10
 Gly Thr Tyr Leu Gly Arg Arg Glu Val Ala Gly Pro Gln His Gly Gln
 -5 1 5 10
 Phe Ser Lys

<210> 1466
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1466
 Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser Phe Leu Leu Ser
 -15 -10 -5
 Pro Glu Gly
 1

<210> 1467
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -66..-1

<400> 1467
 Met Ile Phe Pro His Cys Met Tyr Cys Leu Glu Cys Ile Thr Lys Asn
 -65 -60 -55
 Gly Leu Leu Gly Leu Lys Val Leu Pro Leu Tyr Gly Ile Met Leu Ile
 -50 -45 -40 -35
 Phe Phe Pro Lys Val Val Tyr Asn Asn Gln Pro Leu His Tyr Lys Ser
 -30 -25 -20
 Val Met Val Phe Gln Leu Thr Ser Phe Leu Ser Ile Xaa Ile Phe Val
 -15 -10 -5
 Asn Pro Thr Arg
 1

<210> 1468
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 1468
 Met Val Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser
 -50 -45 -40
 Thr Arg Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu
 -35 -30 -25
 Gly Thr Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr
 -20 -15 -10
 Val Glu Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr
 -5 1 5 10
 Glu Val Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
 15 20 25

<210> 1469
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 1469
 Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr Ser Leu Leu Phe Arg
 -30 -25 -20
 Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg Xaa Xaa Ser Cys Ser
 -15 -10 -5 1
 Ser Xaa Ala Pro Ser Ile Lys Ala Arg Thr Leu Ser Thr Thr Thr Ser
 5 10 15
 Thr Arg Gly Ser Cys Gly Asn Thr Ser Ser Thr Ser Met Arg Thr Ser
 20 25 30
 Ser Ser Leu Glu Ala Pro Ile Gln Ala Arg Arg Thr Arg Ser Thr Gln
 35 40 45
 Gln Leu Phe Ala Gln Ser Trp Ser Leu Ser Xaa Lys Met Met
 50 55 60

<210> 1470
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 1470
 Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu Glu Tyr Leu Tyr Leu
 -40 -35 -30
 Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe Pro Leu His Thr Ser
 -25 -20 -15 -10

Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys Lys Ile Phe Lys Ile
 -5 1 5
 Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp Xaa Ser Leu Leu Arg
 10 15 20
 Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile Ile Ser Arg Gln Glu
 25 30 35
 Leu Pro Pro
 40

<210> 1471
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 1471
 Met Phe Leu Cys Val Cys Tyr Phe Ile Arg Lys Ser Thr Ser Phe Phe
 -10 -5 1
 Ser Ile Ser Ser
 5

<210> 1472
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 1472
 Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr Val
 -45 -40 -35 -30
 Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser Cys
 -25 -20 -15
 Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu Glu
 -10 -5 1
 Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp Leu
 5 10 15
 Ser Pro Gln Leu Ala Pro Arg
 20 25

<210> 1473
 <211> 18
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 1473

Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe Val Phe Leu Gly
-15 -10 -5

Val Val

1

<210> 1474

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37..-1

<400> 1474

Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp
-35 -30 -25

Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met
-20 -15 -10

Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly
-5 1 5 10

<210> 1475

<211> 47

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42..-1

<400> 1475

Met Gln Ala Thr Ala Ser Gln Pro Ile His Phe Phe Xaa Ser Ser Pro
-40 -35 -30

Gln Ala Pro Arg His His Ser Gly His Pro Val Pro Leu Leu Leu Thr
-25 -20 -15

Gln Ala Gly Phe Pro Arg Arg Gly Glu Ala Ala Pro Pro Leu Leu
-10 -5 1 5

<210> 1476

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1476

Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu Lys
-30 -25 -20 -15

Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile Xaa
-10 -5 1

Leu Asp

<210> 1477
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1477
Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala Asp Thr Ala Gln Lys
 -30 -25 -20
Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu Ser Thr Ser Xaa Xaa
 -15 -10 -5
Phe Met Glu Leu Ser Ser Leu Arg
1 5

<210> 1478
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -67..-1

<400> 1478
Met Asn Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn
 -65 -60 -55
Cys Met Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys
 -50 -45 -40
Pro Val Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu
 -35 -30 -25 -20
Leu Ile Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe
 -15 -10 -5
Cys Tyr Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly
 1 5 10
Met Val Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe
 15 20 25
Ser Glu Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly
30 35 40 45

<210> 1479
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1479

Met Gln Ile Ser Ala Ala Ser Leu Asn Phe Ser Ser Lys Asn Gly Ile
 -25 -20 -15
 Phe Phe Ser Leu Thr Leu Ser Gly Cys Lys Phe Ser Lys Leu Leu Cys
 -10 -5 1
 Pro Phe Gly
 5

<210> 1480
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -52..-1

<400> 1480
 Met Ile Phe Glu Pro Val Val Leu Lys Pro Val Phe Leu Asn Ile Phe
 -50 -45 -40
 Phe Phe Ser His His Val Phe Thr Val Phe Phe Ser Gly Ser His Val
 -35 -30 -25
 Asp Ile Leu Ser Arg Thr Val Leu Val Trp Asp Cys Leu Leu Pro Pro
 -20 -15 -10 -5
 Pro Ser Phe Phe Leu Leu Leu Leu Ser Ser Ser Xaa Ser Xaa Leu Leu
 1 5 10
 Leu Xaa Xaa Ser Ser Ser Ser Arg
 15 20

<210> 1481
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1481
 Met Leu Val Pro Leu Leu Ser His Leu Leu Phe Lys Phe Thr Trp Pro
 -10 -5 1
 Lys Xaa Ser Gln
 5

<210> 1482
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 1482
 Met Asp Arg Asn Pro Ser Pro Pro Pro Gly Arg Asp Lys Glu Glu

-45 -40 -35
 Glu Glu Glu Val Ala Gly Gly Asp Cys Ile Gly Ser Thr Val Tyr Ser
 -30 -25 -20
 Lys His Trp Leu Phe Gly Val Leu Ser Gly Leu Xaa Gln Xaa Val Ser
 -15 -10 -5
 Pro Gly Lys His Gln Asn Leu Gly Ser Xaa Xaa Glu Glu Gln Leu Thr
 1 5 10 15
 Glu Leu Asp Glu Arg Asn
 20

<210> 1483
 <211> 37
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400> 1483
 Met Lys Leu Ser Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe
 -20 -15 -10
 Ser Leu Ala Leu Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg
 -5 1 5
 Val Ser Ala Glu Arg
 10

<210> 1484
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 1484
 Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His Gly Val
 -40 -35 -30 -25
 Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala Leu Ser
 -20 -15 -10
 Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser Xaa Thr
 -5 1 5

<210> 1485
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 1485

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
-45 -40 -35
Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
-30 -25 -20
Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
-15 -10 -5
Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
1 5 10 15
Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
20 25 30
Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
35 40 45
Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
50 55 60
Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp
65 70 75

<210> 1486
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1486
Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala Ala Thr
-25 -20 -15
Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln Glu Val
-10 -5 1
Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp Arg Ala
5 10 15
Asp Lys Lys Glu Arg Pro Cys
20 25

<210> 1487
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1487
Met Leu Gln Phe Glu Lys Pro Gly Ser Ala Ile Cys Leu Trp His Ser
-15 -10 -5
Thr Leu Gly Gly Xaa Gly Gly Arg Glu Ile Xaa Ser Leu Arg Pro Ala
1 5 10
Cys Gly
15

<210> 1488

<211> 24
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18..-1

<400> 1488
 Met Leu Ile Ser Tyr Leu Ala Ile Leu Leu Lys Trp Val Ser Asn Ser
 -15 -10 -5
 Lys Ser Phe Leu Val Lys Ala Ser
 1 5

<210> 1489
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 1489
 Met Lys Leu Gln Thr Leu Ala Phe Trp Ser Ala Tyr Val Pro Cys Gln
 -15 -10 -5 1
 Thr Gln Asp Arg Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu
 5 10 15
 Ile Arg Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser
 20 25 30
 Ala Lys Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val
 35 40 45
 Glu Gly Gly His Ser Leu Asp Asn Ser Leu Ser Arg
 50 55 60

<210> 1490
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1490
 Met Pro Ala Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro
 -10 -5 1
 Ser Ser Pro Pro Ser Ile Gly
 5

<210> 1491
 <211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1491
 Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu Gly Ala Ser Ser
 -15 -10 -5
 His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val Asp Cys Gly Phe
 1 5 10 15
 Leu Leu

<210> 1492
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 1492
 Met Cys Cys Pro Gly Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala
 -20 -15 -10 -5
 Pro Ser Thr Ser Trp Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
 1 5 10

<210> 1493
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -54..-1

<400> 1493
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
 -50 -45 -40
 Val Pro Leu Lys Xaa Xaa Xaa Val Asp Asp Asp Asp Ser Lys Ile Trp
 -35 -30 -25
 Ser Xaa Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
 -20 -15 -10
 Leu Xaa Xaa Val Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu
 -5 1 5 10
 Ala Leu Thr Gly Trp
 15

<210> 1494
 <211> 45
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -16..-1

<400> 1494
Met Asp Ala Ser His Ser His Leu Ser Leu Val Gly His Ser Arg Ala
-15 -10 -5
Cys Gly Val Thr Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu
1 5 10 15
Gly Pro Cys Ser Arg Ser Gly Pro Arg Leu Cys Ser Ala
20 25

<210> 1495
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1495
Met Gly Ser Asn Ala Val Val Trp His Thr Lys Pro Ser Leu Leu Asn
-30 -25 -20
His Pro Ala Ser Ser Leu Ile Ser His Asp Pro Trp Pro Arg Gly Ala
-15 -10 -5
Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met Leu Phe Ser Ser Leu
1 5 10
Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys Asn Xaa
15 20 25

<210> 1496
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1496
Met Lys Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val
-15 -10 -5
Tyr Gly Asp Gln Asp Met His Glu Val Val Arg Lys His Xaa Met Asp
1 5 10
Tyr Leu Met Lys Asn Ala Asp Tyr Phe Ser Xaa Tyr Val Thr Glu Asp
15 20 25 30
Phe Thr Thr Tyr Ile Xaa Arg Lys
35

<210> 1497
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1497
Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met Ile Xaa Glu Ala
-20 -15 -10
Xaa Asn Val Trp Cys Gly Asp Ser
-5 1

<210> 1498
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 1498
Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp Ile His Val Val
-45 -40 -35
Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His Ile Phe Tyr Cys
-30 -25 -20
Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu Val Tyr Ser Trp
-15 -10 -5 1
Asn Ile Tyr

<210> 1499
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1499
Met Glu Ser Pro Ser Arg Ala Gly Gly Val Xaa Leu Xaa Lys Ala Ala
-25 -20 -15
Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr Cys Xaa Ala Phe Pro Arg
-10 -5 1
Arg Ser Ala Arg Arg His Leu His Pro Gly His Gly
5 10 15

<210> 1500
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1500

Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
-25 -20 -15 -10
Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
-5 1 5
Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
10 15 20
Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
25 30 35

<210> 1501

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -30..-1

<400> 1501

Met Asp Val Ser Cys Lys Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys
-30 -25 -20 -15
Asn Asn Leu Leu Lys Leu Ser Ser His Ser Pro Thr Cys Ala Cys Lys
-10 -5 1
Leu

<210> 1502

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 1502

Met Ile Phe Lys Asp Val Phe Ser His Leu Ser Gly Ser Ser Leu Gln
-20 -15 -10 -5
Leu Cys Val Ala Gln Phe Leu Xaa Leu Ser Ala Val Asp
1 5

<210> 1503

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44..-1

<400> 1503

Met Lys Leu Thr Lys Asn Ile Leu Xaa Val Ile Ile Gly Cys Phe Lys
-40 -35 -30
Leu Ile Ala Tyr Lys Asn Ser Val Leu Tyr Phe Tyr Ser Asn Phe Ser

-25 -20 -15
 Phe Ser Phe Leu Phe Phe Phe Phe Leu Ser Phe Phe Phe Phe Phe
 -10 -5 1
 Phe Phe
 5

<210> 1504
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -87..-1

<400> 1504
 Met Asn Asn Gln Lys Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe
 -85 -80 -75
 Lys Thr Arg Lys Arg Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe
 -70 -65 -60
 Gln Asp Cys Ile Ile Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu
 -55 -50 -45 -40
 Ala Val Ala Lys Phe Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg
 -35 -30 -25
 Arg Tyr Ala Glu Thr Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu
 -20 -15 -10
 Ala Pro Gly Gly Thr Leu Ala Asp Asp Met Met Xaa
 -5 1 5

<210> 1505
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1505
 Met Ala Asp Ser Leu Glu Ile Lys Leu Pro Phe Leu Pro Phe Ala Gln
 -15 -10 -5
 Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe Phe Phe Xaa Asn Xaa Xaa
 1 5 10 15
 Phe Pro Arg

<210> 1506
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 1506

```
Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu Glu
-35          -30          -25          -20
Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Thr Ala Ala Ser Ala
          -15          -10          -5
Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys Asp
      1          5          10
Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser
    15          20          25
Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro
    30          35          40          45
Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr
          50          55          60
Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr
          65          70          75
Gln Ala Pro
      80
```

<210> 1507

<211> 74

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -43..-1

<400> 1507

```
Met Ala Pro Gln Met Tyr Glu Phe His Leu Pro Leu Ser Pro Glu Glu
          -40          -35          -30
Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr Val Val Gln Glu Val Leu
          -25          -20          -15
Ser Ile Lys His Leu Pro Pro Gln Leu Arg Ala Phe Gln Ala Ala Phe
          -10          -5          1          5
Arg Ala Gln Gly Pro Leu Ala Met Leu Gln His Phe Asp Thr Ile Tyr
          10          15          20
Ser Ile Leu His His Phe Arg Ser Ile Asp
          25          30
```

<210> 1508

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15..-1

<400> 1508

```
Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro Arg
-15          -10          -5          1
Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg Leu
      5          10          15
Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser Ala
```

20 25 30
 Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn Tyr
 35 40 45
 Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu Val
 50 55 60 65
 Gln Ala Cys Gly

<210> 1509
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 1509
 Met Phe His Gly Cys His Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg
 -30 -25 -20 -15
 Gly Phe Leu Phe Phe Leu Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe
 -10 -5 1
 Arg Xaa Xaa Phe Pro Gln Ser Phe Met Leu Glu Ala Phe Val Arg Cys
 5 10 15

<210> 1510
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 1510
 Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val Leu
 -25 -20 -15
 Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp Trp
 -10 -5 1 5
 Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe
 10 15

<210> 1511
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -50..-1

<400> 1511
 Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg Leu
 -50 -45 -40 -35
 Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys Asn

-30 -25 -20
 Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp Cys
 -15 -10 -5
 Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg Ser
 1 5 10
 Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met Gln
 15 20 25 30
 Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly Cys
 35 40 45
 Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln Leu
 50 55 60
 Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys His
 65 70 75
 Gly Thr Asp Leu Trp Leu Asp Ser Cys
 80 85

<210> 1512
 <211> 26
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22..-1

<400> 1512
 Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
 -20 -15 -10
 His Gln Arg Thr Leu Ile Ser Leu Pro Pro
 -5 1

<210> 1513
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 1513
 Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser Ile
 -10 -5 1
 Leu Asp Ser Pro Ala
 5

<210> 1514
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 1514

Met Val Thr Leu Trp Ile Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys
-10 -5 1
Ala Tyr Asn Leu Arg Asn Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa
5 10 15
Val Leu Gly Leu Glu Gln Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa
20 25 30
Phe Leu Gly Leu Lys His Arg Trp
35 40

<210> 1515

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14..-1

<400> 1515

Met Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa
-10 -5 1
Gly Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu
5 10 15
Ala Xaa Ser Glu Ala
20

<210> 1516

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -41..-1

<400> 1516

Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu Ser Phe Asp Phe Val
-40 -35 -30
Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser Val Phe Asn Ile Gly
-25 -20 -15 -10
Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val Ser Pro Gln Ile Pro
-5 1 5
Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg Leu Leu
10 15 20

<210> 1517

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1517

Met Glu Pro Leu Ala Ala Tyr Pro Leu Lys Cys Ser Gly Pro Arg Ala
1 5 10 15

Lys Val Phe Ala Val Leu Leu Ser Ile Val Leu Cys Thr Val Thr Leu
 20 25 30
 Phe Leu Leu Gln Leu Lys Xaa Leu Lys Pro Lys Ile Asn Ser Phe Tyr
 35 40 45
 Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val Ser Leu Glu Lys
 50 55 60
 Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val Ala Ser Asp Cys Gln
 65 70 75 80
 Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys Glu Leu His Lys Glu Phe
 85 90 95
 Gly Pro Ser His Phe Ser Val Leu Ala Phe Pro Cys Asn Gln Phe Gly
 100 105 110
 Glu Ser Glu Pro Arg Pro Ser Lys Glu Val Glu Ser Phe Ala Arg Lys
 115 120 125
 Asn Tyr Gly Val Thr Phe Pro Ile Phe His Lys Ile Lys Ile Leu Gly
 130 135 140
 Ser Glu Gly Glu Leu
 145

<210> 1518

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1518

Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser Arg Cys
 1 5 10 15
 Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln Ser Tyr
 20 25 30
 Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln Ala Tyr
 35 40 45
 Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp Val Arg
 50 55 60
 Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu Phe His
 65 70 75 80
 Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met Ile Gly
 85 90 95
 Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly Glu Xaa
 100 105 110
 Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu Glu Ser
 115 120 125
 Cys Leu Leu His
 130

<210> 1519

<211> 46

<212> PRT

<213> Homo sapiens

<400> 1519

Met Pro Val Thr Arg Ala Ser Gln Pro Arg Lys Pro Ser Ser Ala Gln
 1 5 10 15
 Gln Gln Lys Ala Ala Leu Leu Xaa Asn Asn Thr Ala Leu Gln Ser Val
 20 25 30
 Ser Leu Arg Ser Lys Thr Thr Ile Arg Glu Arg Pro Ser Ser
 35 40 45

<210> 1520

<211> 41

<212> PRT

<213> Homo sapiens

<400> 1520

```
Met Asn Gly Phe Gly Arg Leu Glu His Phe Ser Gly Ala Val Tyr Glu
1          5          10          15
Gly Gln Phe Lys Asp Asn Met Phe His Gly Leu Gly Thr Tyr Thr Phe
          20          25          30
Pro Asn Gly Ala Lys Tyr Thr Gly Ile
          35          40
```

<210> 1521

<211> 131

<212> PRT

<213> Homo sapiens

<400> 1521

```
Met Ala Lys Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg
1          5          10          15
Glu Ile Gln Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly
          20          25          30
Leu Asp Ser Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp
          35          40          45
Ser Arg Phe Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu
          50          55          60
Asp Asp Asp Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys
          65          70          75          80
Lys Pro Gly Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln
          85          90          95
Ser Thr Glu Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile
          100          105          110
Ala Asp Arg Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile
          115          120          125
Ser Gln Ser
          130
```

<210> 1522

<211> 82

<212> PRT

<213> Homo sapiens

<400> 1522

```
Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn Val Lys
1          5          10          15
Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser Met Cys
          20          25          30
Tyr Lys Gln Ala Val Ser Val Asp Glu Met Arg Gly Thr Ile Thr Val
          35          40          45
His Lys Thr Asp Ser Ser Asn Glu Pro Pro Lys Thr Phe Thr Phe Asp
          50          55          60
Thr Val Phe Gly Pro Glu Ser Lys Gln Leu Asp Val Tyr Asn Leu Thr
          65          70          75          80
Ala Arg
```

<210> 1523

<211> 40

<212> PRT

<213> Homo sapiens

<400> 1523

```
Met Pro Asn Arg Gly Gly Asn Gly Leu Ala Pro Gly Glu Asp Arg Phe
1          5          10          15
Lys Pro Val Val Pro Trp Pro His Val Glu Gly Val Glu Val Asp Leu
          20          25          30
Glu Ser Ile Arg Arg Ile Asn Lys
          35          40
```

<210> 1524

<211> 35

<212> PRT

<213> Homo sapiens

<400> 1524

```
Met Ser Leu Trp Leu Cys Phe Gln Cys Pro Leu Gly Val Ser Lys Ser
1          5          10          15
Asn Lys Lys Arg Ile Asn Leu Cys Asn Gly Phe Trp Asn Glu Lys Ile
          20          25          30
Lys Asn Arg
          35
```

<210> 1525

<211> 47

<212> PRT

<213> Homo sapiens

<400> 1525

```
Met Gly Thr His Val Phe Ala Ile Asn Lys Arg Thr Tyr Val Ile Ser
1          5          10          15
Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa Cys Ser Ser Leu Leu
          20          25          30
Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys Pro Leu Gln Thr
          35          40          45
```

<210> 1526

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1526

```
Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His Val
1          5          10          15
Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu Ile
          20          25          30
Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile Phe
          35          40          45
Phe Ser Phe Leu Ser Phe Phe Phe
          50          55
```

<210> 1527

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1527

Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser Cys
1 5 10 15
Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala Ser
20 25 30
Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val Asp
35 40 45
Cys Leu Met Glu Xaa His Gly
50 55

<210> 1528

<211> 121

<212> PRT

<213> Homo sapiens

<400> 1528

Met Glu Gly Gly Gly Ile Pro Leu Glu Thr Leu Lys Glu Glu Ser
1 5 10 15
Gln Ser Arg His Val Leu Pro Ala Ser Phe Glu Val Asn Ser Leu Gln
20 25 30
Lys Ser Asn Trp Gly Phe Leu Leu Thr Gly Leu Val Gly Gly Thr Leu
35 40 45
Val Ala Val Tyr Ala Val Ala Thr Pro Phe Val Thr Pro Ala Leu Arg
50 55 60
Lys Val Cys Leu Pro Phe Val Pro Ala Thr Met Lys Gln Ile Glu Asn
65 70 75 80
Val Val Lys Met Leu Arg Cys Arg Arg Gly Ser Leu Val Asp Ile Gly
85 90 95
Ser Gly Asp Gly Arg Ile Val Ile Ala Ala Ala Lys Lys Gly Phe Xaa
100 105 110
Ala Val Gly Tyr Glu Leu Asn Pro Trp
115 120

<210> 1529

<211> 154

<212> PRT

<213> Homo sapiens

<400> 1529

Met Ala Thr Pro Leu Ala Val Asn Ser Ala Ala Ser Leu Trp Gly Pro
1 5 10 15
Tyr Lys Asp Ile Trp His Lys Val Gly Asn Ala Leu Trp Arg Arg Gln
20 25 30
Pro Glu Ala Val Xaa Leu Leu Asp Lys Ile Leu Lys Lys His Lys Pro
35 40 45
Asp Phe Ile Ser Leu Phe Lys Asn Pro Pro Lys Asn Val Gln Gln His
50 55 60
Glu Lys Val Gln Lys Ala Ser Thr Glu Gly Val Ala Ile Gln Gly Gln
65 70 75 80
Gln Gly Thr Arg Leu Leu Pro Glu Gln Leu Ile Lys Glu Ala Phe Ile
85 90 95
Leu Ser Asp Leu Phe Asp Ile Gly Glu Leu Ala Ala Val Glu Leu Leu
100 105 110
Leu Ala Gly Glu His Gln Gln Pro His Phe Pro Gly Leu Thr Arg Gly
115 120 125
Leu Val Ala Val Leu Leu Tyr Trp Asp Gly Lys Arg Cys Ile Ala Asn

130 135 140
 Ser Leu Lys Ala Leu Ile Gln Ser Arg Arg
 145 150

<210> 1530
 <211> 125
 <212> PRT
 <213> Homo sapiens
 <400> 1530

Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu Val Pro Arg
 1 5 10 15
 Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu Glu Glu Arg
 20 25 30
 Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe Arg Ser Val
 35 40 45
 Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu Ile Ser Lys
 50 55 60
 Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro Lys Leu Ile
 65 70 75 80
 Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser Tyr Val Lys
 85 90 95
 Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro Leu Gly Glu
 100 105 110
 Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro
 115 120 125

<210> 1531
 <211> 35
 <212> PRT
 <213> Homo sapiens
 <400> 1531

Met His Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn
 1 5 10 15
 Leu Leu Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys
 20 25 30
 Xaa Thr Leu
 35

<210> 1532
 <211> 111
 <212> PRT
 <213> Homo sapiens
 <400> 1532

Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser
 1 5 10 15
 Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His
 20 25 30
 Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp
 35 40 45
 Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp
 50 55 60
 Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu
 65 70 75 80
 Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Ser Ala

85 90 95
Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile Pro Pro Gly Asp
100 105 110

<210> 1533

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1533

Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp
1 5 10 15
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp Asp Thr
20 25 30
Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys Ile Arg
35 40 45
Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp Asp Thr
50 55 60
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr Arg Gly
65 70 75 80
Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln Glu Ser Tyr
85 90 95
Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile Asp
100 105

<210> 1534

<211> 31

<212> PRT

<213> Homo sapiens

<400> 1534

Met Asn Ser Lys Ala Xaa Lys Ser Ser Thr Ala Asn Gln Gly Asp Gly
1 5 10 15
Asp Glu Glu Xaa Val Gly Arg Xaa Glu Xaa Ser Val Gly Glu Phe
20 25 30

<210> 1535

<211> 48

<212> PRT

<213> Homo sapiens

<400> 1535

Met Leu Tyr Ser Thr Leu Lys His Thr Leu Gln Tyr Val Ile Ile Asn
1 5 10 15
Cys Gly His His Ala Val Gln Lys Ile Ser Lys Thr Tyr Ser Ser Cys
20 25 30
Leu Thr Glu Xaa Leu Tyr Pro Leu Pro Asn Ile Ser Pro Ile Pro Pro
35 40 45

<210> 1536

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1536

Met Asn Asp Glu Val Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser
1 5 10 15
Glu Val Thr Gln Ile Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val

20 25 30
 Pro Ser Ser Gly Leu Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln
 35 40 45
 Leu Gly Thr Gly His Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys
 50 55 60
 Gly Tyr Trp Ala Ala His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg
 65 70 75 80
 Phe Lys Tyr His Ile Val Lys Gln Ile Phe Ser Gly Gly Asp
 85 90

<210> 1537

<211> 22

<212> PRT

<213> Homo sapiens

<400> 1537

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Val Pro Trp Gly
 1 5 10 15
 Pro Asn His Cys Asp Lys
 20

<210> 1538

<211> 94

<212> PRT

<213> Homo sapiens

<400> 1538

Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met Ala Glu
 1 5 10 15
 Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln Lys Lys
 20 25 30
 Val Lys Glu Val Glu Asp Asp Asp Asp Glu Pro Ile Phe Val Gly
 35 40 45
 Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn Arg Val
 50 55 60
 Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu Ser Arg
 65 70 75 80
 Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr
 85 90

<210> 1539

<211> 67

<212> PRT

<213> Homo sapiens

<400> 1539

Met Val Thr Gln Ala Gln Gln Glu Ile Thr Val Gln Gln Leu Met Ala
 1 5 10 15
 His Leu Asp Ala Ile Arg Lys Asp Met Val Ile Leu Glu Lys Ser Glu
 20 25 30
 Phe Ala Asn Leu Arg Ala Glu Asn Glu Lys Met Lys Ile Glu Leu Asp
 35 40 45
 Gln Val Lys Gln Gln Leu Met His Glu Thr Ser Xaa Ile Arg Ala Asp
 50 55 60
 Asn Lys Leu
 65

<210> 1540
 <211> 38
 <212> PRT
 <213> Homo sapiens
 <400> 1540
 Met Lys Phe Gly Asn Val Arg Met Xaa Ser Ile Gln Ile Phe Ile Val
 1 5 10 15
 Ser Ile Trp Ser Phe Phe Leu Phe Tyr Gly Lys Tyr Thr Tyr Ile Arg
 20 25 30
 Leu Ile Leu Ser Gln Gly
 35

<210> 1541
 <211> 35
 <212> PRT
 <213> Homo sapiens
 <400> 1541
 Met Thr Phe Asp Leu Ser Val Phe Ser Thr Leu Ser Asp His Phe Tyr
 1 5 10 15
 Ser Ser Ser Leu Ser Asn Thr Ala Arg Asn Leu Tyr Ile Cys Leu Phe
 20 25 30
 His Ile Thr
 35

<210> 1542
 <211> 28
 <212> PRT
 <213> Homo sapiens
 <400> 1542
 Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu
 1 5 10 15
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser
 20 25

<210> 1543
 <211> 128
 <212> PRT
 <213> Homo sapiens
 <400> 1543
 Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
 1 5 10 15
 Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
 20 25 30
 Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
 35 40 45
 Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
 50 55 60
 Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
 65 70 75 80
 Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
 85 90 95
 Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
 100 105 110
 Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val

115

120

125

<210> 1544

<211> 33

<212> PRT

<213> Homo sapiens

<400> 1544

Met Ala Asn Arg Tyr Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu
 1 5 10 15
 Leu Ser Leu Ser Pro Asp Val Thr Leu Thr His Phe Ala His Cys Asn
 20 25 30
 Leu

<210> 1545

<211> 68

<212> PRT

<213> Homo sapiens

<400> 1545

Met Met Glu Glu Ser Gly Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro
 1 5 10 15
 Pro Asn Pro Ala Gly Leu Ala Ala Thr Ala Met Ser Ser Thr Pro Val
 20 25 30
 Pro Leu Ala Ala Thr Ser Ser Phe Ser Ser Pro Asn Val Ser Ser Met
 35 40 45
 Glu Ser Phe Pro Pro Leu Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro
 50 55 60
 Pro Val Arg Pro
 65

<210> 1546

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1546

Met Leu Cys Leu Thr Glu Gly Ala Lys Asp Glu Cys Asn Val Val Glu
 1 5 10 15
 Val Val Ala Arg Asn His Asp His Gln Glu Ile Ala Val Pro Val Ala
 20 25 30
 Xaa Leu Lys Leu Ser Cys Gln Pro Met Leu Ser Leu Asp Asp Phe Gln
 35 40 45
 Leu Gln
 50

<210> 1547

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1547

Met Pro Thr Val Ser Val Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly
 1 5 10 15
 Arg Thr Tyr Thr Asp Glu Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly
 20 25 30
 Leu Glu Leu Asp Glu Ile Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu
 35 40 45

Gln Gly Asn Val Lys Ala Ala Gly Ala Ser Asp Val Val Leu Tyr Lys
50 55 60
Ile Asp Val Pro Ala Asn Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu
65 70 75 80
Val Arg Gly Leu Gln Val Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr
85 90 95
Lys Arg Val Met Pro Asp Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu
100 105 110
Glu Thr Ala Lys Ile Arg Pro Phe Ala Val Ala Ala Val Leu Arg Asn
115 120 125
Ile Lys Phe Thr Lys Asp Arg Tyr Asp Ser Phe
130 135

<210> 1548

<211> 71

<212> PRT

<213> Homo sapiens

<400> 1548

Met Phe Ser Glu Glu Leu Trp Leu Glu Asn Glu Lys Lys Cys Ala Val
1 5 10 15
Val Arg Lys Ser Lys Gln Gly Arg Lys Arg Gln Glu Leu Leu Ala Val
20 25 30
Ala Phe Gly Val Lys Val His Thr Phe Arg Gly Pro His Trp Cys Glu
35 40 45
Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile Ala Gln Gly Val Arg Cys
50 55 60
Ser Asp Cys Gly Leu Asn Val
65 70

<210> 1549

<211> 29

<212> PRT

<213> Homo sapiens

<400> 1549

Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser Phe
1 5 10 15
Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu
20 25

<210> 1550

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1550

Met Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser
1 5 10 15
Leu Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu
20 25 30
Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr
35 40 45
Gln Thr
50

<210> 1551

<211> 68
 <212> PRT
 <213> Homo sapiens
 <400> 1551
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
 1 5 10 15
 Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
 20 25 30
 Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
 35 40 45
 Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
 50 55 60
 Ala Lys Asp Gly
 65

<210> 1552
 <211> 52
 <212> PRT
 <213> Homo sapiens
 <400> 1552
 Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr Ile
 1 5 10 15
 Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val Gly
 20 25 30
 Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr Arg
 35 40 45
 Ile Leu Ala Gly
 50

<210> 1553
 <211> 37
 <212> PRT
 <213> Homo sapiens
 <400> 1553
 Met Arg Leu Gly Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu
 1 5 10 15
 Ala Leu Ser Arg Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys
 20 25 30
 Pro Thr Val Pro Gly
 35

<210> 1554
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13..-1

<400> 1554
 Met Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp Lys Gly
 -10 -5 1
 Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala Ser Ala

[illegible]

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<220>
<221> SIGNAL
<222> -18..-1
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<210> 1556
<211> 95
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -31..-1
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<210> 1557
<211> 101

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1557
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
-30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
-15 -10 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
20 25 30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
35 40 45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Lys
50 55 60
Lys Ser Arg Lys Pro
65

<210> 1558
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1558
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val Gly
-50 -45 -40
Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
-35 -30 -25 -20
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
-15 -10 -5
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
1 5 10
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
15 20 25
Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
30 35 40 45
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
50 55 60
Arg Thr Phe

<210> 1559
<211> 126
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 1559

Met	Asp	Lys	Ser	Leu	Leu	Leu	Glu	Leu	Pro	Ile	Leu	Leu	Cys	Cys	Phe
			-20						-15					-10	
Arg	Ala	Leu	Ser	Gly	Ser	Leu	Ser	Met	Arg	Asn	Asp	Ala	Val	Asn	Glu
			-5					1				5			
Ile	Val	Ala	Val	Lys	Asn	Asn	Phe	Pro	Val	Ile	Glu	Ile	Val	Arg	Cys
	10					15					20				
Arg	Met	Cys	His	Leu	Gln	Phe	Pro	Gly	Glu	Lys	Cys	Ser	Arg	Gly	Arg
25					30					35				40	
Gly	Ile	Cys	Thr	Ala	Thr	Thr	Glu	Glu	Ala	Cys	Met	Val	Gly	Arg	Met
			45						50					55	
Phe	Lys	Arg	Asp	Gly	Asn	Pro	Trp	Leu	Thr	Phe	Met	Gly	Cys	Leu	Lys
			60					65				70			
Asn	Cys	Ala	Asp	Val	Lys	Gly	Ile	Arg	Trp	Ser	Val	Tyr	Leu	Val	Asn
		75					80					85			
Phe	Arg	Cys	Xaa	Arg	Ser	His	Asp	Leu	Cys	Asn	Glu	Asp	Leu		
	90					95					100				

<210> 1560
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 1560

Met	Asp	Leu	Leu	Trp	Ile	Leu	Pro	Ser	Leu	Trp	Leu	Leu	Leu	Leu	Gly
	-15				-10					-5					
Gly	Pro	Ala	Cys	Leu	Lys	Thr	Gln	Glu	His	Pro	Ser	Cys	Pro	Gly	Pro
1			5					10						15	
Arg	Glu	Leu	Glu	Ala	Ser	Lys	Val	Val	Leu	Leu	Pro	Ser	Cys	Pro	Gly
		20					25					30			
Ala	Pro	Gly	Ser	Pro	Gly	Glu	Lys	Gly	Ala	Pro	Gly	Pro	Gln	Gly	Pro
		35				40					45				
Pro	Gly	Pro	Pro	Gly	Lys	Met	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Asp	Pro
	50				55						60				
Val	Asn	Leu	Leu	Arg	Cys	Gln	Glu	Gly	Pro	Arg	Asn	Cys	Arg	Glu	Leu
65					70				75					80	
Leu	Ser	Arg	Ala	Pro	Pro										
				85											

<210> 1561
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -19..-1

<400> 1561

```
Met Glu Ser Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln
      -15                      -10                      -5
Ala Ser Ala Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln
      1                      5                      10
Pro Met Ser Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser
      15                      20                      25
Phe Asn Ser Ser Xaa Asn Val Val Asn Val Leu Lys
      30                      35                      40
```

<210> 1562

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 1562

```
Met Asp Phe Trp Leu Trp Pro Leu Tyr Phe Leu Pro Val Ser Gly Ala
      -15                      -10                      -5
Leu Arg Ile Leu Pro Glu Val Lys Val Glu Gly Glu Leu Gly Gly Ser
      1                      5                      10                      15
Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu
      20                      25                      30
Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
      35                      40                      45
Thr Asn Phe Ile Xaa Ala Glu Tyr Lys Gly Arg Val Thr Leu Arg Ala
      50                      55                      60
Ile Pro Thr Gln Glu Ser Val Pro Ser Gly Gly Asn Thr Ala Asp Arg
      65                      70                      75                      80
Lys
```

<210> 1563

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34..-1

<400> 1563

```
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala
      -30                      -25                      -20
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
      -15                      -10                      -5
Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
      1                      5                      10
Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa Leu Pro
      15                      20                      25                      30
```

Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Ser
 35 40 45
 Xaa Xaa

<210> 1564
 <211> 48
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 1564
 Met Ala Gln Leu Trp Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val
 -15 -10 -5
 Ser Val Ala Ala Asn Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser
 1 5 10 15
 Val Ile Leu Pro Glu Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp
 20 25 30

<210> 1565
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 1565
 Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Ala Val Ala
 -30 -25 -20
 Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
 -15 -10 -5
 Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
 1 5 10
 Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro
 15 20 25 30
 Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Cys
 35 40 45
 Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
 50 55 60
 Val Met Met Lys Asn Arg Arg Ser Ser
 65 70

<210> 1566
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 1566

```
Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu Ala Phe Ser Leu
      -15                      -10                      -5
Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp Asp Phe Asn Leu
      1                      5                      10
Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln Pro Trp Asp His
      15                      20                      25
Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala
      30                      35                      40                      45
Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln
      50                      55                      60
Asp Asp Gly Arg Arg Asn Arg Val
      65
```

<210> 1567

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -53..-1

<400> 1567

```
Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp
      -50                      -45                      -40
Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His Ile Arg Met
      -35                      -30                      -25
Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu
      -20                      -15                      -10
Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr
      -5                      1                      5                      10
Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser
      15                      20                      25
Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys Tyr Pro Leu
      30                      35                      40
Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val
      45                      50                      55
Ala Val Val Val Thr Val Leu
      60                      65
```

<210> 1568

<211> 104

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -55..-1

<400> 1568

```
Met Ser Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His
      -55                      -50                      -45                      -40
```

Gln Asn Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln
 -35 -30 -25
 Thr Lys Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe
 -20 -15 -10
 Cys Cys Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu
 -5 1 5
 Pro Pro Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val
 10 15 20 25
 Gly Leu Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu
 30 35 40
 Lys Lys Met Leu Leu Ser Val Ser
 45

<210> 1569
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -62..-1

<400> 1569
 Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr
 -60 -55 -50
 Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn
 -45 -40 -35
 Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val
 -30 -25 -20 -15
 Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val
 -10 -5 1
 Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr
 5 10 15
 Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu
 20 25 30
 Leu Gln Ser Ala His Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg
 35 40 45 50
 Leu Gln Ser Cys Arg Pro Asn Ser Pro Gly Ser Ala Ser Xaa
 55 60

<210> 1570
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -56..-1

<400> 1570
 Met Ala Pro Thr Lys Pro Ser Phe Gln Gln Asp Pro Ser Arg Arg Glu
 -55 -50 -45
 Arg Leu Gln Ala Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser
 -40 -35 -30 -25

Arg Arg Gly Lys Glu Asn Phe Glu Phe Tyr Glu Leu Ala Lys Leu Leu
-20 -15 -10
Pro Leu Pro Ala Ala Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile
-5 1 5
Arg Leu Thr Ile Ser Tyr Leu Lys Met Arg Asp Phe Ala Asn Gln Gly
10 15 20
Asp Pro Pro Trp Asn Leu Arg Met Glu Gly Pro Pro Pro Asn Thr Ser
25 30 35 40
Val Lys Val Ile Gly Ala Gln Arg Arg Arg Ser Pro Ser Ala Leu Ala
45 50 55
Ile Glu Val Phe Glu Ala His Leu Gly Ser His Ile Leu Gln Ser Trp
60 65 70
Met Ala Leu Tyr Leu His
75

<210> 1571
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1571
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20 -15 -10 -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
1 5

<210> 1572
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1572
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20 -15 -10 -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
1 5

<210> 1573
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1573

```
Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr Thr Leu
-45          -40          -35          -30
Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro Trp Asn
          -25          -20          -15
Ile Cys Cys Ala Ala Ala Ala Ala Ala Ala Gly Ser Arg Ile
          -10          -5          1
```

<210> 1574

<211> 137

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -52...-1

<400> 1574

```
Met Lys Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu
          -50          -45          -40
Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly
          -35          -30          -25
Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu
-20          -15          -10          -5
Val Ile Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg
          1          5          10
Gly Pro Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu
          15          20          25
Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val
          30          35          40
Gly Thr Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn
45          50          55          60
Trp Ala Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu
          65          70          75
Thr Cys Ser Thr Ser Val Thr Thr Cys
          80          85
```

<210> 1575

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -71...-1

<400> 1575

```
Met Ala Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser
          -70          -65          -60
Tyr Cys Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His
-55          -50          -45          -40
Gln Thr Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val
          -35          -30          -25
Ile Gln Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser
```

-20 -15 -10
 Leu Leu Thr Arg Gly Ser Gly Asn Gln Glu Gln Arg Gln Leu Lys
 -5 1 5
 Lys Leu Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu
 10 15 20 25
 Leu Gly Phe Leu Leu
 30

<210> 1576
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -69...-1

<400> 1576
 Met Ala Thr His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly
 -65 -60 -55
 Ile Leu Ser Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg
 -50 -45 -40
 Ser Arg Val Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe
 -35 -30 -25
 Pro Asp Cys His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu
 -20 -15 -10
 Gly Asp Thr Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
 -5 1 5 10

<210> 1577
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 1577
 Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser Trp Val Ser Ala Thr
 -35 -30 -25 -20
 Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys His Ser Leu Arg Lys
 -15 -10 -5
 Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu Val Lys Gln Ser Leu
 1 5 10
 Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser
 15 20 25
 His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro Asp Asp Val Xaa Pro
 30 35 40 45
 Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr
 50 55 60
 Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp Phe
 65 70

<210> 1578
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -51..-1

<400> 1578
 Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln
 -50 -45 -40
 Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr
 -35 -30 -25 -20
 Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser
 -15 -10 -5
 Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe
 1 5 10
 Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala
 15 20 25
 Xaa
 30

<210> 1579
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -93..-1

<400> 1579
 Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His Arg
 -90 -85 -80
 Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Gly Arg Gly Gln Ser
 -75 -70 -65
 His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala Ser
 -60 -55 -50
 Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile Ile
 -45 -40 -35 -30
 Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu Tyr
 -25 -20 -15
 Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln Lys
 -10 -5 1
 Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln
 5 10 15

<210> 1580
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -16..-1

<400> 1580

Met Ala Ala Ala Gly Leu Ala Leu Leu Xaa Arg Arg Val Ser Ser Ala
-15 -10 -5
Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val Pro Ala Cys Thr
1 5 10 15
Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro Asn Val Thr Ser
20 25 30
Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser Arg Lys Gly Leu
35 40 45
Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln Glu Lys Val Lys
50 55 60
Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn Lys Ser Asn Glu
65 70 75 80
Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu Arg Asn Met Leu
85 90 95
Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu Pro Met Pro Ser
100 105 110
Pro Glu Arg Leu Asp Arg
115

<210> 1581

<211> 64

<212> PRT

<213> Homo sapiens

<400> 1581

Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys Val Phe
1 5 10 15
Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys Lys Thr
20 25 30
Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu Met Ser
35 40 45
Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met Val Phe
50 55 60

<210> 1582

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1582

Met Ala Val Ala Arg Ala Gly Val Leu Gly Val Gln Trp Leu Gln Arg
1 5 10 15
Ala Ser Arg Asn Val Met Pro Leu Gly Ala Arg Thr Ala Ser His Met
20 25 30
Thr Lys Asp Met Phe Pro Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg
35 40 45
Ala Ala Ala Ala Lys Lys Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro
50 55 60
Tyr Pro Asp Asp Gly Met Gly Tyr Gly Asp Leu Phe Leu Xaa Val
65 70 75

<210> 1583

<211> 66
 <212> PRT
 <213> Homo sapiens
 <400> 1583
 Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg Asp Gly Leu Arg Glu
 1 5 10 15
 Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn Phe Asp Val Arg Pro
 20 25 30
 Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser Tyr Trp Leu Asp Leu
 35 40 45
 Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe Leu Phe Val Tyr Phe
 50 55 60
 Leu Pro
 65

<210> 1584
 <211> 45
 <212> PRT
 <213> Homo sapiens
 <400> 1584
 Met Tyr Val Tyr Val Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser
 1 5 10 15
 Lys Leu Glu Asn Ser Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa
 20 25 30
 Lys Lys Ile Phe Thr Phe Val Thr Phe Leu Phe Pro Pro
 35 40 45

<210> 1585
 <211> 25
 <212> PRT
 <213> Homo sapiens
 <400> 1585
 Met Gly Pro Gly Gly Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro
 1 5 10 15
 Trp Thr Ala Arg Ala Ser Arg Ser Pro
 20 25

<210> 1586
 <211> 98
 <212> PRT
 <213> Homo sapiens
 <400> 1586
 Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser
 1 5 10 15
 Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His
 20 25 30
 Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp
 35 40 45
 Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp
 50 55 60
 Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu
 65 70 75 80
 Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Val Xaa
 85 90 95

Asn Ile

<210> 1587

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1587

```
Met Cys Leu Leu Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg
1          5          10          15
Arg Thr Leu Lys Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu
          20          25          30
Ala Leu Leu Leu Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys
          35          40          45
Thr Glu
          50
```

<210> 1588

<211> 32

<212> PRT

<213> Homo sapiens

<400> 1588

```
Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
1          5          10          15
Xaa Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
          20          25          30
```

<210> 1589

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1589

```
Met Ala Ser Ser Gly Ala Gly Asp Pro Leu Asp Ser Lys Arg Gly Glu
1          5          10          15
Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
          20          25          30
Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Pro Ser Gly Arg Arg
          35          40          45
Ser Tyr His Gly Gly Glu Pro Gly Thr Ser
          50          55
```

<210> 1590

<211> 98

<212> PRT

<213> Homo sapiens

<400> 1590

```
Met Ser Ser Asp Asp Lys Ser Lys Ser Asn Asp Pro Lys Thr Glu Pro
1          5          10          15
Lys Asn Cys Asp Pro Lys Cys Glu Gln Lys Cys Glu Ser Lys Cys Gln
          20          25          30
Pro Ser Cys Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys Pro
          35          40          45
Trp Glu Lys Cys Pro Ala Pro Pro Lys Cys Leu Pro Cys Pro Ser Gln
          50          55          60
Ser Pro Ser Ser Cys Pro Pro Gln Pro Cys Thr Lys Pro Cys Pro Pro
```

65 70 75 80
 Lys Cys Pro Ser Ser Cys Pro His Ala Cys Pro Xaa Pro Cys Pro Pro
 85 90 95

Pro Glu

<210> 1591

<211> 43

<212> PRT

<213> Homo sapiens

<400> 1591

Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
 1 5 10 15
 Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
 20 25 30
 Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
 35 40

<210> 1592

<211> 157

<212> PRT

<213> Homo sapiens

<400> 1592

Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
 1 5 10 15
 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
 20 25 30
 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
 35 40 45
 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
 50 55 60
 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
 65 70 75 80
 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
 85 90 95
 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
 100 105 110
 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
 115 120 125
 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
 130 135 140
 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
 145 150 155

<210> 1593

<211> 119

<212> PRT

<213> Homo sapiens

<400> 1593

Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
 1 5 10 15
 Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
 20 25 30
 Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu
 35 40 45

Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala
50 55 60
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala
65 70 75 80
Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu
85 90 95
Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala
100 105 110
Ala Val Ile Ala Arg Phe Tyr
115

<210> 1594

<211> 81

<212> PRT

<213> Homo sapiens

<400> 1594

Met Tyr Ile Gln Cys Cys Glu Trp Leu Gln Ser Trp Arg Ser Lys Asp
1 5 10 15
Glu Phe Cys Leu Glu Glu Ser Gly Lys Ala Ser Trp Arg Arg Glu Gln
20 25 30
Trp His Gly Pro Xaa Xaa Val Arg Ser Phe Gln Phe Ile Pro Phe Lys
35 40 45
His Cys Ser His Val Ala Phe Lys His Ser Ile Val Leu Ala Val Thr
50 55 60
Gln Ala His Ser Ala Lys Gly Ser Thr Ser Phe Ser Ala Met Arg Thr
65 70 75 80
Tyr

<210> 1595

<211> 65

<212> PRT

<213> Homo sapiens

<400> 1595

Met Val Gly Val Ser Val Cys His His Ile Arg Val Gly Ile Lys Arg
1 5 10 15
Arg Lys Ala Ala Leu Leu Glu Leu Cys Gly Leu Leu Gln Val Arg Val
20 25 30
Ala Gly Asn Arg Thr Thr Leu Leu Glu Glu Lys Arg Asn Ser Phe
35 40 45
Ser Ala Xaa Thr Arg Lys Ala Val Phe Phe Ser Gly Asp Leu His Phe
50 55 60
Ser
65

<210> 1596

<211> 111

<212> PRT

<213> Homo sapiens

<400> 1596

Met Pro Ser Arg Thr Ala Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg
1 5 10 15
Arg Arg Arg Met Leu Ala Asp Arg Ser Val Arg Phe Pro Asn Asp Val
20 25 30
Leu Phe Leu Asp His Ile Arg Gln Gly Asp Leu Glu Gln Val Gly Arg

35 40 45
 Phe Ile Arg Thr Arg Lys Val Ser Leu Ala Thr Ile His Pro Ser Gly
 50 55 60
 Leu Ala Ala Leu His Glu Ala Val Leu Ser Gly Asn Leu Glu Cys Val
 65 70 75 80
 Lys Leu Leu Val Lys Tyr Gly Ala Asp Ile His Gln Arg Asp Glu Ala
 85 90 95
 Gly Trp Thr Pro Leu His Ile Ala Cys Ser Asp Gly Tyr Leu Thr
 100 105 110

<210> 1597

<211> 33

<212> PRT

<213> Homo sapiens

<400> 1597

Met Ala Trp Gly Gly Trp Gly Ala His Ser Ala Cys Ser Glu Glu Arg
 1 5 10 15
 Ala Thr Arg Pro Val Glu Gly Ala Tyr Ser Gly Arg Trp Gly Gln Ala
 20 25 30

Gln

<210> 1598

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1598

Met Asp Pro Asn Pro Arg Ala Ala Leu Glu Arg Gln Gln Leu Arg Leu
 1 5 10 15
 Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu Gln Pro Glu Thr Glu
 20 25 30
 Phe Val Phe Pro Leu Ser His Leu His Leu Glu Ser Gln Arg Pro Pro
 35 40 45
 Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val Asp Thr Leu Glu Gln
 50 55 60
 Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala Asp Val Phe Leu
 65 70 75 80
 Pro Cys Glu Asp Pro Pro Thr Pro Gln Ser Ser Gly Val Asp Asn
 85 90 95
 His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr Ile Arg Gln Asp His
 100 105 110

Ile

<210> 1599

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1599

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 1 5 10 15
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Asp Thr Lys Tyr Ile
 20 25 30
 Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe Leu Trp Asn Ile Leu
 35 40 45
 Lys Leu Pro Val Gln Thr Leu Leu Gln Gly

50

55

<210> 1600

<211> 247

<212> DNA

<213> Homo sapiens

<400> 1600

gaaaattact	ttgacctttt	gttagtgatc	ccattcagct	agtaccaagc	tgaagattga	60
tattcgttaa	tggttaatat	aaattttactg	ctctagggtta	agcctaacat	atgtaattgc	120
tactagccta	ttacttttta	gtccattggg	aatcactaaa	aaaagtagag	gcttttagctt	180
cattcctcgg	ctgcttaaat	catattgtaa	tgttttaaat	tgttatgtcg	tcctgtataa	240
ccttagg						247

<210> 1601

<211> 225

<212> DNA

<213> Homo sapiens

<400> 1601

aaaattattt	tgagacaaaa	catgggaaag	gagggagttg	gccaggagtt	tatcatgaag	60
catatacagg	agtcatcccc	tacgttgaca	ctggtaagtt	gacttcagtc	acatgaaaca	120
tgtcaccttt	ccataaatac	tccattccct	tttgtgattt	tggtctttgc	acatgttggt	180
ctatctctgc	ctggaatgtg	ttctccacct	tttgattgtc	tgcca		225

<210> 1602

<211> 258

<212> DNA

<213> Homo sapiens

<400> 1602

gtgaccacag	tctgcagagg	ccagagagag	caggaaagga	aatggaaagg	aacctcacct	60
tcattgcttg	ggaaaaggag	aaacctgtgt	taatgtgtct	tcccaacatc	ccactctctt	120
cagcaatcgc	tggaacagcc	atgggccatc	cctgctgagt	caggaaagaa	gctgagggaa	180
gagtcgggat	tgaaaagcag	cagacaaggg	aaatgtggac	acaagcacat	gaagagaaca	240
ccatgtgaac	ataaagat					258

<210> 1603

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1603

aaggttactt	gactgggagt	tctcagacct	ccagtttcag	ccctgccctc	agcctccaat	60
ccgtaagaga	yaccagccc	cagcaattgg	attgggcagc	ccgtcttgac	acaccactgt	120
getgagtgt	tgaggacgtg	tttcaacaga	tggttggggt	tagtgtgtgt	catcacattc	180
gagtggggat	taagagaagg	aaggctgcct	tgtctggagt	gtgtgggtctt	ctccaagtga	240
gagtcgcagg	caatagaact	actttgtctt	tggaggaaaa	ggaggaattc	attttcagca	300
gacacaagaa	aagcagtttt	tttttcaggt	gctgacggcc	a		341

<210> 1604

<211> 292

<212> DNA

<213> Homo sapiens

<400> 1604

cactggcgcg	ggttgagttc	cctgttgccc	ttggtctcgg	ggtcgctgtm	ggcgctgagg	60
ctgcagctat	catgggtgaac	ttacttcaga	ttgtgcggga	ccactggggt	catgttcttg	120
tccctatggg	atttgtcatt	ggatgttatt	tagacagaaa	gagtgatgaa	cggctaactg	180

ccttccggaa	caagagtatg	ttatttaaaa	gggaattgca	acccagtga	gaagttacct	240
ggaagtaaag	actggctaga	ttatcgaatg	ttcacatttt	aaagttctga	ga	292

<210> 1605

<211> 357

<212> DNA

<213> Homo sapiens

<400> 1605

ctgctctaag	ctgcagcaag	agaaactgtg	tgtgagggga	agaggcctgt	ttcgctgtcg	60
gggtctctagt	tcttgcaagc	tctttaagag	tctgcactgg	aggaactcct	gccattacca	120
gctcccttct	tgcagaagg	agggggaaac	atacatttat	tcatgccagt	ctgttgcatg	180
caggcttttt	ggcttcttac	cttgcaacaa	aataattgca	ccaactcctt	agtgccgatt	240
ccgcccacag	agagtcttg	arccacagtc	ttttttgctt	tgcattgtag	gagagggact	300
aagtgtctaga	gactatgtcg	ctttcctgag	ctaccgagag	cgctcgtgaa	ctggaat	357

<210> 1606

<211> 293

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 13

<223> n=a, g, c or t
Oligonucleotide

<400> 1606

attccctacc	cancagccct	cgcgcggtcc	ggcacagcgg	acaccaggac	tccaaaatgg	60
cgtcagttgg	tgagtgtccg	gccccagtac	cagtgaagga	caagaaactt	ctggagggtca	120
aactggggga	gctgccaaag	tggatcttga	tgcggractt	cagtcctagt	ggcattttcg	180
gagcgtttca	aaragggttac	accggtacta	caacaagtac	atcaatgtga	agaaggggag	240
catctcgggg	attaccatgg	tgctacccta	ccacacattc	gaagaacccg	tat	293

<210> 1607

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 323

<223> n=a, g, c or t
Oligonucleotide

<400> 1607

tgttgtcttt	atcagactta	cattgcctct	gtgaatatca	gccttggtct	actccaagtg	60
caggacaaac	acaaagaact	ctctgcacag	ttcattactc	cattagggtg	ttcagatgca	120
attccagccc	ttagtcaggt	tctttccagt	gtcctcaaac	acagtaagga	gagtgtctta	180
agtgactctt	tgtgtctcac	acaatctctt	gggttcccag	gtcactgggt	tagtagccag	240
ctgcatccaa	gaagccaggt	gagcctgtgc	caccaatcac	agatactcct	taccaaccat	300
ctgccaaccc	atgccagccc	tgntgcccac	ggatgtgcgg	ctgtccatgt	gccacgcccc	360
c						361

<210> 1608

<211> 305
 <212> DNA
 <213> Homo sapiens
 <400> 1608
 aagacggaag ctcggttgat gtttctgcag aagttttccc ccttggtcgg tggcggastg 60
 ctgagcgcga tagtagcagc tccggcggca gcaacattga ctacgaggaa tggcggcggc 120
 tgccgcagga cctgcagcat cccagaggtg cagatttttaa tttcagtgc tgaattaaaa 180
 ggtgtcaaga agctcgaaatg gtatgtaggc ctcccatggc atttcaattt aaaaagaagt 240
 aagcacttga aatttttttg ttttaagcaaa tttgttttta cttttataat ttatttttaa 300
 taata 305

<210> 1609
 <211> 242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 152
 <223> n=a, g, c or t
 Oligonucleotide

<400> 1609
 aatctggtct ttctgtagac ccaagtcaga aggaaccatt tgtggagtta aatagaatat 60
 tagaggcatt aaaggtcaga gttctgagac ctgctctgga gtgggcagtg tcaaaccggg 120
 aaatgcttat agctcaaaca gctccttgga anttaagcta cacagactgt attttattag 180
 cttgttaatg ggtggaacca caaatcagcg agaggcatta caatatgcta aaaattttca 240
 gc 242

<210> 1610
 <211> 196
 <212> DNA
 <213> Homo sapiens

<400> 1610
 ggaagcgatt tcatagccac ggtttttggc tttcatcgct ttttctacat gtttttagcc 60
 tcaccagaag tctttcatct cggtggtcca actcaggatc tcagcctcat tattttctta 120
 cccttctgga gtgcatatgt gcctttacag ttctgtttgc aaacgctgtc tagcatacta 180
 agaggatgtt agcaaa 196

<210> 1611
 <211> 228
 <212> DNA
 <213> Homo sapiens

<400> 1611
 atattgaata agcgacccgg cctcctaggg ggtcgtcgtg gtgcagacag tttagcagaa 60
 cagcctccgc ggctccgggg agaaggtgag gtcttgatg gatgggaagg gtgaggtgcg 120
 tcggccagag gcttatttat tgacgggact gtttcccttg gccacgcga cgtagcttct 180
 gttgtccttg actgggcgcc gcctcccgcc ccgcgcctc ggaagccc 228

<210> 1612
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 108
 <223> n=a, g, c or t
 Oligonucleotide

<400> 1612
 tattttagag atggaacaaa gagaacacat agatattcaa taatttactc aaaagtctgt 60
 gaggagccct agaaagaaat tcagggtctcc tatgtactga tcacagcnca gaaccccagg 120
 aagccagagg tgttccaccc caatccttca cctcaccccc acatcatggt ggcccctggg 180
 acctggatgg aaaacctctg gcwtcctggg gttctgggct g 221

<210> 1613
 <211> 360
 <212> DNA
 <213> Homo sapiens
 <400> 1613

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 gctactttct gaatcctaaa gcgctcttcc agctttcaca tttgattccg tggcagaagg 180
 ctcacagcct cacaaagtgg agacaggcag acagtccac ctcatattcaa ctccagagtt 240
 ggggaacgtg ctgggggtgc tcagccagag cctctcagcc aggccttggt aggcagaggg 300
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<210> 1614
 <211> 171
 <212> DNA
 <213> Homo sapiens
 <400> 1614

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 gacatttaaa atttttctgg ttgtagcctc attactgtat agaaatcaac taccagatga 120
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<210> 1615
 <211> 193
 <212> DNA
 <213> Homo sapiens
 <400> 1615

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 gcgtgagcac cacgtccggc cacaaaagag ctttgatgca cacggtgaca gccacatggt 120
 gcacccggaa gaacaagggg cctgaagtta gttagaccct ccttgctggt tctaccacag 180
 tcgcacgccc cac 193

<210> 1616
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 99
 <223> n=a, g, c or t
 Oligonucleotide

<400> 1616
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atatcaagca aagaaaatgc caattctcag ccaaagatg aagatgcctc ctctgatgcc 180
tactgctttg agctgctctc tatggtttta gcactgagtg gctctaactg tggccggcaa 240
tatctggctc aacagctaac cctgcttcag gatctcttcc gctgcttcac acagcctctc 300
ctagagtcca gagacaggta cctctttact agaagagttt gctgaagta 349

<210> 1617

<211> 155

<212> DNA

<213> Homo sapiens

<400> 1617

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attctgaacc catctgaatg accaaggcct gaggc 155

<210> 1618

<211> 185

<212> DNA

<213> Homo sapiens

<400> 1618

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tctctctttt ccagctacct ttactccctc tccttcaatt ccactttcct ctgcttactt 180
ttttt 185

<210> 1619

<211> 169

<212> DNA

<213> Homo sapiens

<400> 1619

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gttttgagaga agcgggatgg tacagtgcta cgaactacagc agtatagctc cgggtggcgtg 120
ggtgcgttgt gtgggacgct gccattgtcc tttctaaata cctggaaac 169

<210> 1620

<211> 246

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 122

<223> n=a, g, c or t
Oligonucleotide

<400> 1620

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anstgggcag ttttattcac cataagtatt ccaagcccta gtggttcctg gcacattttg 180
tattcacaat aaatatttgt taagtcaatg accagatgaa tggcgtttta actcaagata 240
gttttt 246

<210> 1621

<211> 280

<212> DNA

<213> Homo sapiens

<400> 1621

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ggccaaagac	atttttggac	aagtttaacc	acgaagccga	agacctgttc	tatcaaagtt	180
cacttgcttc	ttggaattat	aacaccaata	ttactgaaga	gaatgtccaa	aacatgaata	240
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<210> 1622

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 43

<223> n=a, g, c or t
Oligonucleotide

<400> 1622

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gagcgagctc	ctgctgcaac	tctgtccag	cacggccagc	gccagcgccc	gccgtcggtg	180
cactctacga	gccgtgcagc	gtgcccactg	gagttgttgt	gtatcaagga	tcgatcccct	240
atatgcacac	acacacctcc	acctccacca	atgcactctt	cttcctcctc	cttctccaga	300
caactgctgg	gaaaaaaata	aaacaccaac	cccaaccgtc	agcaacaagg	taasmgagcg	360
attcgacatc	atTTTTTTTc	ctgttcaatt	ttttccttgt			400